

PS Example 52; Page 79; 110pp; English.

XX The present invention relates to C3' methylene hydrogen phosphate

CC oligomers. The oligomers may be used as research reagents, for

CC treating disease caused by undesired production of proteins

CC and for diagnosing and treating AIDS and atherosclerosis.

XX

SQ Sequence 13 BP; 0 A; 0 C; 0 G; 12 T; 1 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAA 1096

DB 13 AAAAAAAAAAAAA 1

RESULT 1233

ABC07004/c

ID ABC07004 standard; DNA; 13 BP.

XX

AC ABC07004;

XX

DT 20-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 6995 for detecting SNP TSC0002084.

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

XX WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

PI WPI; 2001-657177/75.

XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status -

XX

PS Claim 1; SEQ ID 6995; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAA 1096

DB 13 AAAAAAAAAAAAA 1

RESULT 1235

ABC10866

ID ABC10866 standard; DNA; 13 BP.

XX

AC ABC10866;

XX

DT 20-FEB-2002 (first entry)

XX

XX


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PS Claim 1; SEQ ID 11933; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 11 A; 0 C; 0 G; 2 T; 0 other;
    Query Match      1.2%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 6.7e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1082 TTAAAAA 1094
    DB 13 TTAAAAA 1
    RESULT 1238
    ABC11927/c
    ID ABC11927 standard; DNA; 13 BP.
    AC ABC11927;
    XX
    DT 20-FEB-2002 (first entry)
    DE Oligonucleotide SEQ ID NO 11934 for detecting SNP TSC0002863.
    XX
    KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
    KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
    KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
    XX
    OS Homo sapiens.
    XX
    PN WO200177384-A2.
    XX
    PD 18-OCT-2001.
    XX
    DT 20-FEB-2002 (first entry)
    DE Oligonucleotide SEQ ID NO 11934 for detecting SNP TSC0002863.
    XX
    KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
    KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
    KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
    XX
    OS Homo sapiens.
    XX
    PN WO200177384-A2.
    XX
    PD 18-OCT-2001.
    XX
    PF 06-APR-2001; 2001WO-IB00713.
    XX
    PR 07-APR-2000; 2000DE-1019173.
    XX
    PA (EPIG-) EPIGENOMICS AG.
    XX
    PI Olek A, Piepenbrock C, Berlin K;
    XX
    WIPI; 2001-657177/75.
    XX
    PT Set of oligonucleotides, useful for diagnosis and cell typing, is
    PT designed to detect single nucleotide polymorphisms and cytosine
    PT methylation status -
    XX
    PS Claim 1; SEQ ID 11934; 29pp + Sequence Listing; German.
    CC This invention describes novel oligonucleotide primers or peptide nucleic
    CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
    CC and cytosine methylation status in chemically pretreated genomic DNA. The
    CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
    CC range of diseases including immune system, gastrointestinal, respiratory,
    CC central nervous system, cardiovascular and metabolic disorders. The
    CC oligomers are also used for detecting cell type differentiation.
    CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
    CC AB100010-AB182073 represent the oligomers described in the invention.
    CC NOTE: The sequence data for this patent did not form part of the printed
    CC specification, but was obtained in electronic format from WIPO at
    CC ftp.wipo.int/pub/published_pct_sequences.
    XX
    SQ Sequence 13 BP; 11 A; 0 C; 0 G; 2 T; 0 other;
    Query Match      1.2%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 6.7e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1082 TTAAAAA 1094
    DB 13 TTAAAAA 1
    RESULT 1238
    ABC20592
    ID ABC20592 standard; DNA; 13 BP.
    AC ABC20592;
    XX
    DT 20-FEB-2002 (first entry)
    DE Oligonucleotide SEQ ID NO 20609 for detecting SNP TSC0004197.
    XX
    KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
    KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
    KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
    XX
    OS Homo sapiens.
    XX
    PN WO200177384-A2.
    XX
    PD 18-OCT-2001.
    XX
    DT 06-APR-2001; 2001WO-IB00713.
    XX
    PR 07-APR-2000; 2000DE-1019173.
    XX
    PA (EPIG-) EPIGENOMICS AG.
    XX
    PI Olek A, Piepenbrock C, Berlin K;
    XX
    WIPI; 2001-657177/75.
    XX
    PT Set of oligonucleotides, useful for diagnosis and cell typing, is
    PT designed to detect single nucleotide polymorphisms and cytosine
    PT methylation status -
    XX
    PS Claim 1; SEQ ID 20609; 29pp + Sequence Listing; German.
    CC This invention describes novel oligonucleotide primers or peptide nucleic
    CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
    CC and cytosine methylation status in chemically pretreated genomic DNA. The
    CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
    CC range of diseases including immune system, gastrointestinal, respiratory,
    CC central nervous system, cardiovascular and metabolic disorders. The
    CC oligomers are also used for detecting cell type differentiation.
    CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
    CC AB100010-AB182073 represent the oligomers described in the invention.
    CC NOTE: The sequence data for this patent did not form part of the printed
    CC specification, but was obtained in electronic format from WIPO at
    CC ftp.wipo.int/pub/published_pct_sequences.
    XX
    SQ Sequence 13 BP; 10 A; 0 C; 0 G; 3 T; 0 other;
    Query Match      1.2%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 6.7e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1080 TATTA 1092
    DB 1 TATTA 13
    RESULT 1238
    ABC20592
    ID ABC20592 standard; DNA; 13 BP.
    AC ABC20592;
    XX
    DT 20-FEB-2002 (first entry)
    DE Oligonucleotide SEQ ID NO 20609 for detecting SNP TSC0004197.
    XX
    KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
    KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
    KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
    XX
    OS Homo sapiens.
    XX
    PN WO200177384-A2.
    XX
    PD 18-OCT-2001.
    XX
    DT 06-APR-2001; 2001WO-IB00713.
    XX
    PR 07-APR-2000; 2000DE-1019173.
    XX
    PA (EPIG-) EPIGENOMICS AG.
    XX
    PI Olek A, Piepenbrock C, Berlin K;
    XX
    WIPI; 2001-657177/75.
    XX
    PT Set of oligonucleotides, useful for diagnosis and cell typing, is
    PT designed to detect single nucleotide polymorphisms and cytosine
    PT methylation status -
    XX
    PS Claim 1; SEQ ID 11934; 29pp + Sequence Listing; German.
    CC This invention describes novel oligonucleotide primers or peptide nucleic
    CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
    CC and cytosine methylation status in chemically pretreated genomic DNA. The
    CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
    CC range of diseases including immune system, gastrointestinal, respiratory,
    CC central nervous system, cardiovascular and metabolic disorders. The
    CC oligomers are also used for detecting cell type differentiation.
    CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
    CC AB100010-AB182073 represent the oligomers described in the invention.
    CC NOTE: The sequence data for this patent did not form part of the printed
    CC specification, but was obtained in electronic format from WIPO at
    CC ftp.wipo.int/pub/published_pct_sequences.
    XX
    SQ Sequence 13 BP; 10 A; 0 C; 0 G; 3 T; 0 other;
    Query Match      1.2%; Score 13; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 6.7e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1080 TATTA 1092
    DB 1 TATTA 13
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RESULT 1240
ABC20593/c
ID ABC20593 standard; DNA; 13 BP.
XX
XX AC ABC20593;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 20610 for detecting SNP TSC0004197.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX PS Claim 1; SEQ ID 20610; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABH00010-ABH82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABH00010-ABH82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1080 TATTAAAAAAA 1092
Db 13 TATTAAAAAAA 1

RESULT 1241
ABC22352/c
ID ABC22352 standard; DNA; 13 BP.
XX
XX AC ABC22352;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 22369 for detecting SNP TSC0004431.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX PS Claim 1; SEQ ID 22369; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABH00010-ABH82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1076 CAACTATTAAAAA 1088
Db 13 CAACTATTAAAAA 1

RESULT 1242
ABC22353
ID ABC22353 standard; DNA; 13 BP.
XX
XX AC ABC22353;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 22370 for detecting SNP TSC0004431.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX PS Claim 1; SEQ ID 22369; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABH00010-ABH82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;

```


PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 22370; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1076 CCACTATTAAAAA 1088
 DB 1 CCACTATTAAAAA 13
 RESULT 1243
 ID ABC24966/c
 AC ABC24966;
 XX 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 24983 for detecting SNP TSC0006050.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 24983; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 1 A; 0 C; 0 G; 12 T; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAA 1095
 DB 13 TAAAAAATAAAAA 1
 RESULT 1244
 ID ABC24967
 AC ABC24967;
 XX 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 24984 for detecting SNP TSC0006050.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 24984; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 12 A; 0 C; 0 G; 1 T; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 13;

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Best Local Similarity 100.0%; Pred. No. 6.7e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1083 TAAAAAAAAAAAAA 1093
   |||||
Db 1 TAAAAAAAAAAAAA 13

RESULT 1245
ABC65478
ID ABC65478 standard; DNA; 13 BP.
XX
AC ABC65478;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 65495 for detecting SNP TSC0017239.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 65495; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
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CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 11 A; 0 C; 0 G; 2 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAAAAAAAAA 1093
   |||||
Db 1 ATTAAAAAAAAAAAA 13

RESULT 1246
ABC65479/C
ID ABC65479 standard; DNA; 13 BP.
XX
AC ABC65479;
XX

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XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 65496 for detecting SNP TSC0017239.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 65496; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH99989 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 2 A; 0 C; 0 G; 11 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAAAAAAAAA 1093
   |||||
Db 13 ATTAAAAAAAAAAAA 1

RESULT 1247
ABC98802
ID ABC98802 standard; DNA; 13 BP.
XX
AC ABC98802;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 98819 for detecting SNP TSC0024557.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX

```


CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 123 GAAGAAAGGATGT 135
 Db 1 GAAGAAAGGATGT 13
 RESULT 1250
 ABH00841/c
 ID ABH00841 standard; DNA; 13 BP.
 XX
 AC ABH00841;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 200818 for detecting SNP TSC0049407.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 200818; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 123 GAAGAAAGGATGT 135
 Db 1 GAAGAAAGGATGT 135
 RESULT 1251
 ABH13166/c
 ID ABH13166 standard; DNA; 13 BP.
 XX
 AC ABH13166;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 213143 for detecting SNP TSC0001557.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 213143; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1077 AACTATTAAAAA 1089
 Db 13 AACTATTAAAAA 1
 RESULT 1252
 ABH13167
 ID ABH13167 standard; DNA; 13 BP.
 XX
 AC ABH13167;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 213144 for detecting SNP TSC0001557.
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell-type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI99989 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIFO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 other;
SQ
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 AGGTTTGTGTTTA 945
Db 13 AGGTTTGTGTTTA 1

RESULT 1255
ABS78383/c
ID ABS78383 standard; DNA; 13 BP.

XX ABS78383;

XX 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #867.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW macular degeneration; corneal graft rejection; neovascular glaucoma;
KW retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW haemophiliac joint; angiofibroma; wound granulation;
KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

XX Synthetic.

XX WO200253141-A2.

XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US48458.

XX 14-DEC-2000; 2000US-255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

XX WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least
PT one antiangiogenic nucleic acid molecule to the subject -

XX Claim 2; Page 34; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.

CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,

CC retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardial
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
CC joints, angiofibroma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.

XX Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
Db 13 AAAAAAAAAAAAAA 1

RESULT 1256
ABS78384/c
ID ABS78384 standard; DNA; 13 BP.

XX ABS78384;

XX 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #868.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW macular degeneration; corneal graft rejection; neovascular glaucoma;
KW retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW haemophiliac joint; angiofibroma; wound granulation;
KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

XX Synthetic.

XX WO200253141-A2.

XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US48458.

XX 14-DEC-2000; 2000US-255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

XX WPI; 2002-566690/60.

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PT one antiangiogenic nucleic acid molecule to the subject -

XX Claim 2; Page 34; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,
CC retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardial
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
CC joints, angiofibroma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.

XX Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;


```
AC ABL39399;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 835.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 13
FT /*tag= a
FT /mod_base= OTHER
FT /note= "modified by FITC"
XX
FN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 308; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1
RESULT 1260
ABL39400/c
ID ABL39400 standard; DNA; 13 BP.
XX
AC ABL39400;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 836.
```

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XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 13
FT /*tag= a
FT /mod_base= OTHER
FT /note= "modified by FITC"
XX
FN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 308; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1
RESULT 1261
ABZ59804/c
ID ABZ59804 standard; RNA; 13 BP.
XX
AC ABZ59804;
XX
DT 01-APR-2003 (first entry)
XX
DE Potato gene PCR primer Roth-JT11-AA.
XX
KW Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW transferrin binding protein; receptor-like protein kinase; helicase;
KW non-long terminal repeat retroelement reverse transcriptase;
KW overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
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XX OS Synthetic.
XX PN DEL0114063-A1.
XX XX
XX PD 10-OCT-2002.
XX XX
XX PF 22-MAR-2001; 2001DE-1014063.
XX XX
XX PR 22-MAR-2001; 2001DE-1014063.
XX XX
XX PA (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX XX
XX PI Buelow L, Tscharnatke M, Haussuehl K;
XX XX
XX DR WPI; 2003-041808/04.
XX XX
XX PT New DNA sequences from potato, useful for producing plants with altered
XX PT properties, e.g. tolerance of flooding, also related proteins,
XX PT antibodies and inhibitory sequences
XX XX
XX PS Example 1; Page 8; 26pp; German.
XX XX
XX CC The invention relates to DNA sequences (I) that encode six specific plant
XX CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
XX CC activity (IIa); (ii) a protein (ABP60426) with transferrin binding
XX CC protein activity (IIb); (iii) a protein (ABP60427) with receptor-like
XX CC protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation
XX CC factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long
XX CC terminal repeat retroelement reverse transcriptase activity (IIf); or
XX CC (vi) a protein (ABP60430) with helicase activity (IIIf). (I), also related
XX CC sequences, derived ribozymes and antisense sequences, expression vectors,
XX CC encoded proteins and antibodies against the proteins, are used to produce
XX CC plants with altered properties, including tolerance of overwatering. The
XX CC antibodies are also used for isolation of the proteins and in
XX CC immunoassays. Also (i) or their primer or probe fragments are used to
XX CC screen for terminators and constitutively, aerobically or anaerobically
XX CC inducible plant promoters, specifically for use in potatoes and the
XX CC sequence that encodes (IId) is used to alter the translation profile in
XX CC plants. Since (I) are derived from potato, their promoters and
XX CC terminators provide high level transgene expression in potato, with
XX CC improved tissue specificity and inducibility, and can also be used to
XX CC control endogenous genes. The present sequence is that of a PCR primer
XX CC used in the first strand synthesis of cDNAs derived from potato.
XX XX
XX SQ Sequence 13 BP; 2 A; 0 C; 0 G; 11 T; 0 other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1082 TTAAAAAATAAAAA 1094
Db 13 TTAAAAAATAAAAA 1

RESULT 1262
AAL54076
ID AAL54076 standard; DNA; 13 BP.
XX
XX AC AAL54076;
XX XX
XX DT 06-MAR-2003 (first entry)
XX XX
XX DE Oligo-homodeoxyribonucleotide sequence, oligo dA.
XX XX
XX KW Detection; single-stranded sensor; detectable fluorescence emission;
XX KW forensic testing; paternity testing; tissue typing; hereditary disorder;
XX KW human population genetics; human evolutionary history; cystic fibrosis;
XX KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX XX
XX OS Unidentified.
XX XX

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PN W0200284271-A2.
XX
XX PD 24-OCT-2002.
XX XX
XX PF 16-APR-2002; 2002WO-US12176.
XX XX
XX PR 16-APR-2001; 2001US-0836579.
XX XX
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (CHAJ/) CHA J N.
XX
XX PI Cha JN, Morse DE, Stucky GD;
XX XX
XX DR WPI; 2003-103378/09.
XX XX
XX PT Detecting polynucleotides, for pharmacogenetic testing, comprises
XX PT contacting a target polynucleotide with a predetermined single-stranded
XX PT sensor polynucleotide and an agent that allows the sensor to fluoresce
XX PT upon excitation
XX XX
XX PS Example 1; Page 25; 41pp; English.
XX XX
XX CC The invention relates to a novel assay for detecting a polynucleotide in
XX CC a sample, which comprises: contacting a sample suspected of containing a
XX CC target polynucleotide with a predetermined single-stranded sensor
XX CC polynucleotide complementary to the target polynucleotide, in a solution
XX CC comprising an agent that is a nonaqueous solvent that allows the sensor
XX CC polynucleotide to produce a detectable fluorescence emission; exciting
XX CC the sensor polynucleotide; and determining fluorescence emission. The
XX CC assay is useful for detecting a single or double-stranded target
XX CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
XX CC wide variety of different applications including pharmacogenetic testing,
XX CC forensic testing to identify the species or individual which was the
XX CC source of a forensic specimen, in anthropological setting, paternity
XX CC testing, testing for compatibility between prospective tissue or blood
XX CC donors and patients and in screening for hereditary disorders. The method
XX CC is also useful to study alterations of gene expression in response to a
XX CC stimulus, disease, drug or medication, and other applications include
XX CC characterisation of human haplotype diversity. The method is useful for
XX CC detecting polynucleotide sequences from contaminants or pathogens
XX CC including bacteria, yeast, and viruses to detect single nucleotide
XX CC polymorphisms, which may be associated with particular alleles or subsets
XX CC of alleles. The method is useful for detection of mutations and to detect
XX CC nucleotide sequences associated with increased risk of diseases or
XX CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
XX CC This polynucleotide sequence represents an oligonucleotide sequence used
XX CC in a fluorescence technique of the invention.
XX
XX SQ Sequence 13 BP; 13 A; 0 C; 0 G; 0 U; 0 other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAATAAAAA 1096
Db 1 AAAAAAATAAAAA 13

RESULT 1263
AAT36896/c
ID AAT36896 standard; DNA; 14 BP.
XX
XX AC AAT36896;
XX XX
XX DT 23-OCT-1996 (first entry)
XX XX
XX DE Candida albicans leukotriene A4 hydrolase cDNA PCR primer.
XX XX
XX KW Leukotriene A4 hydrolase; pro-inflammatory; reduced;
XX KW 5,6-dihydroxy-7,9,11,14-eicosatetraenoic acid; immune response;
XX KW expression vector; recombinant production; antibody generation;
XX KW

```

KW diagnostic agent; passive immunisation; vaccine; treatment;
 KW prevention; infection; reagent; detection; modulation;
 KW inflammatory response; antisense; prevention; PCR; primer;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 OS
 XX US5529916-A.
 PN
 XX
 XX 25-JUN-1996.
 PD
 XX
 XX 01-NOV-1994; 94US-0332838.
 PF
 XX
 XX 01-NOV-1994; 94US-0332838.
 PR
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX
 XX Cormack BP, Falkow S;
 PI
 XX
 XX WPI; 1996-308739/31.
 DR
 XX
 XX Recombinant DNA encoding yeast leukotriene A4 hydrolase - and
 PT related vectors and transformed cells, producing yeast hydrolase
 PT useful, e.g. as vaccine against Candida infection and as diagnostic
 PT reagent
 XX
 XX
 PS Example 1; Columns 23-24; 24pp; English.
 XX
 XX The present sequence is a primer for the C. albicans leukotriene A4
 CC (LTA4) hydrolase, cDNA. The hydrolase converts LTA4 to (probably)
 CC 5,6-dihydroxy-7,9,11,14-eicosatetraenoic acid, which is less
 CC pro-inflammatory than the LTB4 produced by the mammalian enzyme,
 CC therefore reducing the immune response to C. albicans. An
 CC expression vector contg. the hydrolase cDNA can be used to produce
 CC the hydrolase, which can be used to generate antibodies (as
 CC diagnostic agents, or for passive immunisation), as a vaccine to
 CC treat or prevent Candida infection, as a reagent to detect
 CC antibodies and to reduce/modulate an inflammatory response by
 CC systemic or topical application. Nucleic acid antisense to the
 CC hydrolase cDNA may prevent hydrolase expression.
 XX
 XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAATAAAAAAAAAA 1095
 DB |||||
 13 TAAATAAAAAAAAAA 1
 RESULT 1264
 AAX83329/C
 ID AAX83329 standard; DNA; 14 BP.
 XX
 XX
 AC AAX83329;
 XX
 XX 31-AUG-1999 (first entry)
 DT
 XX
 DE Breast cancer tumour specific cDNA anchored primer.
 XX
 XX Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
 KW human endogenous retrovirus; vaccine; primer; PCR; amplification; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX WO9725426-A2.
 PN
 XX
 XX 17-JUL-1997.
 PD
 XX
 PF 10-JAN-1997; 97WO-US00485.

XX
 PR 20-AUG-1996; 96US-0700014.
 PR 11-JAN-1996; 96US-0585392.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX
 XX Prudakis TN, Reed SG, Smith JM;
 PI
 XX
 XX WPI; 1997-372865/34.
 DR
 XX
 XX Breast cancer-related DNA from retrovirus antigen (s) - useful for
 PT diagnosis and treatment of breast cancer
 PT
 XX
 XX Example 1; Page 24; 221pp; English.
 PS
 XX
 XX Primers AAX83286-X83329 were used to PCR amplify breast cancer tumour
 CC specific clones (AAX83201-X83285 and AAX83331-X83415) which are
 CC expressed from a genomic region containing a human endogenous retrovirus
 CC (AAX83330). Detection of the clone sequences allows determination of the
 CC presence of breast cancer in a mammal. Progression of breast cancer can
 CC be monitored by detecting the level of clone expression. Polypeptides
 CC encoded by the clones can be used in vaccines to inhibit or prevent
 CC breast cancer.
 XX
 XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAATAAAAAAAAAA 1095
 DB |||||
 13 TAAATAAAAAAAAAA 1
 RESULT 1265
 AAT75017/C
 ID AAT75017 standard; DNA; 14 BP.
 XX
 XX AAT75017;
 AC
 XX
 XX 06-OCT-1997 (first entry)
 DT
 XX
 XX Breast tumour cDNA primer (T)12AG.
 DE
 XX
 XX Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine;
 KW retrovirus; polymerase chain reaction; PCR; primer; ss.
 KW
 XX Synthetic.
 OS
 XX WO9725431-A1.
 PN
 XX
 XX 17-JUL-1997.
 PD
 XX
 XX 10-JAN-1997; 97WO-US00398.
 PF
 XX
 XX 10-JAN-1996; 96US-0587329.
 PR
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX
 XX Prudakis TN, Smith JM;
 PI
 XX
 XX WPI; 1997-384982/35.
 DR
 XX
 XX Endogenous human tumour-associated retroviral element, B18Ag1 - used
 PT for the prognosis, diagnosis and monitoring of human cancers,
 PT especially breast cancer
 PT
 XX
 XX Example 3; Page 21; 74pp; English.
 PS
 XX
 XX Primer (T)12AG (AAT75017) is used for first strand cDNA synthesis
 CC from RNA prep. from human breast tumour tissue. The cDNA can
 CC subsequently be amplified using primers B18Ag1-2 and B18Ag1-3
 CC

CC (see also AAT75013 and AAT75014) to isolate tumour-associated
 CC retroviral element B18Ag1 (see also AAT75002).

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAA 1095
 |||||
 Db 13 TAAAAAATAAAAA 1

RESULT 1266
 AAV69039/c
 ID AAV69039 standard; DNA; 14 BP.

XX AC AAV69039;

XX 22-JAN-1999 (first entry)

DE Human breast tumour RNA anchor primer #1.

KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
 KW vaccine; epitope; endogenous; retroviral element; primer; ss.

OS Synthetic.

XX Homo sapiens.

XX WO9845328-A2.

PN 15-OCT-1998.

XX 09-APR-1998; 98WO-US06939.

XX 11-DEC-1997; 97US-0991789.

PR 09-APR-1997; 97US-0838762.

XX (CORI-) CORIXA CORP.

XX Prudakis TN, Reed SG, Smith JM;

XX WPI; 1998-557473/47.

XX New DNA sequences isolated from endogenous human retroviral element
 PT - and related vectors, transformed cells, proteins and antibodies,
 PT useful for diagnosis, treatment and prevention of breast cancer

PS Example 1; Page 76; 173pp; English.

XX The present sequence represents an anchor primer used to convert normal
 CC breast and tumour RNA to cDNA. The present invention describes nucleotide
 CC sequences which encode human breast cancer specific polypeptides.
 CC Detection or measurement of human breast tumour specific polypeptides
 CC and nucleotide sequences, or the corresponding RNA in a sample, is used
 CC for diagnosis and monitoring of breast cancer. Human breast tumour
 CC specific polypeptides and nucleotide sequences, and the vectors
 CC containing the DNAs, are also useful in vaccines for inhibiting
 CC development (for prevention or therapy) of breast cancer. The
 CC polypeptides may also be used to raise monoclonal antibodies, used as
 CC immunoassay reagents.

XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAA 1095
 |||||
 Db 13 TAAAAAATAAAAA 1

RESULT 1267
 AAV54446/c
 ID AAV54446 standard; DNA; 14 BP.

XX AC AAV54446;

XX 21-DEC-1998 (first entry)

DE Nucleotide sequence of the T12MX PCR primer 2.

XX PCR; primer; amplification; cGMP-dependent kinase; ss.

XX Synthetic.

XX JP10225292-A.

XX 25-AUG-1998.

XX 13-FEB-1997; 97JP-0028750.

XX 13-FEB-1997; 97JP-0028750.

XX (KAOS) KAO CORP.

XX WPI; 1998-513902/44.

XX DNA coding cGMP-dependent kinase - useful for obtaining drugs
 PT related to expression of the gene

XX Disclosure; Page 3; 4pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used for
 CC amplification in the method of the invention involving the use of
 CC cGMP-dependent kinase, used in the method of the invention,
 CC where it is used to obtain drugs related to expression of the gene.

XX Sequence 14 BP; 1 A; 0 C; 0 G; 12 T; 1 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAATAAAAA 1095

Db 14 TTAATAAATAAAAA 1

RESULT 1268
 AAV54447/c
 ID AAV54447 standard; DNA; 14 BP.

XX AC AAV54447;

XX 21-DEC-1998 (first entry)

DE Nucleotide sequence of the T12MX PCR primer 3.

XX PCR; primer; amplification; cGMP-dependent kinase; ss.

XX Synthetic.

XX JP10225292-A.

XX 25-AUG-1998.

XX 13-FEB-1997; 97JP-0028750.

XX 13-FEB-1997; 97JP-0028750.

XX (KAOS) KAO CORP.

XX WPI; 1998-513902/44.

XX DNA coding cGMP-dependent kinase - useful for obtaining drugs
 PT related to expression of the gene
 XX
 XX Disclosure; Page 3; 4pp; Japanese.
 XX This is the nucleotide sequence of a PCR primer used for
 CC amplification in the method of the invention involving the use of
 CC cGMP-dependent kinase, used in the method of the invention,
 CC where it is used to obtain drugs related to expression of the gene.
 XX
 XX Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 1 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 | | | | | | | | | |
 Db 14 ANAAAAAAAAAAAA 1

RESULT 1269
 AAV54451/c
 ID AAV54451 standard; cDNA; 14 BP.
 XX
 AC AAV54451;
 XX
 DT 21-DEC-1998 (first entry)
 XX
 DE Nucleotide sequence of the T12MX PCR primer 2.
 XX
 KW PCR; primer; amplification; MSS-1-like protein; Tat protein; HIV; ss.
 XX
 OS Synthetic.

XX JP10225291-A.
 XX
 PD 25-AUG-1998.
 XX
 PF 13-FEB-1997; 97JP-0028749.
 XX
 PR 13-FEB-1997; 97JP-0028749.
 XX
 PA (KAOS) KAO CORP.
 XX
 DR WPI; 1998-513901/44.
 XX

XX DNA coding MSS-1-like protein - useful for developing drug related
 PT to gene expression through Tat protein formed at early period of HIV
 PT infection
 XX
 XX Disclosure; Page 3; 4pp; Japanese.
 XX
 CC This is the nucleotide sequence of a T12MX PCR primer used for
 CC amplification in the method of the invention, involving the use of
 CC MSS-1-like protein. The rat-derived MSS-1-like protein is used to
 CC develop a drug related to gene expression through Tat protein formed
 CC at early period of HIV infection.
 XX
 XX Sequence 14 BP; 1 A; 0 C; 0 G; 12 T; 1 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
 | | | | | | | | | |
 Db 14 TNAATAAAAAAAAAA 1

RESULT 1270
 AAV54452/c

ID AAV54452 standard; cDNA; 14 BP.
 XX
 AC AAV54452;
 XX
 DT 21-DEC-1998 (first entry)
 XX
 DE Nucleotide sequence of the T12MX PCR primer 3.
 XX
 KW PCR; primer; amplification; MSS-1-like protein; Tat protein; HIV; ss.
 XX
 OS Synthetic.
 XX
 PN JP10225291-A.
 XX
 PD 25-AUG-1998.
 XX
 PF 13-FEB-1997; 97JP-0028749.
 XX
 PR 13-FEB-1997; 97JP-0028749.
 XX
 PA (KAOS) KAO CORP.
 XX
 DR WPI; 1998-513901/44.
 XX
 PT DNA coding MSS-1-like protein - useful for developing drug related
 PT to gene expression through Tat protein formed at early period of HIV
 PT infection
 XX
 PS Disclosure; Page 3; 4pp; Japanese.
 XX
 CC This is the nucleotide sequence of a T12MX PCR primer used for
 CC amplification in the method of the invention, involving the use of
 CC MSS-1-like protein. The rat-derived MSS-1-like protein is used to
 CC develop a drug related to gene expression through Tat protein formed
 CC at early period of HIV infection.
 XX
 XX Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 1 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 | | | | | | | | | |
 Db 14 ANAAAAAAAAAAAA 1

RESULT 1271
 AAV09229/c
 ID AAV09229 standard; DNA; 14 BP.
 XX
 AC AAV09229;
 XX

XX 07-JUL-1998 (first entry)
 XX
 DE 3' poly(T) primer 5.
 XX
 KW 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
 KW oxidative metabolism; P450RA1; retinoic acid; RA; promoter; ss.
 XX
 OS Synthetic.
 XX
 PN WO9749832-A2.
 XX
 PD 31-DEC-1997.
 XX
 PF 23-JUN-1997; 97WO-CA00488.
 XX
 PR 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX
 PA (TOOH) UNIV QUEENS KINGSTON.

PI Petkovich PM;
XX WPI; 1998-077193/07.
XX Identifying DNA encoding inducible or suppressible cytochrome P450 -
PT by screening for drugs which reduce the catabolism of retinoic acid,
PT useful in cancer chemotherapy and the treatment of acne and
PT psoriasis
XX Example 1; Page 50; 113pp; English.
XX This is a 3' poly(T) PCR primer used in the amplification of the
CC inducible cytochrome P450RAI gene which specifically metabolises a
CC derivative of the retinoic acid (RA). The cytochrome P450 gene in
CC general produces enzymes involved in the oxidative metabolism of
CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
CC sequence can be used to induce or suppress the expression of its
CC protein. P450RAI is highly induced by RA in cell lines and tissues.
CC This allows for the development of a drug screen using promoters and
CC nucleotide sequences to identify drugs which are useful for reducing
CC the catabolism of RA.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1
|||||
RESULT 1272
AAV09231/C
ID AAV09231 standard; DNA; 14 BP.
XX
AC AAV09231;
XX
DT 07-JUL-1998 (first entry)
XX
DE 3' poly(T) primer 7.
XX
DE 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
KW
XX Synthetic.
OS
XX WOI749832-A2.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-CA00488.
XX
XX 01-OCT-1996; 96US-0724466.
XX 21-JUN-1996; 96US-0667546.
XX (TOOH) UNIV QUEENS KINGSTON.
XX
XX Petkovich PM;
XX
XX WOI749832-A2.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-CA00488.
XX
XX 01-OCT-1996; 96US-0724466.
XX 21-JUN-1996; 96US-0667546.
XX (TOOH) UNIV QUEENS KINGSTON.
XX
XX Petkovich PM;
XX
XX WPI; 1998-077193/07.
XX
XX Identifying DNA encoding inducible or suppressible cytochrome P450 -
PT by screening for drugs which reduce the catabolism of retinoic acid,
PT useful in cancer chemotherapy and the treatment of acne and
PT psoriasis
XX Example 1; Page 50; 113pp; English.
XX This is a 3' poly(T) PCR primer used in the amplification of the
CC inducible cytochrome P450RAI gene which specifically metabolises a
CC derivative of the retinoic acid (RA). The cytochrome P450 gene in

CC general produces enzymes involved in the oxidative metabolism of
CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
CC sequence can be used to induce or suppress the expression of its
CC protein. P450RAI is highly induced by RA in cell lines and tissues.
CC This allows for the development of a drug screen using promoters and
CC nucleotide sequences to identify drugs which are useful for reducing
CC the catabolism of RA.
XX
SQ Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1
|||||
RESULT 1273
AAV09232/C
ID AAV09232 standard; DNA; 14 BP.
XX
AC AAV09232;
XX
DT 07-JUL-1998 (first entry)
XX
DE 3' poly(T) primer 8.
XX
DE 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
KW
XX Synthetic.
OS
XX WOI749832-A2.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-CA00488.
XX
XX 01-OCT-1996; 96US-0724466.
XX 21-JUN-1996; 96US-0667546.
XX (TOOH) UNIV QUEENS KINGSTON.
XX
XX Petkovich PM;
XX
XX WPI; 1998-077193/07.
XX
XX Identifying DNA encoding inducible or suppressible cytochrome P450 -
PT by screening for drugs which reduce the catabolism of retinoic acid,
PT useful in cancer chemotherapy and the treatment of acne and
PT psoriasis
XX Example 1; Page 51; 113pp; English.
XX This is a 3' poly(T) PCR primer used in the amplification of the
CC inducible cytochrome P450RAI gene which specifically metabolises a
CC derivative of the retinoic acid (RA). The cytochrome P450 gene in
CC general produces enzymes involved in the oxidative metabolism of
CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
CC sequence can be used to induce or suppress the expression of its
CC protein. P450RAI is highly induced by RA in cell lines and tissues.
CC This allows for the development of a drug screen using promoters and
CC nucleotide sequences to identify drugs which are useful for reducing
CC the catabolism of RA.
XX
SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

RESULT 1275
AAV12223/c
ID AAV12223 standard; DNA; 14 BP.

KW retinoic acid; zebrafish; inhibitor; antisense; cancer;
 KW actinic keratosis; oral leukoplakia; head tumour; neck tumour;
 KW non-small cell lung carcinoma; basal cell carcinoma;
 KW acute promyelocytic leukemia; skin cancer; acne; psoriasis;
 KW ichthyosis; therapy; diagnosis; screening; differential display;
 KW PCR; primer; ss.
 XX
 OS Synthetic.
 PN WO9749815-A1.
 XX
 XX 31-DEC-1997.
 PD
 XX
 XX 23-JUN-1997; 97WO-CA00440.
 PF
 XX 01-OCT-1996; 96US-0724466.
 PR
 XX 21-JUN-1996; 96US-0667546.
 PR
 XX (TOOH) UNIV QUEENS KINGSTON.
 PA
 XX Beckett BR, Jones G, Petkovich PM, White JA;
 PI WPI; 1998-077178/07.
 XX
 XX Retinoid metabolising protein - useful to develop products to treat,
 PT e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
 PT ichthyosis
 PT
 XX
 PS Disclosure; Page 14; 110pp; English.
 XX
 CC PolyT oligonucleotides (see AAV12217-28) were used in reverse
 CC transcription reactions on polyA+ RNA isolated from the fins of
 CC control or retinoic acid-treated zebrafish (Danio rerio). Several
 CC combinations of the polyT primers were used with degenerate
 CC upstream primers (see AAV12229-33) for differential display PCR.
 CC Bands demonstrating reproducible differential amplifications were
 CC found using the primers given in AAV12221 and AAV12231. This PCR
 CC product was reamplified (see AAV12234-35). A differential display
 CC product (see AAV12213) which exhibited a dependence on the presence
 CC of retinoic acid for its expression was isolated, and was used to
 CC isolate a full-length clone (see AAV12203) coding for a novel
 CC retinoid metabolising protein (see AAV44159), designated zp450RA1.
 XX
 SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;
 XX

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1093 TAAAAAATAAAAA 1095
 DB |||||
 13 TAAAAAATAAAAA 1

RESULT 1277
 AAV04013/C
 ID AAV04013 standard; cDNA; 14 BP.
 XX
 AC AAV04013;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Oligo-dT primer used in CGR11 gene RT-PCR.
 XX
 XX Cell growth regulatory gene; CGR11; rat; tumour; cancer;
 KW diagnosis; gene therapy; RT-PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9745542-A2.
 PN
 XX 04-DEC-1997.
 PD
 XX

PF 29-MAY-1997; 97WO-US09584.
 XX
 PR 29-MAY-1996; 96US-0018557.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 XX Beaudry GA, Bertelsen AH, Galella E, Madden SI;
 PI WPI; 1998-032649/03.
 DR
 XX
 XX DNA encoding mammalian growth response protein CGR11 or CGR19 -
 PT useful to suppress or diagnose cancer, also similar use of SM20 or
 PT MEH protein
 PT
 XX
 PS Example 2; Page 16; 46pp; English.
 XX
 CC This oligo-dT primer was used with a random 10-mer primer (see
 CC AAV04014) in an RT-PCR amplification of rat embryo fibroblast REF-112
 CC cell RNA. This was performed in order to identifying novel p53
 CC regulated genes. One transcript that was upregulated specifically
 CC in cells harboring wild-type p53 protein was identified. A
 CC previously uncharacterised cDNA (see AAV04008), the cell regulatory
 CC gene CGR11, was isolated. The CGR11 gene and CGR11 protein (see
 CC AAV38423) can be used in methods for the diagnosis and treatment
 CC of cancer.
 CC
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 other;
 XX

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAA 1095
 DB |||||
 13 TAAAAAATAAAAA 1

RESULT 1278
 AAV23414
 ID AAA23414 standard; RNA; 14 BP.
 XX
 AC AAA23414;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 target site SEQ ID NO:6640.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipapillary; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiodioma;
 KW tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 XX 07-OCT-1999.
 PD
 XX
 XX 24-MAR-1999; 99WO-US06507.
 PF
 XX 27-MAR-1998; 98US-0079678.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.
 XX
 XX

PT Novel ribozymes for modulating the synthesis, expression and/or
PT stability of an mRNA encoding an angiogenic factors
PS Claim 54; Page 277; 305pp; English.
XX The present invention describes enzymatic cleavage of nucleic acid molecules with
CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
CC and AA17168 to AA17560 and AA17623 to AA17684 represent their
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
CC and AA19155 to AA19222 represent their corresponding target sequences;
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA21596 to AA21688 and
CC AA21689 to AA22475 and AA22476 to AA22476 represent ribozyme sequences
CC for integrin subunit beta 3, and AA22476 to AA22476 represent ribozyme sequences
CC AA22476 to AA22476 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX Sequence 14 BP; 1 A; 2 C; 6 G; 5 U; 0 other;
SQ Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 61.5%; Pred. No. 7.2e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 134 GTCGCTTTGGG 146
Db 2 GUCGCUUGGG 14
RESULT 1279
AAZ08326/c
ID AAZ08326 standard; DNA; 14 BP.
XX AAZ08326;
AC AAZ08326;
XX 13-OCT-1999 (first entry)
DE Human lung tumour RNA conversion primer (dt)12AG anchored 3' primer.
XX Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;
XX immunotherapy; detection; inhibition; primer; ss.
OS Synthetic.
OS Homo sapiens.
XX WO9938973-A2.
XX 05-AUG-1999.
XX 26-JAN-1999; 99WO-US01642.
XX 22-DEC-1998; 98US-0219245.
XX 28-JAN-1998; 98US-0015022.
XX 28-JAN-1998; 98US-0015029.
XX 18-MAR-1998; 98US-0040828.
XX 18-MAR-1998; 98US-0040831.
XX 23-JUL-1998; 98US-0122191.
XX 23-JUL-1998; 98US-0122192.
XX (CORI-) CORIXA CORP.

XX Frudakis TN, Lodes MJ, Mohamath R, Reed SG;
XX WPI; 1999-479187/40.
XX Lung tumour specific polynucleotides for inhibiting the development
XX of lung cancer
XX Example 1; Page 82; 171pp; English.
XX The present invention describes lung tumour specific polynucleotides
XX and tumour antigens. AA201144 to AA207246 and AA208301 to AA208325
XX represent specifically claimed polynucleotides, and AA29486 to AA29571
XX represent amino acid sequences from the present invention. The lung
XX tumour specific polynucleotides and polypeptides can be used in
XX pharmaceutical compositions and vaccines to inhibit the development of
XX lung cancer. They can also be used to detect lung cancer in a patient.
XX Probes and antibodies derived from the lung tumour sequences are useful
XX in detection of lung cancer. The present sequence represents a primer
XX used in an example from the present invention.
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
SQ Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1083 TAAAAAATAAAAA 1095
Db 13 TAAAAAATAAAAA 1
RESULT 1280
AAZ21821/c
ID AAZ21821 standard; DNA; 14 BP.
XX AAZ21821;
AC AAZ21821;
XX 18-MAY-1999 (first entry)
DE Primer for Mouse tag7 clone coding sequence.
XX Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma;
XX melanoma; leukaemia; apoptosis inducer; mouse; PCR primer; ss.
XX Synthetic.
XX Mus sp.
XX WO9902686-A1.
XX 21-JAN-1999.
XX 10-JUL-1998; 98WO-EP04287.
XX 11-JUL-1997; 97US-0893764.
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX Georgiev G, Kiselev S, Ostermann E, Prokhorchouk E;
XX WPI; 1999-120887/10.
XX New nucleic acid encoding tag7 - used to inhibit tumour growth and
XX induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
XX leukaemia
XX Example 1; Page 56; 138pp; English.
XX This sequence is a PCR primer for DNA encoding the murine tag7 of the
XX invention. Cells containing the tag7 DNA sequence are used to express
XX recombinant tag7. Tag7 is used to produce and purify antibodies; to
XX inhibit growth of mammalian tumours, especially for treating carcinoma
XX (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder,

CC testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma
 CC or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas),
 CC melanoma or leukaemia; and as a molecular weight marker. The tag7
 CC polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding
 CC sequences are also useful as probes for gene mapping and detection of
 CC tag7 gene expression, and as primers. Antibodies against tag7 are used as
 CC reagents for detecting tag7; as an antagonist of tag7; for isolating tag7
 CC and therapeutically to inhibit or delay tumour metastasis.
 XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
 |||||
 Db 13 TAAAAAATAAAAAA 1

RESULT 1281

AAAX19471/c
 ID AAAX19471 standard; DNA; 14 BP.

XX AC AAAX19471;

DT 21-MAY-1999 (first entry)

DE Human senescence factor p23 T12 anchor primer SEQ ID NO:13.

XX Human; senescence factor; p23; cancer; persistent inflammation;
 KW proliferative disorder; degenerative disorder; primer; ss.

OS Synthetic.
 OS Homo sapiens.

XX WO9907893-A1.

XX 18-FEB-1999.

XX 05-AUG-1998; 98WO-US16343.

XX 08-AUG-1997; 97US-0908873.

XX (UNIW) UNIV WASHINGTON.

XX Hosier S, Kubbies M, Swissshelm K;

XX WPI; 1999-167454/14.

XX Newly isolated nucleic acid molecule (designated p23) encoding a p23
 PT polypeptide - useful for inducing a senescence phenotype in a cell

XX Example 1; Page 18; 44pp; English.

XX The present invention describes human senescence factor p23. An
 CC expression vector for p23 is useful for inducing a senescent phenotype
 CC in a cell (preferably eukaryotic). This may help in regulating diseases,
 CC including cancer, persistent inflammation, and various proliferative and
 CC degenerative disorders. These transgenic cells are useful in gene
 CC therapy for treating cancer, particularly where antisense
 CC oligonucleotides are useful for blocking normal or mutant p23 expression
 CC in cancer cells or other proliferating cells. Transgenic cells are also
 CC useful for producing the p23 polypeptide in large quantities. The
 CC antibodies are useful for raising antiserum against p23, and for
 CC identifying senescent cells in culture and tissue biopsies. The p23
 CC polynucleotides are useful for modulating or altering p23 activity in a
 CC cell, and for identifying and isolating the whole gene encoding p23,
 CC and variants of p23. Assays based on p23 elements, which detect p23,
 CC levels and activity are useful as diagnostic markers for staging tumours,
 CC determining prognosis, and/or predicting therapeutic success. These
 CC elements also provide an assay for detecting chromosomal rearrangements
 CC in chromosome 3 in a human cell. The isolation of the p23 polynucleotide

CC permits the manipulation of malignant growth in cancer. The present
 CC sequence represents a primer used in an example from the present
 CC invention.

XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
 |||||
 Db 13 TAAAAAATAAAAAA 1

RESULT 1282

AAAX19474/c
 ID AAAX19474 standard; DNA; 14 BP.

XX AC AAAX19474;

XX DT 21-MAY-1999 (first entry)

XX Human senescence factor p23 T12 anchor primer SEQ ID NO:16.

XX Human; senescence factor; p23; cancer; persistent inflammation;
 KW proliferative disorder; degenerative disorder; primer; ss.

OS Synthetic.
 OS Homo sapiens.

XX WO9907893-A1.

XX 18-FEB-1999.

XX 05-AUG-1998; 98WO-US16343.

XX 08-AUG-1997; 97US-0908873.

XX (UNIW) UNIV WASHINGTON.

XX Hosier S, Kubbies M, Swissshelm K;

XX WPI; 1999-167454/14.

XX Newly isolated nucleic acid molecule (designated p23) encoding a p23
 PT polypeptide - useful for inducing a senescence phenotype in a cell

XX Example 1; Page 18; 44pp; English.

XX The present invention describes human senescence factor p23. An
 CC expression vector for p23 is useful for inducing a senescent phenotype
 CC in a cell (preferably eukaryotic). This may help in regulating diseases,
 CC including cancer, persistent inflammation, and various proliferative and
 CC degenerative disorders. These transgenic cells are useful in gene
 CC therapy for treating cancer, particularly where antisense
 CC oligonucleotides are useful for blocking normal or mutant p23 expression
 CC in cancer cells or other proliferating cells. Transgenic cells are also
 CC useful for producing the p23 polypeptide in large quantities. The
 CC antibodies are useful for raising antiserum against p23, and for
 CC identifying senescent cells in culture and tissue biopsies. The p23
 CC polynucleotides are useful for modulating or altering p23 activity in a
 CC cell, and for identifying and isolating the whole gene encoding p23,
 CC and variants of p23. Assays based on p23 elements, which detect p23,
 CC levels and activity are useful as diagnostic markers for staging tumours,
 CC determining prognosis, and/or predicting therapeutic success. These
 CC elements also provide an assay for detecting chromosomal rearrangements
 CC in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
 CC permits the manipulation of malignant growth in cancer. The present
 CC sequence represents a primer used in an example from the present
 CC invention.

XX Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAA 1095
| | | | | | | | | | | | | | | |
Db 13 TAAAAAAAAAAAAA 1

RESULT 1283
AAAX19468/c
ID AAX19468 standard; DNA; 14 BP.
XX
AC AAX19468;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:10.
XX
KW Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9907893-A1.
XX
PD 18-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US16343.
XX
PR 08-AUG-1997; 97US-0908873.
XX
PA (UNIW) UNIV WASHINGTON.
XX
XX Hosier S, Kubbies M, Swissshelm K;
XX
DR WPI; 1999-167454/14.
XX

Newly isolated nucleic acid molecule (designated p23) encoding a p23 polypeptide - useful for inducing a senescence phenotype in a cell
Example 1; Page 18; 4pp; English.
XX
CC The present invention describes human senescence factor p23. An expression vector for p23 is useful for inducing a senescent phenotype in a cell (preferably eukaryotic). This may help in regulating diseases, including cancer, persistent inflammation, and various proliferative and degenerative disorders. These transgenic cells are useful in gene therapy for treating cancer, particularly where antisense oligonucleotides are useful for blocking normal or mutant p23 expression in cancer cells or other proliferating cells. Transgenic cells are also useful for producing the p23 polypeptide in large quantities. The antibodies are useful for raising antiserum against p23, and for identifying senescent cells in culture and tissue biopsies. The p23 polynucleotides are useful for modulating or altering p23 activity in a cell, and for identifying and isolating the whole gene encoding p23, and variants of p23. Assays based on p23 elements, which detect p23 levels and activity are useful as diagnostic markers for staging tumours, determining prognosis, and/or predicting therapeutic success. These elements also provide an assay for detecting chromosomal rearrangements in chromosome 3 in a human cell. The isolation of the p23 polynucleotide permits the manipulation of malignant growth in cancer. The present sequence represents a primer used in an example from the present invention.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAA 1095
| | | | | | | | | | | | | | | |
Db 13 TAAAAAAAAAAAAA 1

RESULT 1284
AAAX02695/c
ID AAX02695 standard; DNA; 14 BP.
XX
AC AAX02695;
XX
DT 10-MAY-1999 (first entry)
XX
DE Barley HPPD primer #1.
XX
KW HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
KW transgenic; plant cell; callus tissue; protoplast; electroporation;
KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
KW sunflower; tobacco; ss.
XX
OS Hordeum vulgare.
XX
PN DE19730066-A1.
XX
PD 21-JAN-1999.
XX
XX 14-JUL-1997; 97DE-1030066.
XX
PR 14-JUL-1997; 97DE-1030066.
XX
PA (BADI) BASF AG.
XX
XX Falk J, Kurpinska K, Lerchl J, Schmidt R, Seulberger H;
XX WPI; 1999-096742/09.
XX
XX DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing plants with increased vitamin E content, etc.
XX
PS Example 1; Page 9; 26pp; German.
XX
CC AAX02695-X02708 are primers used in the isolation of a novel barley (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This protein is useful for plant transformation to produce transgenic plants especially where an expression cassette is introduced into a plant cell, callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens transformation, electroporation or particle bombardment and where the plants are selected from soya, barley, wheat, oilseed rape, maize and sunflower, or where the DNA is expressed in tobacco plants, especially in leaves or seeds.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAA 1095
| | | | | | | | | | | | | | | |
Db 13 TAAAAAAAAAAAAA 1

RESULT 1285
AAAX02697/c
ID AAX02697 standard; DNA; 14 BP.
XX
AC AAX02697;
XX
DT 10-MAY-1999 (first entry)
XX
DE Barley HPPD primer #3.
XX
KW HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;

KW transgenic; plant cell; callus tissue, protoplast; electroporation;
 KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
 XX sunflower; tobacco; ss.

OS Hordeum vulgare.

PN DEL9730066-A1.

XX 21-JAN-1999.

XX 14-JUL-1997; 97DE-1030066.

XX 14-JUL-1997; 97DE-1030066.

XX (BADI) BASF AG.

XX Falk J, Kurpinska K, Lerchl J, Schmidt R, Seulberger H;
 XX WPI; 1999-096742/09.

XX DNA encoding barley hydroxyphenylpyruvate dioxygenase - for
 PT producing plants with increased vitamin E content, etc.

XX Example 1; Page 9; 26pp; German.

XX AAX02695-X02708 are primers used in the isolation of a novel barley
 CC (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
 CC protein is useful for plant transformation to produce transgenic plants
 CC especially where an expression cassette is introduced into a plant cell,
 CC callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
 CC transformation, electroporation or particle bombardment and where the
 CC plants are selected from soya, barley, wheat, oilseed rape, maize and
 CC sunflower, or where the DNA is expressed in tobacco plants, especially
 CC in leaves or seeds.

XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAA 1095
 DB |||||||
 13 TAAAAAATAAAAA 1

RESULT 1286
 AAC79077/C
 ID AAC79077 standard; DNA; 14 BP.

XX AAC79077;
 XX 05-FEB-2001 (first entry)
 XX (dT)12AG primer.

XX Lung tumour protein; lung cancer; cytostatic; vaccine; ss.

XX Synthetic.

XX WO200060077-A2.

XX 12-OCT-2000.

XX 30-MAR-2000; 2000WO-US08560.

XX 02-APR-1999; 99US-0285323.

XX 09-AUG-1999; 99US-0370838.

XX 30-DEC-1999; 99US-0476235.

XX 03-MAR-2000; 2000US-0518809.

XX (CORI-) CORIXA CORP.

PI Reed SG, Lodes MJ, Mohamath R, Secrist H;
 XX WPI; 2000-638466/61.

XX Novel lung tumor polypeptides and polynucleotides, useful for
 PT detecting, monitoring or treating cancer, especially lung cancer -

XX Claim 1; Page 106; 243pp; English.

XX The present sequence is given in a specification relating to compounds
 CC for therapy and diagnosis of lung cancer. Polypeptides comprising at
 CC least an immunogenic part of a lung tumour protein are disclosed.
 CC The polypeptides are useful for inhibiting the development of cancer,
 CC especially lung cancer. Samples of T cells expressing the polypeptides
 CC may be used to inhibit the development of cancer. The polypeptides are
 CC also useful for detecting and monitoring the progression of cancer,
 CC especially lung cancer.

XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAA 1095
 DB |||||||
 13 TAAAAAATAAAAA 1

RESULT 1287
 AAC80852/C
 ID AAC80852 standard; DNA; 14 BP.

XX AAC80852;

XX 13-FEB-2001 (first entry)

XX Human B18Ag1 cDNA anchored 3' PCR primer.

XX Human; breast tumour-specific antigen; cytostatic; vaccine;
 XX breast cancer; B18Ag1; B11Ag1; B15Ag1; PCR primer; ss.

XX Homo sapiens.

XX WO200061753-A2.

XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-US09312.

XX 09-APR-1999; 99US-0289198.

XX 28-OCT-1999; 99US-0429755.

XX 23-MAR-2000; 2000US-0534825.

XX (CORI-) CORIXA CORP.

XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
 XX WPI; 2000-628403/60.

XX An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -

XX Example 1; Page 33; 187pp; English.

XX The present sequence is a PCR primer which was used in the isolation of
 CC human breast tumour-specific antigens. Methods for the treatment and
 CC diagnosis of breast cancer are disclosed. Nucleotide sequences that are
 CC preferentially expressed in breast tumour tissue, and the polypeptides
 CC encoded by such nucleotide sequences, are used in compositions and
 CC vaccines to inhibit the development of cancer, especially breast cancer.
 CC The progression of a cancer may be monitored by carrying out detection of

CC tumour-specific antigens at subsequent time points and comparing the
 CC results from the different time points. CD4+ and/or CD8+ T-cells isolated
 CC from the cancer patient may be treated with tumour-specific polypeptides,
 CC polynucleotides encoding the polypeptides or antigen presenting cells
 CC expressing the polypeptides. The cells are then administered to the
 CC patient to inhibit development of cancer.
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAA 1095
 DB 13 TAAAAAATAAAAA 1

RESULT 1289
 AAZ60813/c
 ID AAZ60813 standard; DNA; 14 BP.
 AC AAZ60813;
 DT 16-MAY-2000 (first entry)
 DE 3' PCR primer used to screen for differentially expressed genes.
 KW Differentially expressed gene; effector gene; dft-A;
 KW FOS transforming pathway; RAS transforming pathway; cancer;
 KW neurological disorder; central nervous system disease; PCR primer; ss.
 OS Rattus sp.
 PN CR2271326-A1.
 XX 11-NOV-1999.
 PD 10-MAY-1999; 99CA-2271326.
 PF 11-MAY-1998; 98US-0075215.
 PR (RECL-) INST RECH CLINIQUES MONTREAL.
 PA Jolicoeur P, Balsalobre A;
 PI WPI; 2000-171736/16.
 DR Antibodies specific for dft-A proteins useful for diagnosing cancers
 PT and neurological disorders characterized by inappropriate dft-A
 PT expression -
 XX Disclosure; Page 6; 45pp; English.

CC PCR primers AAZ60744-55 and AAZ60812-13 were used to screen for
 CC differentially expressed genes in normal versus Fos-transformed rat-1
 CC cells, to identify effector genes. From the amplified fragments, dft-A
 CC was identified. Dft-A protein is a member of the immunoglobulin (Ig)
 CC gene superfamily, and contains C2-type Ig-like domain and on potential
 CC transmembrane domain. The predicted dft-A protein shares extensive
 CC homology with MFAP3, an extracellular protein associated with
 CC microfibrils. The specification describes an antibody which recognizes
 CC a dft-A protein encoded by a dft-A gene. The dft-A gene is regulated
 CC by the FOS and RAS transforming pathways. The antibodies may be used
 CC to detect levels of dft-A protein expression in sample from patients
 CC according to standard immunoassay techniques (e.g. enzyme linked
 CC immunosorbant assays (ELISA)). Levels of dft-A expression can be used
 CC to diagnose cancers, neurological disorders and other central nervous
 CC system diseases.
 XX
 SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 ABQ63270

Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAA 1095
 DB 13 TAAAAAATAAAAA 1

RESULT 1289
 AAD23152/c
 ID AAD23152 standard; DNA; 14 BP.
 AC AAD23152;
 XX 26-FEB-2002 (first entry)
 DT Human lung tumour-specific cDNA synthesising 3' RT-PCR anchored primer.
 DE Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
 KW antisense-therapy; vaccine; immune response; lung cancer; RT-PCR primer;
 KW ss.
 OS Homo sapiens.
 XX WO200172295-A2.
 PN 04-OCT-2001.
 PD 28-MAR-2001; 2001WO-US09991.
 PF 29-MAR-2000; 2000US-0538037.
 PR 05-JUN-2000; 2000US-0588937.
 PR 18-AUG-2000; 2000US-0640878.
 PR 22-SEP-2000; 2000US-234517P.
 PR 01-NOV-2000; 2000US-0704512.
 PR 14-DEC-2000; 2000US-0738973.
 XX (CORI-) CORIXA CORP.
 PA Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indrias CV;
 PI Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
 PI WPI; 2001-639201/73.
 DR New human lung-specific polynucleotides and polypeptides for the
 PT diagnosis and treatment of disease e.g. lung cancer -
 PT Example 1; Page 162; 378pp; English.

CC The invention relates to isolated lung tumour-specific proteins and
 CC their corresponding cDNA molecules. Lung tumour-specific proteins and
 CC their antigen-presenting cells are useful for stimulating and/or
 CC expanding T cells specific for a tumour protein, and for inhibiting
 CC the development of cancer. The invention also relates to a composition
 CC useful for stimulating an immune response, and for treating cancer. The
 CC lung tumour specific oligonucleotide is useful in gene therapy and for
 CC diagnosis, detection and treatment of lung cancer. The present DNA
 CC sequence is 3' RT (reverse transcriptase)-PCR anchored primer which is
 CC used for synthesising human lung tumour-specific cDNA.
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAA 1095
 DB 13 TAAAAAATAAAAA 1

RESULT 1290
 ABQ63270

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ID ABQ83270 standard; DNA; 14 BP.
XX AC
XX ABQ83270;
XX DT
XX 18-JAN-2003 (first entry)
XX DE
XX EGI cDNA tag related oligonucleotide SEQ ID NO:43.
XX KW
XX cDNA tag; identification; gene expression analysis; linker;
XX KW
XX expressed gene identification; EGI; ss.
XX OS
XX Synthetic.
XX PN
XX WO200274951-A1.
XX PD
XX 26-SEP-2002.
XX PF
XX 13-MAR-2002; 2002WO-JP02338.
XX PR
XX 15-MAR-2001; 2001JP-0073959.
XX PA
XX (KURE ) KUREHA CHEM IND CO LTD.
XX PA
XX (YAMA/) YAMAMOTO M.
XX PA
XX (YAMA/) YAMAMOTO N.
XX PI
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX DR
XX Construction of cDNA tags for identifying expressed genes with specific
XX PT
XX linkers and recognition sequences, applicable in gene expression
XX PT
XX analysis, disease diagnosis and identifying target for gene therapy -
XX PS
XX Example 1; Page 24; 59pp; Japanese.
XX CC
XX The present invention describes a method for constructing a cDNA tag for
XX CC
XX identifying an expressed gene. The method comprises: (a) preparation of
XX CC
XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX CC
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX CC
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX CC
XX linker Y ligated material; and (e) cleaving the amplification product.
XX CC
XX The method can be used for the construction of cDNA tags for identifying
XX CC
XX expressed genes, which is applicable in gene expression analysis, disease
XX CC
XX diagnosis and identifying target for gene therapy, including the
XX CC
XX clarification of difference in function or morphology of cells under
XX CC
XX physiological or pathological conditions. The cDNA or cells for assay can
XX CC
XX be specifically expressed, with reproducibility and accuracy in the
XX CC
XX detection of genes. The present sequence represents an expressed gene
XX CC
XX identification (EGI) cDNA tag related oligonucleotide which is used in
XX CC
XX an example from the present invention.
XX SQ
XX Sequence 14 BP; 13 A; 1 C; 0 G; 0 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 1 AAAAAAAAAAAAAA 13

RESULT 1291
ABQ83271
ID ABQ83271 standard; DNA; 14 BP.
XX AC
XX ABQ83271;
XX DT
XX 18-JAN-2003 (first entry)
XX DE
XX EGI cDNA tag related oligonucleotide SEQ ID NO:44.
XX KW
XX cDNA tag; identification; gene expression analysis; linker;

```

```

KM expressed gene identification; EGI; ss.
XX OS
XX Synthetic.
XX PN
XX WO200274951-A1.
XX PD
XX 26-SEP-2002.
XX PF
XX 13-MAR-2002; 2002WO-JP02338.
XX PR
XX 15-MAR-2001; 2001JP-0073959.
XX PA
XX (KURE ) KUREHA CHEM IND CO LTD.
XX PA
XX (YAMA/) YAMAMOTO M.
XX PA
XX (YAMA/) YAMAMOTO N.
XX PI
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX DR
XX Construction of cDNA tags for identifying expressed genes with specific
XX PT
XX linkers and recognition sequences, applicable in gene expression
XX PT
XX analysis, disease diagnosis and identifying target for gene therapy -
XX PS
XX Example 1; Page 24; 59pp; Japanese.
XX CC
XX The present invention describes a method for constructing a cDNA tag for
XX CC
XX identifying an expressed gene. The method comprises: (a) preparation of
XX CC
XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX CC
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX CC
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX CC
XX linker Y ligated material; and (e) cleaving the amplification product.
XX CC
XX The method can be used for the construction of cDNA tags for identifying
XX CC
XX expressed genes, which is applicable in gene expression analysis, disease
XX CC
XX diagnosis and identifying target for gene therapy, including the
XX CC
XX clarification of difference in function or morphology of cells under
XX CC
XX physiological or pathological conditions. The cDNA or cells for assay can
XX CC
XX be specifically expressed, with reproducibility and accuracy in the
XX CC
XX detection of genes. The present sequence represents an expressed gene
XX CC
XX identification (EGI) cDNA tag related oligonucleotide which is used in
XX CC
XX an example from the present invention.
XX SQ
XX Sequence 14 BP; 13 A; 0 C; 1 G; 0 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 1 AAAAAAAAAAAAAA 13

RESULT 1292
ABQ83272
ID ABQ83272 standard; DNA; 14 BP.
XX AC
XX ABQ83272;
XX DT
XX 18-JAN-2003 (first entry)
XX DE
XX EGI cDNA tag related oligonucleotide SEQ ID NO:45.
XX KW
XX cDNA tag; identification; gene expression analysis; linker;
XX KW
XX expressed gene identification; EGI; ss.
XX OS
XX Synthetic.
XX PN
XX WO200274951-A1.
XX PD
XX 26-SEP-2002.
XX PS
XX 13-MAR-2002; 2002WO-JP02338.

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XX PR 15-MAR-2001; 2001JP-0073959.
XX PA (KURE ) KUREHA CHEM IND CO LTD.
XX PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX DR WPI; 2002-759896/82.
XX PT Construction of cDNA tags for identifying expressed genes with specific
XX PT linkers and recognition sequences, applicable in gene expression
XX PT analysis, disease diagnosis and identifying target for gene therapy -
XX PS Example 1; Page 24; 59pp; Japanese.
XX CC The present invention describes a method for constructing a cDNA tag for
XX CC identifying an expressed gene. The method comprises: (a) preparation of
XX CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX CC linker Y ligated material; and (e) cleaving the amplification product.
XX CC The method can be used for the construction of cDNA tags for identifying
XX CC expressed genes, which is applicable in gene expression analysis, disease
XX CC diagnosis and identifying target for gene therapy, including the
XX CC clarification of difference in function or morphology of cells under
XX CC physiological or pathological conditions. The cDNA or cells for assay can
XX CC be specifically expressed, with reproducibility and accuracy in the
XX CC detection of genes. The present sequence represents an expressed gene
XX CC identification (EGI) cDNA tag related oligonucleotide which is used in
XX CC an example from the present invention.
XX SQ Sequence 14 BP; 13 A; 0 C; 0 G; 1 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 1 AAAAAAAAAAAAAA 13

RESULT 1293
ABQ83276/c
ID ABQ83276 standard; DNA; 14 BP.
XX AC ABQ83276;
XX DT 18-JAN-2003 (first entry)
XX DE EGI cDNA tag related oligonucleotide SEQ ID NO:49.
XX KW cDNA tag; identification; gene expression analysis; linker;
XX KW expressed gene identification; EGI; ss.
XX OS Synthetic.
XX PN WO200274951-A1.
XX PD 26-SEP-2002.
XX PF 13-MAR-2002; 2002WO-JP02338.
XX PR 15-MAR-2001; 2001JP-0073959.
XX PA (KURE ) KUREHA CHEM IND CO LTD.
XX PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX DR WPI; 2002-759896/82.
XX PT Construction of cDNA tags for identifying expressed genes with specific
XX PT linkers and recognition sequences, applicable in gene expression
XX PT analysis, disease diagnosis and identifying target for gene therapy -
XX PS Example 1; Page 24; 59pp; Japanese.
XX CC The present invention describes a method for constructing a cDNA tag for

```

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DR XX WPI; 2002-759896/82.
PT XX Construction of cDNA tags for identifying expressed genes with specific
PT XX linkers and recognition sequences, applicable in gene expression
PT XX analysis, disease diagnosis and identifying target for gene therapy -
XX PS Example 1; Page 24; 59pp; Japanese.
XX CC The present invention describes a method for constructing a cDNA tag for
XX CC identifying an expressed gene. The method comprises: (a) preparation of
XX CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX CC linker Y ligated material; and (e) cleaving the amplification product.
XX CC The method can be used for the construction of cDNA tags for identifying
XX CC expressed genes, which is applicable in gene expression analysis, disease
XX CC diagnosis and identifying target for gene therapy, including the
XX CC clarification of difference in function or morphology of cells under
XX CC physiological or pathological conditions. The cDNA or cells for assay can
XX CC be specifically expressed, with reproducibility and accuracy in the
XX CC detection of genes. The present sequence represents an expressed gene
XX CC identification (EGI) cDNA tag related oligonucleotide which is used in
XX CC an example from the present invention.
XX SQ Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1

RESULT 1294
ABQ83277/c
ID ABQ83277 standard; DNA; 14 BP.
XX AC ABQ83277;
XX DT 18-JAN-2003 (first entry)
XX DE EGI cDNA tag related oligonucleotide SEQ ID NO:50.
XX KW cDNA tag; identification; gene expression analysis; linker;
XX KW expressed gene identification; EGI; ss.
XX OS Synthetic.
XX PN WO200274951-A1.
XX PD 26-SEP-2002.
XX PF 13-MAR-2002; 2002WO-JP02338.
XX PR 15-MAR-2001; 2001JP-0073959.
XX PA (KURE ) KUREHA CHEM IND CO LTD.
XX PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX DR WPI; 2002-759896/82.
XX PT Construction of cDNA tags for identifying expressed genes with specific
XX PT linkers and recognition sequences, applicable in gene expression
XX PT analysis, disease diagnosis and identifying target for gene therapy -
XX PS Example 1; Page 24; 59pp; Japanese.
XX CC The present invention describes a method for constructing a cDNA tag for

```

identifying an expressed gene. The method comprises: (a) preparation of complementary deoxyribonucleic acid; (b) producing cDNA fragment by cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA fragment ligated material; (d) amplification of the linker X-cDNA tag-linker Y ligated material; and (e) cleaving the amplification product. The method can be used for the construction of cDNA tags for identifying expressed genes, which is applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy, including the clarification of difference in function or morphology of cells under physiological or pathological conditions. The cDNA or cells for assay can be specifically expressed, with reproducibility and accuracy in the detection of genes. The present sequence represents an expressed gene identification (EGI) cDNA tag related oligonucleotide which is used in an example from the present invention.

Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1

RESULT 1295

ABV73026/c

ID ABV73026 standard; DNA; 14 BP.

XX AC ABV73026;

DT 08-JAN-2003 (first entry)

DE Murine sFRP-1 differential display (DD PCR) primer T12VA.

XX KW Frizzled-related protein; FRP; sFRP-1; osteopathic; anti-HIV; virucide;
XX KW antiinflammatory; immunosuppressive; antibacterial; antiparasitic;
XX KW cytostatic; antiarthritic; antirheumatic; PCR; primer; ss.

OS Mus sp.

XX FN WO200255547-A2.

XX PD 18-JUL-2002.

XX PF 10-JAN-2002; 2002WO-US00869.

XX PR 10-JAN-2001; 2001US-260908P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA (SVIN-) ST VINCENTS INST MEDICAL RES.

XX PI Rubin JS, Uren A, Horwood NJ, Gillespie MT, Kay BK, Weisblum B;

XX DR WPI; 2002-740678/80.

XX PS Example 1; Page 31; 81pp; English.

XX CC The invention relates to a purified peptide that binds to secreted

XX CC Frizzled-related protein (sFRP)-1. The peptide is useful for enhancing or

XX CC stimulating osteoclast differentiation, or to modify T-cell activity in a

XX CC subject with abnormal bone remodeling, achondroplasia, Albright's

XX CC osteodystrophy or osteopetrosis. The sFRP-1 is useful for inhibiting

XX CC osteoclast formation in a subject with a bone disorder or unwanted bone

XX CC resorption, e.g. postmenopausal osteoporosis, Paget's disease, lytic bone

XX CC metastases, multiple myeloma, rheumatoid arthritis or hypercalcemia of

XX CC malignancy. Modulating T-cell activity is useful in subjects suspected of

CC having toxic shock, sepsis, graft-versus-host reactions or acute
CC inflammatory reactions. The immunostimulatory sFRP-1-binding peptide is
CC useful in activating the immune system against bacterial, viral and
CC parasitic infections, and in the treatment of human immunodeficiency
CC virus (HIV). The present sequence represents a differential display
CC (DD PCR) primer used for murine sFRP-1.

XX SQ Sequence 14 BP; 1 A; 0 C; 0 G; 12 T; 1 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
DB 14 TNAATAAAAAAAAAA 1

RESULT 1296

ABS54141/c

ID ABS54141 standard; DNA; 14 BP.

XX AC ABS54141;

XX DT 25-NOV-2002 (first entry)

XX DE Oligo-dT primer #2.

XX KW PCR; primer; Zis-SR; neuroendocrine phenotype; diabetes; ss;

XX KW Parkinson's disease; Alzheimer's disease; neurodegenerative disease;

XX KW zinc finger splicing with extended Ser-Arg domain; secretory pathway;

XX KW zinc finger protein.

XX OS Synthetic.

XX PN WO200261082-A2.

XX PD 08-AUG-2002.

XX PF 29-JAN-2002; 2002WO-CA00101.

XX PR 29-JAN-2001; 2001US-264296P.

XX PA (UYSH) UNIV SHERBROOKE.

XX PI Day R;

XX DR WPI; 2002-682683/73.

XX PT New Zis-SR nucleic acid molecules and polypeptides, useful for

XX PT restoring or increasing the secretory properties of a cell, or for

XX PT treating diseases or conditions associated with a loss of function,

XX PT e.g. diabetes or Parkinson's disease -

XX PS Disclosure; Page 35; 70pp; English.

XX CC The invention relates to an isolated nucleic acid molecule, Zis-SR,
XX CC encoding a protein involved in the secretory pathway in a cell (or its
XX CC homologue or variant) or nucleic acid molecules that hybridise under high
XX CC stringency condition to the Zis-SR nucleic acid. Also included are
XX CC an isolated polypeptide involved in the formation of secretory

XX CC granules in cells comprising the amino acid sequence spanning amino

XX CC acids 243-310 of the Zis-SR protein, restoring the neuroendocrine

XX CC differentiation of a cell using the nucleic acid molecule or polypeptide

XX CC cited above, identifying a gene and/or protein involved in inducing

XX CC regulated secretion comprising a comparison at the molecular level of a

XX CC secretion-defective cell line under conditions that restore

XX CC differentiation of the secretion-defective cell, such that secretion is

XX CC restored, and the secretion-defective cell line in the absence of the

XX CC conditions cited. Also included are modulating the secretory properties

XX CC of a cell comprising modulating the activity and/or level of Zis-SR and

XX CC an assay to identify a modulator of regulated secretion in a cell

XX CC comprising an assessment of a biological activity of Zis-SR, its part

CC or derivative in the presence of a candidate agent, where a modulator
CC of regulated secretion is selected when the biological activity of
CC Zis-SR, its part or derivative is measurably different in the presence
CC of the candidate compound as compared in its absence. The nucleic acid
CC molecules or polypeptides are useful for restoring or increasing
CC the secretory properties of a cell, for regulating neuroendocrine
CC phenotype, and for long term therapies to treat diseases or conditions
CC associated with a loss of function, e.g. diabetes, neurodegenerative
CC diseases such as Alzheimer's disease or Parkinson's disease. The assay is
CC useful for screening compounds for treating diseases or conditions
CC associated with a defect in the regulated secretory pathways in cells.
CC The nucleic acid molecules can also be used to locate gene regions
CC associated with genetic diseases. The present sequence is an
CC oligo-dT PCR primer used to isolate the cDNA encoding mouse
CC Zis-SR (zinc finger splicing with extended Ser-Arg domain).
XX

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1297

ABK46742/c
ID ABK46742 standard; DNA; 14 BP.

AC ABK46742;

XX 05-JUN-2002 (first entry)

XX Human breast tumour-specific cDNA B18Agl, RT-PCR primer.

XX Human; breast tumour-specific protein; vaccine; breast cancer;
KW primer; ss.

XX Homo sapiens.

XX US6344550-B1.

XX 05-FEB-2002.

XX 17-APR-1998; 98US-0062451.

XX 01-JAN-1996; 96US-0585392.

XX 20-AUG-1996; 96US-0700014.

XX 10-JAN-1997; 97WO-US00485.

XX 09-APR-1997; 97US-0838762.

XX 11-DEC-1997; 97US-0991789.

XX (CORI-) CORIXA CORP.

XX Frudakis TN, Smith JM, Reed SG;

XX WPI; 2002-215084/27.

XX Polynucleotide encoding breast-specific tumour polypeptides useful as

XX vaccine for preventing and treating breast cancer in a subject -

XX Example 1; Column 16; 128pp; English.

XX The invention relates to an isolated DNA molecule (I) encoding breast-
XX tumour-specific polypeptides. (I) is useful as a vaccine for preventing
XX and treating breast cancer in a subject. The polypeptide encoded by (I)
XX is used for production of compounds such as antibodies useful in
XX diagnosing and monitoring the progression of breast cancer. ABK4614-
XX ABK46899 represent human breast tumour-specific coding sequences and
XX related PCR primers of the invention.

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1298

ABL88472/c
ID ABL88472 standard; DNA; 14 BP.

XX ABL88472;

XX 16-MAY-2002 (first entry)

XX Oligo dT 3P1 primer 2.

XX Pain; analgesic; gene therapy; neurological disorder;
KW neurodegenerative disease; primer; ss.

XX Synthetic.

XX WO200212338-A2.

XX 14-FEB-2002.

XX 03-AUG-2001; 2001WO-BP09011.

XX 03-AUG-2000; 2000DE-1037759.

XX (CHEF) GRUENENTHAL GMBH.

XX Gillen C, Wetzels I, Wnendt S, Weihe E, Schaefer MK;

XX WPI; 2002-257469/30.

XX Identifying pain-regulating compounds, useful for treating chronic pain
XX and for diagnosis, by measuring binding of compounds to specific
XX peptides and proteins -

XX Example 1; Page 62; 213pp; German.

XX The invention relates to identifying pain-regulating substances (A)
XX comprises (i) incubating a test substance with a cell (or preparation
XX from it) that has synthesised a peptide or protein (B) and (ii) measuring
XX either binding of the test substance to (B) or some functional parameter
XX that is altered by this binding. The method is useful for identifying
XX pain-regulating substances (A) with analgesic activity. (A) along with
XX nucleic acid (ABL88411-ABL88441) that encode proteins (B,
XX ABB85006-ABB85037) that interact with (A); (B); vectors containing the
XX nucleic acid; antibodies against (B); cells that express (B) and agents
XX that bind to (B), are all useful for treating pain, particularly chronic
XX pain, including use in gene therapy. The same materials can also be used
XX for diagnosis, e.g. of neurological and neurodegenerative diseases. The
XX present sequence is that of a PCR primer, used in examples of the
XX invention.

SQ Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1299


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AAD24491/c
ID AAD24491 standard; DNA; 14 BP.
XX
AC AAD24491;
XX
DT 07-MAR-2002 (first entry)
XX
DE Retinoid-regulated gene isolating poly(T) PCR primer #5.
XX
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.
XX
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.
XX
PR 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 2002-033254/04.
XX
PT New DNA fragments having promoter activity, useful in retinoid
PT metabolism, as well as in producing retinoic acid metabolizing
PT cytochrome P450s that are useful as targets for the treatment of
PT certain cancers -
XX
PS Disclosure; Column 13; 75pp; English.
XX
CC The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers
CC such as prostate cancer. The invention also relates to a method of
CC screening drugs for their effect on activity of RA inducible proteins.
CC The present DNA sequence is poly(T) PCR primer which is used for
CC isolating retinoid regulating genes by differential display of mRNAs.
CC Note: This sequence is incorrectly referred as SEQ ID NO: 6 in column
CC 14 of the specification.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1300
AAD24493/c
ID AAD24493 standard; DNA; 14 BP.
XX
AC AAD24493;
XX
DT 07-MAR-2002 (first entry)
XX
DE Retinoid-regulated gene isolating poly(T) PCR primer #7.
XX
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.
XX
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.
XX
PR 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 2002-033254/04.
XX
PT New DNA fragments having promoter activity, useful in retinoid
PT metabolism, as well as in producing retinoic acid metabolizing
PT cytochrome P450s that are useful as targets for the treatment of
PT certain cancers -
XX
PS Disclosure; Column 13; 75pp; English.
XX
CC The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers
CC such as prostate cancer. The invention also relates to a method of
CC screening drugs for their effect on activity of RA inducible proteins.
CC The present DNA sequence is poly(T) PCR primer which is used for
CC isolating retinoid regulating genes by differential display of mRNAs.
CC Note: This sequence is incorrectly referred as SEQ ID NO: 6 in column
CC 14 of the specification.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1300
AAD24491/c
ID AAD24491 standard; DNA; 14 BP.
XX
AC AAD24491;
XX
DT 07-MAR-2002 (first entry)
XX
DE Retinoid-regulated gene isolating poly(T) PCR primer #5.
XX
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.
XX
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.
XX
PR 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 2002-033254/04.
XX
PT New DNA fragments having promoter activity, useful in retinoid
PT metabolism, as well as in producing retinoic acid metabolizing
PT cytochrome P450s that are useful as targets for the treatment of
PT certain cancers -
XX
PS Disclosure; Column 13; 75pp; English.
XX
CC The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers
CC such as prostate cancer. The invention also relates to a method of
CC screening drugs for their effect on activity of RA inducible proteins.
CC The present DNA sequence is poly(T) PCR primer which is used for
CC isolating retinoid regulating genes by differential display of mRNAs.
CC Note: This sequence is incorrectly referred as SEQ ID NO: 6 in column
CC 14 of the specification.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1301
AAD24494/c
ID AAD24494 standard; DNA; 14 BP.
XX
AC AAD24494;
XX
DT 07-MAR-2002 (first entry)
XX
DE Retinoid-regulated gene isolating poly(T) PCR primer #8.
XX
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.
XX
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.

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KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.
XX
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.
XX
PR 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 2002-033254/04.
XX
PT New DNA fragments having promoter activity, useful in retinoid
PT metabolism, as well as in producing retinoic acid metabolizing
PT cytochrome P450s that are useful as targets for the treatment of
PT certain cancers -
XX
PS Disclosure; Column 13; 75pp; English.
XX
CC The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers
CC such as prostate cancer. The invention also relates to a method of
CC screening drugs for their effect on activity of RA inducible proteins.
CC The present DNA sequence is poly(T) PCR primer which is used for
CC isolating retinoid regulating genes by differential display of mRNAs.
XX
SQ Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1095
DB 13 TAAAAAATAAAAAA 1

RESULT 1301
AAD24494/c
ID AAD24494 standard; DNA; 14 BP.
XX
AC AAD24494;
XX
DT 07-MAR-2002 (first entry)
XX
DE Retinoid-regulated gene isolating poly(T) PCR primer #8.
XX
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.
XX
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.

```

XX 21-JUN-1996; 96US-0667546.
 PR 01-OCT-1996; 96US-0724466.
 PR 23-JUN-1997; 97WO-CA00440.
 XX
 PA (TOOH) UNIV QUEENS KINGSTON.
 XX
 PI Petkovich PM, White JA, Beckett BR, Jones G;
 XX
 XX WPI; 2002-033254/04.
 DR
 XX New DNA fragments having promoter activity, useful in retinoid
 PT metabolism, as well as in producing retinoic acid metabolizing
 PT cytochrome P450s that are useful as targets for the treatment of
 PT certain cancers -
 XX
 XX Disclosure; Column 13; 75pp; English.
 XX
 CC The present invention relates to retinoid (e.g., retinoic acid (RA),
 CC vitamin A) metabolising proteins and nucleic acid sequences encoding
 CC them. RA metabolising proteins contain a haeme-binding motif which is
 CC characteristic of the group of proteins known as cytochrome P450s. The
 CC sequences of the invention are useful in retinoid metabolism and in
 CC producing retinoic acid metabolising cytochrome P450s. They are
 CC particularly useful as targets for the treatment of certain cancers
 CC such as prostate cancer. The invention also relates to a method of
 CC screening drugs for their effect on activity of RA inducible proteins.
 CC The present DNA sequence is poly(T) PCR primer which is used for
 CC isolating retinoid regulating genes by differential display of mRNAs.
 XX
 XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1095
 Db 13 TAAAAAATAAAAAA 1
 RESULT 1302
 AAS99698/C
 ID RAS99698 standard; DNA; 14 BP.
 XX
 AC RAS99698;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Breast tumour-specific cDNA B18Ag1, RT-PCR primer.
 XX
 KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
 KW tumour; vaccine; immunogenic.
 XX
 OS Homo sapiens.
 XX
 PN WO200190152-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-US16776.
 XX
 PR 24-MAY-2000; 2000US-0577505.
 PR 08-JUN-2000; 2000US-0590583.
 PR 26-OCT-2000; 2000US-0699295.
 PR 16-MAR-2001; 2001US-0810936.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 PI Wang A, Skeiky YAW, Harlocker SL, Day CH;
 XX
 XX WPI; 2002-089919/12.

XX New breast tumour proteins and polynucleotides encoding them, useful for
 PT treating and/or preventing cancer, particularly breast cancer, and for
 PT eliciting humoral and/or cellular immune response -
 XX
 XX Example 1; Page 93; 245pp; English.
 XX
 CC The invention relates to novel breast tumour polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response.
 CC particularly humoral and/or cellular immune response. The polynucleotides
 CC may be used as probes or primers for nucleic acid hybridisation, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
 CC represent novel human breast cancer protein coding sequences and
 CC PCR primers of the invention.
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1095
 Db 13 TAAAAAATAAAAAA 1
 RESULT 1303
 ABX79769/C
 ID ABX79769 standard; cDNA; 14 BP.
 XX
 AC ABX79769;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #94.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-0475947.
 XX
 PR 31-DEC-1999; 99US-0475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 XX WPI; 2003-208818/20.
 DR
 XX Identifying a candidate polymorphic repeat within a coding sequence,
 PT for understanding or treating genetic disease, comprises detecting
 PT tandem repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability -
 XX
 XX Examples; Column 343; 588pp; English.
 PS
 XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring

CC angiogenesis, particularly retinopathy, rheumatoid arthritis, Crohn's
CC disease, atherosclerosis, ovarian hyperstimulation, psoriasis,
CC endometriosis, restenosis after balloon angioplasty, overproduction of
CC tissue during wound healing, peripheral vascular diseases, hypertension,
CC vascular inflammation, Raynaud disease, aneurysm, arterial restenosis,
CC thrombophlebitis, lymphagitis, lymphodema, ischemia, angina, myocardial
CC infarction, chronic heart disease, (congestive) cardiac insufficiency,
CC age-related macular degeneration and osteoporosis. It is also used to
CC prevent cell multiplication, especially as antitumor agents, and as
CC research reagents for in vitro or in vivo studies on signalling pathways.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

```
Query Match      1.2%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 13 TAAAAAAAAAAAAA 1

RESULT 1305
AAT52132/c
ID AAT52132 standard; RNA; 15 BP.

KW human immunodeficiency virus; acquired immune deficiency syndrome;
KW AIDS: ss.

XX Homo sapiens.

XX
PN WO9523225-A2.XX
PD 31-ATTG-1995XX
PF 23-FEB-1995.

XX
FF
93 FEB-1993; 93MO-TB00158.

PR 30-JAN-1995;
PR 23-FEB-1994;

PR 29-MAR-1994;
PR 04-APR-1994;

PR 04-APR-1994;
PR 07-APR-1994;

PR 15-APR-1994; 94US-0227958.
PR 15-APR-1994; 94US-0228041

PR 15-AUG-1994;
PR 16-AUG-1994;

94US-02914433
94US-0292620.
94US-0292620.
94US-0293520.
94US-0293520.
94US-0300000.
94US-0303039.
94US-0311486.
94US-0311749.
94US-0314397.
94US-0316771.
94US-0319492.
94US-0319492.

PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX PT Ribozymes having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX PS Claim 2; Page 175; 407pp; English.
 CC The present sequence represents a preferred target sequence for
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and
 CC thereby inhibit ICAM-1 expression, making them useful for reducing
 CC transplant rejection and alleviating symptoms in patients with
 CC rheumatoid arthritis, asthma and other inflammatory disorders.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 15 BP; 1 A; 0 C; 1 G; 13 U; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1096
 Db |||||
 15 AAAAAAAAAAAAAA 3
 RESULT 1306
 AAX18364/C
 ID AAX18364 standard; DNA; 15 BP.
 XX AC AAX18364;
 XX DT 11-MAY-1999 (first entry)
 XX DE RT-PCR primer of the invention SEQ ID 5.
 XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX OS Synthetic.
 XX PN JP11032765-A.
 XX PD 09-FEB-1999.
 XX PF 18-JUL-1997; 97JP-0208312.
 XX PR 18-JUL-1997; 97JP-0208312.
 XX PA (TAKI) TAKARA SHUZO CO LTD.
 XX DR WPI; 1999-183822/16.
 XX PT Peptides having at least two new nucleotides - useful as primers in

PT RT-PCR
 XX Disclosure; Page 10; 19pp; Japanese.
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = a natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
 CC guanine and/or cytosine. The new nucleotides are useful as primers for
 CC RT-PCR and determination of base sequences. The new sequences allow for
 CC reproductive and highly efficient analysis of gene sequences.
 XX SQ Sequence 15 BP; 0 A; 0 C; 2 G; 13 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1096
 Db |||||
 13 AAAAAAAAAAAAAA 1
 RESULT 1307
 AAX18361/C
 ID AAX18361 standard; DNA; 15 BP.
 XX AC AAX18361;
 XX DT 11-MAY-1999 (first entry)
 XX DE RT-PCR primer of the invention SEQ ID 2.
 XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX OS Synthetic.
 XX PN JP11032765-A.
 XX PD 09-FEB-1999.
 XX PF 18-JUL-1997; 97JP-0208312.
 XX PR 18-JUL-1997; 97JP-0208312.
 XX PA (TAKI) TAKARA SHUZO CO LTD.
 XX DR WPI; 1999-183822/16.
 XX PT Peptides having at least two new nucleotides - useful as primers in
 XX OS RT-PCR
 XX Disclosure; Page 10; 19pp; Japanese.
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = a natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
 CC guanine and/or cytosine. The new nucleotides are useful as primers for
 CC RT-PCR and determination of base sequences. The new sequences allow for
 CC reproductive and highly efficient analysis of gene sequences.
 XX SQ Sequence 15 BP; 0 A; 2 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAA 1096
| | | | | | | | | | | | | | | | |
DB 13 AAAAAAAAAAAAA 1

RESULT 1308
AAZ62807/c
ID AAZ62807 standard; RNA; 15 BP.
XX
AC AAZ62807;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV-7901 which cleaves HCV RNA at nt. 7901.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US09027.
XX
PR 27-APR-1998; 98US-0083217.
PR 18-SEP-1998; 98US-0100842.
PR 25-FEB-1999; 99US-0257608.
PR 23-MAR-1999; 99US-0274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection -
XX
PS Claim 1; Page 64; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given
CC in the descriptor line.
CC The HCV sequence was screened for optimal ribozyme target sites using
CC a computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases.
CC The ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer.
XX
SQ Sequence 15 BP; 4 A; 2 C; 3 G; 6 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 CATAGCCAAATTT 722
| | | | | | | | | | | | | | | | |
DB 13 CATAGCCAAATTT 722

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 772 TGGAGAGAGAGTG 784
| | | | | | | | | | | | | | | | |
DB 13 TGGAGAGAGAGTG 1

RESULT 1310
AAZ64410/c
ID AAZ64410 standard; RNA; 15 BP.
XX
AC AAZ64410;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8887.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US09027.
XX
PR 27-APR-1998; 98US-0083217.
PR 18-SEP-1998; 98US-0100842.
PR 25-FEB-1999; 99US-0257608.
PR 23-MAR-1999; 99US-0274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection -
XX
PS Claim 1; Page 91; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given
CC in the descriptor line.
CC The HCV sequence was screened for optimal ribozyme target sites using
CC a computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases.
CC The ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer.
XX
SQ Sequence 15 BP; 2 A; 7 C; 0 G; 6 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 772 TGGAGAGAGAGTG 784
| | | | | | | | | | | | | | | | |
DB 13 TGGAGAGAGAGTG 1

RESULT 1310
AAZ64410/c
ID AAZ64410 standard; RNA; 15 BP.
XX

AC AAF69537;
 XX 18-APR-2001 (first entry)
 DT
 XX Human IL4Ralpha gene probe #177.
 DE
 XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
 KW allergic disease; probe; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200104270-A1.
 PN
 XX 18-JAN-2001.
 PD
 XX 13-JUL-2000; 2000WO-US19094.
 PF
 XX 13-JUL-1999; 99US-0143435.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
 PI Windemuth AK;
 PI
 XX WPI; 2001-103078/11.
 DR
 XX
 XX New isolated polynucleotide useful for the identification of
 PT therapeutics in allergic diseases is new -
 PT
 XX Claim 15; Page 45; 18pp; English.
 PS
 XX The present invention relates to polymorphisms of the human interleukin 4
 CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
 CC sequence). Polynucleotides comprising polymorphic gene variants are
 CC useful for therapeutic purposes. For example, where a patient may benefit
 CC from expression of a particular IL4Ralpha protein isoform, an expression
 CC vector encoding the isoform may be administered to the patient. It may
 CC desirable to decrease or block expression of a particular IL4Ralpha
 CC isogene, which may be done by turning off by transforming a targeted
 CC organ, tissue or cell population with an expression vector that expresses
 CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
 CC identified by these methods may be useful for allergic diseases. The
 CC present sequence is a probe for human IL4R-alpha.
 XX
 SQ Sequence 15 BP; 2 A; 8 C; 4 G; 1 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 143 GGGGGCTGCAGCT 155
 DB |||||
 14 GGGGGCTGCAGCT 2
 RESULT 1311
 AAF53329/c
 ID AAF53329 standard; DNA; 15 BP.
 XX
 AC AAF53329;
 XX
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #4289.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 XX WO200078341-A1.
 XX
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU00693.
 PF
 XX 21-JUN-1999; 99US-0140345.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX
 XX Example 8; Page 88; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX
 SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 322 GCAGAGAGAGCTCT 334
 DB |||||
 15 GCAGAGAGAGCTCT 3
 RESULT 1312
 AAF53334/c
 ID AAF53334 standard; DNA; 15 BP.
 XX
 AC AAF53334;
 XX
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #4294.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200078341-A1.

XX PD 28-DEC-2000.

XX PA 21-JUN-2000; 2000WO-AU00693.

XX PF (ROBE) ROBERTS B.

XX PR (PVC) PAVCO P A.

XX XX (MURD-) MURDOCH CHILDRENS RES INST.

XX PA Wraight CJ, Werther GA, Edmondson SR;

XX PI WPI; 2001-041421/05.

XX DR Ameliorating the effects of a disorder, e.g. psoriasis, by

XX XX administering UV (ultra-violet) treatment (optional) and an antisense

XX PT nucleic acid that inhibits or reduces growth factor mediated cell

XX PT proliferation and/or inflammation -

XX XX Example 8; Page 89; 201pp; English.

XX PS The present invention relates to a method for ameliorating the effects

XX CC of skin disorders. The method comprises contacting the skin with an

XX CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1

XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

XX CC inhibiting or reducing growth factor mediated cell proliferation,

XX CC inflammation and/or other disorders. The present sequence is an

XX CC oligonucleotide which can be used to design the antisense

XX CC oligonucleotides of the present invention (see AAF45151 and

XX CC AAF5153-F45161). The method is useful for ameliorating the effects of

XX CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids,

XX CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the

XX CC skin, a hyperneovascular condition such as a neovascular condition of the

XX CC retina, brain or skin, growth factor-mediated malignancies, other

XX CC sclerotic disease, kidney disease, hyperproliferation of the inside of

XX CC blood vessels or any other hyperplasia.

XX SQ Sequence 15 BP; 3 A; 4 C; 3 G; 5 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 ACTGCAGAGAGC 331

DB 13 ACTGCAGAGAGC 1

RESULT 1313

ABX00658/c

ID ABX00658 standard; RNA; 15 BP.

XX AC ABX00658;

XX DT 23-DEC-2002 (first entry)

XX DE Hepatitis C virus substrate #440 for HCV hammerhead ribozyme #440.

XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;

XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;

XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;

XX KW type I interferon; interferon alpha; interferon beta; cytosstatic;

XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;

XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX OS Hepatitis C virus.

XX PN US2002082225-A1.

XX XX 27-JUN-2002.

XX PD 23-MAR-1999; 99US-0274553.

XX PF 23-MAR-1999; 99US-0274553.

XX PR 23-MAR-1999; 99US-0274553.

XX (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PF (ROBE) ROBERTS B.

XX PA (PVC) PAVCO P A.

XX XX (MACE/) MACEJACK D.

XX PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;

XX DR WPI; 2002-617759/66.

XX XX New ribozymes targeting RNA derived from hepatitis C virus inhibit

XX PT viral replication and are useful to treat hepatitis C virus infections

XX PT and cirrhosis, liver failure or hepatocellular carcinoma -

XX PS Claim 1; Page 33; 80pp; English.

XX XX The present invention relates to enzymatic nucleic acids which

XX CC specifically cleave RNA derived from Hepatitis C virus (HCV). The

XX CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or

XX CC hairpin (HP) motif where the binding arms comprise sequences

XX CC complementary to one of the substrate sequences defined in the

XX CC specification. The HCV ribozymes are useful for modulating the

XX CC expression and/or replication of HCV. They can be used to treat

XX CC cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV

XX CC ribozymes are also useful for treating a condition associated with

XX CC HCV infection in conjunction with one or more other drug therapies,

XX CC particularly type I interferon, especially interferon alpha, beta or

XX CC gamma or consensus interferon. The present sequence represents a

XX CC substrate for a HCV hammerhead (HH) ribozyme.

XX CC Note: Some of the sequence data for this patent did not form part of

XX CC the printed specification. The complete sequence data for this patent

XX CC was obtained in electronic format directly from the USPTO web site

XX CC at segdata.uspto.gov/psipsideEntry.html.

XX SQ Sequence 15 BP; 4 A; 2 C; 3 G; 6 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 CATAGCCCAATTT 722

DB 15 CATAGCCCAATTT 3

RESULT 1314

ABX01463/c

ID ABX01463 standard; RNA; 15 BP.

XX AC ABX01463;

XX DT 23-DEC-2002 (first entry)

XX DE Hepatitis C virus substrate #1245 for HCV hammerhead ribozyme #1245.

XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;

XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;

XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;

XX KW type I interferon; interferon alpha; interferon beta; cytosstatic;

XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;

XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX OS Hepatitis C virus.

XX PN US2002082225-A1.

XX XX 27-JUN-2002.

XX PD 23-MAR-1999; 99US-0274553.

XX PF 23-MAR-1999; 99US-0274553.

XX PR 23-MAR-1999; 99US-0274553.

XX Human; 3-hydroxy-3-methylglutaryl coenzyme A lyase; HMGCL; primer; ss;
KW single nucleotide polymorphism; SNP; haplotyping; genotyping; ASO.
XX
OS Homo sapiens.
XX WO200198315-A2.
FN 27-DEC-2001.
XX
PD 20-JUN-2001; 2001WO-US19834.
PF 20-JUN-2000; 2000US-212782P.
PR (GENA-) GENAISSANCE PHARM INC.
XX Duda A, Kliem SE, Koshy B, Parks KE;
XX WPI; 2002-130786/17.
DR Novel genetic variants of 3-hydroxy-3-methylglutaryl coenzyme A lyase
XX useful in screening drugs to treat disease associated with the protein
PT e.g. 3-hydroxy-3-methylglutaryl coenzyme A deficiency -
PT Claim 17; Page 13; 84pp; English.
PS The present invention relates to a new polynucleotide having a sequence
XX comprising a 3-hydroxy-3-methylglutaryl coenzyme A lyase (HMGCL) isogene,
CC selected from 6 isogenes, and defined by a corresponding set of
CC polymorphisms whose locations and identities are given in the
CC specification. The method of the invention is useful for haplotyping the
CC HMGCL gene in an individual and in design of clinical trials of
CC candidate drugs for treating a specific condition or disease
CC predicted to be associated with HMGCL activity and is useful for
CC genotyping HMGCL gene of an individual. The method of the invention
CC is also useful for identifying an association between a trait and at
CC least one haplotype or haplotype pair of HMGCL gene. ASO is useful as
CC probes and primers and for assaying a polymorphism in the target region.
CC The invention is useful for genotyping and/or haplotyping the HMGCL gene
CC in an individual. Without requiring any prior knowledge of the
CC phenotypic effect of any particular HMGCL haplotype or haplotype pair,
CC the method of the invention provides the scientist with a tool to
CC identify lead compounds that are more likely to show efficacy in clinical
CC trials. The present nucleic acid sequence represents one of a collection
CC of ASO primers (ABK14046-ABK14050 and ABK14427-ABK14433) that were used
CC in the invention to detect polymorphisms in the human HMGCL gene.
XX
SQ Sequence 15 BP; 3 A; 6 C; 2 G; 3 T; 1 other;
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 953 ACAGCTGGGCGAGGT 967
DB 15 ATATCTGGCGAGGT 1
RESULT 1317
AAD26137/c
ID AAD26137 standard; DNA; 15 BP.
XX
AC AAD26137;
XX
DT 26-MAR-2002 (first entry)
XX Human endothelin 2 (EDN2) gene polymorphism detecting ASO primer #10.
DE Human; endothelin 2; EDN2; polymorphic site; PS; therapy; hypertension;
XX drug screening; cardiovascular disorder; renal insufficiency; ASO;
KW allele specific oligonucleotide; cerebroprotective; polymorphism;
KW hypotensive; cerebrovascular condition; primer; ss.
PF
XX

OS Homo sapiens.
XX WO200190118-A2.
FN 29-NOV-2001.
XX
PD 21-MAY-2001; 2001WO-US16433.
PF 19-MAY-2000; 2000US-205761P.
PR (GENA-) GENAISSANCE PHARM INC.
XX Kazemi A, Koshy B, Tanguay DA;
XX WPI; 2002-083075/11.
DR New human endothelin 2 (EDN2) polymorphic variants and encoding genes,
XX useful in expressing EDN2 protein for screening candidate drugs to
PT treat diseases related to EDN2 activity -
PT Claim 16; Page 14; 91pp; English.
PS The invention relates to genetic variants of human endothelin 2 (EDN2)
XX gene. EDN2 gene contains 17 polymorphic sites PS1-PS17. The polymorphic
CC variants are useful in studying the expression and function of EDN2,
CC in expressing EDN2 protein for use in screening for candidate drugs to
CC treat diseases related to EDN2 activity, in studying the effect of the
CC variation on the biological activity of EDN2, and the binding affinity
CC of candidate drugs targeting EDN2 for the treatment of hypertension,
CC cardiovascular disorders, renal insufficiency and cerebrovascular
CC conditions. The haplotyping methods are useful in validating EDN2 as
CC a candidate target for treating a specific condition or disease
CC predicted to be associated with EDN2 activity, or in the design of
CC clinical trials of candidate drugs for treating a specific condition
CC or disease associated with EDN2 activity. Allele specific
CC oligonucleotides (ASO) are used as probes and primers, and for
CC detecting polymorphism in EDN2 gene. The present sequence is an
XX ASO primer used to detect polymorphism in human EDN2 gene.
SQ Sequence 15 BP; 3 A; 2 C; 8 G; 1 T; 1 other;
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 399 CACACCTGCTCCAG 413
DB 15 CRCTCCTGCTCCAG 1
RESULT 1318
ABK09399/c
ID ABK09399 standard; DNA; 15 BP.
XX
AC ABK09399;
XX
DT 14-MAR-2002 (first entry)
XX Human NPR1 gene allele-specific oligonucleotide sequencing primer #21.
DE Human; natriuretic peptide receptor A/quanlylate cyclase A; NPR1; ss;
XX atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
KW haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
KW drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
OS Homo sapiens.
XX WO200179231-A2.
FN 25-OCT-2001.
PD 16-APR-2001; 2001WO-US12300.
PF
XX

PR 14-APR-2000; 2000US-197330P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Bentivegna SC, Choi JY, Kliem SE, Nandabalan K;
XX WPI; 2002-066340/09.
XX Genotyping human natriuretic peptide receptor A/guanylate cyclase gene
XX of an individual, involves determining identity of nucleotide pair at
XX specific polymorphic sites for two copies of the gene -
XX
XX Claim 15; Page 14; 96pp; English.
XX The invention relates to single nucleotide polymorphisms in the gene
XX encoding the human natriuretic peptide receptor A/guanylate cyclase A
XX (atriuretic peptide receptor A) or NPRI polypeptide. A method for
XX haplotyping the NPRI gene in an individual comprises identifying the
XX nucleotide at one or more polymorphic sites and determining whether one
XX of the copies of the gene is defined by one of the NPRI haplotypes given
XX in the specification or whether both copies are defined by a haplotype
XX pair. This method is useful in genotyping, whereby all possible haplotype
XX pairs can be assigned to specific genotypes. An association between a
XX trait and a haplotype or haplotype pair of the NPRI gene can be
XX identified by comparing the frequency of the haplotype or haplotype pair
XX in a population exhibiting the trait with the frequency of the haplotype
XX or haplotype pair in a reference population, where a higher haplotype
XX frequency in the trait population indicates the trait is associated with
XX the haplotype or haplotype pair. NPRI and its corresponding DNA are used
XX for studying the expression and function of NPRI, for use in screening
XX for candidate drugs to treat diseases related to NPRI activity, such as
XX hypertension. The sequences are also useful for studying the effect of
XX variation on the biological activity of NPRI as well as on the binding
XX affinity of candidate drugs targeting NPRI. Sequences AAS9959-AAS9990
XX and ABK0930-ABK09462 represent probes, sequencing primers and PCR
XX primers used to detect NPRI gene polymorphisms.
SQ Sequence 15 BP; 1 A; 4 C; 5 G; 4 T; 1 other;
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 261 GACAGGACCACTTC 275
DB 15 GRCAGGACCACTAC 1
RESULT 1319
AAS95901/c
ID AAS95901 standard; DNA; 15 BP.
XX AAS95901;
XX
XX 26-FEB-2002 (first entry)
XX Human CALM1 gene allele-specific oligonucleotide #10.
XX Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
XX haplotyping; SCYA3; Alzheimer's disease; drug screening;
XX calcium-dependent signal transduction; PCR primer; ss.
XX Homo sapiens.
XX WO200179218-A2.
XX
XX 25-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US11509.
XX
XX 12-APR-2000; 2000US-196340P.
XX (GENA-) GENAISSANCE PHARM INC.
PA

XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
XX WPI; 2002-049190/06.
XX New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
XX expressing CALM1 protein for use in screening for candidate drugs to
XX treat diseases related to CALM1 activity such as Alzheimer's disease -
XX
XX Claim 15; Page 13; 82pp; English.
XX The invention relates to an isolated polynucleotide comprising a
XX sequence selected from a polymorphic variant of calmodulin 1 (CALM1).
XX The polymorphic variant comprises an CALM1 isogene defined by a
XX haplotype selected from haplotypes 1-21 given in the specification.
XX The polymorphisms are useful for studying the biological function of
XX CALM1 as well as in identifying drugs targeting this protein for the
XX treatment of a disorder related to its abnormal expression or function.
XX The polymorphic variants may also be used in screening for compounds
XX targeting CALM1 to treat a specific condition or disease predicted to
XX be associated with CALM1 activity. Establishing CALM1 haplotype or
XX haplotype pair of an individual is useful for improving the efficiency
XX and reliability of several steps in the discovery and development of
XX drugs for treating diseases associated with SCYA3 activity, e.g.
XX Alzheimer's disease and diseases involving defects in calcium-dependent
XX signal transduction. Haplotyping the CALM1 gene in an individual is
XX also useful in the design of clinical trials of candidate drugs for
XX treating a specific condition or disease predicted to be associated
XX with CALM1 activity. AAS95892-AAS96018 represent human CALM1 allele-
XX specific oligonucleotides and PCR primers of the invention.
SQ Sequence 15 BP; 2 A; 2 C; 10 G; 0 U; 1 other;
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 420 CTCGGCTGCCCTT 434
DB 15 CTCGGCTGCCCTT 1
RESULT 1320
ABK30004/c
ID ABK30004 standard; DNA; 15 BP.
XX
XX AC ABK30004;
XX
XX 23-APR-2002 (first entry)
XX Hepatitis B virus preS1 promoter domain 5 mutant.
XX
XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
XX HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
XX vanH promoter; androgen receptor promoter; AR promoter;
XX human epidermal growth factor receptor 2 promoter; her2 promoter;
XX beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
XX colon cancer; immunological disorder; prostate cancer; cytostatic;
XX autoimmune disease; HBV pre-S promoter; HBV-X promoter;
XX Enterococcus infection; immunosuppressive; antibacterial; antiviral;
XX gene expression modulator; multiple sclerosis; MS;
XX chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
XX systemic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
XX familial adenomatous polyposis; rheumatoid arthritis; PCR, primer;
XX mutant; transgenic; ds.
XX
XX Hepatitis B virus.
XX
XX WO200194600-A2.
XX
XX 13-DEC-2001.
XX
XX 06-JUN-2001; 2001WO-US18343.
XX PF


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PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 146; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
XX Sequence 17 BP; 4 A; 3 C; 7 G; 3 U; 0 other;
XX
XX Query Match 1.2%; Score 13; DB 1; Length 17;
XX Best Local Similarity 84.6%; Pred. No. 8.6e+02;
XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 49 GCGGTTAAGGCT 61
XX 3 GCGGUAAGGCU 15
XX
XX RESULT 1323
XX AAX69797/c
XX ID AAX69797 standard; RNA; 17 BP.
XX AC AAX69797;
XX
XX DT 28-JUL-1999 (first entry)
XX
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1092.
XX
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9715662-A2.
XX
XX PD 01-MAY-1997.
XX
XX PF 25-OCT-1996; 96WO-US17480.
XX
XX PR 11-JAN-1996; 96US-0584040.
XX
XX PR 26-OCT-1995; 95US-0005974.
XX
XX PA (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate

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CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
XX Sequence 17 BP; 1 A; 2 C; 0 G; 14 U; 0 other;
XX
XX Query Match 1.2%; Score 13; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 8.6e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAA 1096
XX 17 AAAAAAAAAA 5
XX
XX RESULT 1324
XX AAX69427/c
XX ID AAX69427 standard; RNA; 17 BP.
XX AC AAX69427;
XX
XX DT 28-JUL-1999 (first entry)
XX
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #722.
XX
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9715662-A2.
XX
XX PD 01-MAY-1997.
XX
XX PF 25-OCT-1996; 96WO-US17480.
XX
XX PR 11-JAN-1996; 96US-0584040.
XX
XX PR 26-OCT-1995; 95US-0005974.
XX
XX PA (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 68; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
XX Sequence 17 BP; 4 A; 0 C; 3 G; 10 U; 0 other;
XX

```

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 ACTATTAAAAAA 1090
|||||
Db 17 ACTATTAAAAAA 5

RESULT 1325
AAX69428/c
ID AAX69428 standard; RNA; 17 BP.
XX
AC AAX69428;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #723.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 68; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 4 A; 0 C; 3 G; 10 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 ACTATTAAAAAA 1090
|||||
Db 16 ACTATTAAAAAA 4

RESULT 1326

AAX69429/c
ID AAX69429 standard; RNA; 17 BP.
XX
AC AAX69429;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #724.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 68; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 4 A; 1 C; 3 G; 9 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 ACTATTAAAAAA 1090
|||||
Db 15 ACTATTAAAAAA 3

RESULT 1327
AAX69430/c
ID AAX69430 standard; RNA; 17 BP.
XX
AC AAX69430;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #725.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 XX foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 FN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 XX 25-OCT-1996; 96WO-US17480.
 XX
 PR 11-JAN-1996; 96US-0584040.
 PR 26-OCT-1995; 95US-0005974.
 XX
 PA (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX WPI; 1997-259017/23.
 DR
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PS Claim 4; Page 68; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 XX Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1078 ACTATTAAAAAA 1090
 Db 14 ACTATTAAAAAA 2
 RESULT 1328
 AAA23035
 ID AAA23035 standard; RNA; 17 BP.
 XX
 AC AAA23035;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6261.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9950403-A2.

XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US06507.
 PF
 XX 27-MAR-1998; 98US-0079678.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 PT
 XX Claim 54; Page 258; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23442 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 XX Sequence 17 BP; 3 A; 2 C; 7 G; 5 U; 0 other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 17;
 Best Local Similarity 61.5%; Pred. No. 8.6e+02;
 Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 134 GTCGCTTGGGG 146
 Db 2 GUCUGCUUGGG 14
 RESULT 1329
 AAA23036
 ID AAA23036 standard; RNA; 17 BP.
 XX
 AC AAA23036;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6262.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;


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XX DR WPI; 2002-643480/69.
XX PT Identifying hematopoietic stem cells, by targeting two reporter DNAs
XX PT into different genomic loci of hematopoietic cells to produce
XX PT targeted cell population, and selecting cells under specific survival
XX PT conditions -
XX PS Disclosure; Fig 4; 36pp; English.
XX CC This invention relates to a novel method for identifying haematopoietic
XX CC stem cells (HSCs) involving targeting two different reporter DNAs into
XX CC different functionally important genomic loci of HSCs such that reporter
XX CC DNA (RD) expression is driven by genomic locus promoter into which RD
XX CC is targeted, to produce a population of successfully targeted HSCs and
XX CC other cells and subjecting that population to conditions so that HSCs
XX CC survive and other cells do not. The method of the invention is useful
XX CC for identifying HSCs and for exploring, for e.g., the conditions to
XX CC expand HSCs in vitro, and to identify signal molecules that control HSC
XX CC self-renewal and lineage commitment, which may provide improvements in
XX CC current bone marrow transplantation and leukemia therapy. The present
XX CC sequence represents an intermediate product shown in an example of
XX CC a DNA amplification method shown in the specification.
XX SQ Sequence 17 BP; 0 A; 0 C; 3 G; 13 T; 1 other;
Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1096
DB 17 AAAAAAAAAAAAAA 5
RESULT 1332
ABN01766
ID ABN01766 standard; DNA; 17 BP.
XX AC ABN01766;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1758.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX FN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 05-FEB-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.
XX XX
PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX DR WPI; 2002-179446/23.
XX XX
XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1
XX PT proteins, or as specific biomolecule capture probes for
XX PT surface-enhanced laser desorption/ionization, comprises human
XX PT myosin-like protein hGDMPLP-1 -
XX PS Disclosure; SEQ ID 1758; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
XX CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
XX CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
XX CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
XX CC substrates, to provide initial substrates for the recombinant engineering
XX CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
XX CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
XX CC be used as immunogens to raise antibodies that specifically recognise
XX CC hGDMPLP-1 proteins, as standards in assays used to determine the
XX CC concentration and/or amount specifically of hGDMPLP proteins, as specific
XX CC biomolecule capture probes for surface-enhanced laser desorption
XX CC ionisation, as therapeutic supplement in patients having specific
XX CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
XX CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
XX CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
XX CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
XX CC chromosome 22. The present sequence represents an oligomer used in the
XX CC screening of the hGDMPLP-1 sequence in the exemplification of the present
XX CC invention.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence.
XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 other;
Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 CTAAGGCCAGATG 453
DB 5 CTAAGGCCAGATG 17
RESULT 1333
ABN01767
ID ABN01767 standard; DNA; 17 BP.
XX AC ABN01767;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1759.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX FN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 05-FEB-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.
XX XX
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PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 1759; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 other;
SQ Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 CTAAGCCAGATG 453
DB 4 CTAAGCCAGATG 16
RESULT 1334
ABN01768
ID ABN01768 standard; DNA; 17 BP.
XX AC ABN01768;
XX 29-MAY-2002 (first entry)
DT Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1760.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW

XX skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
XX WO2001192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US16981.
XX 26-MAY-2000; 2000US-207456P.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 05-FEB-2001; 2001US-266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 1760; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 other;
SQ Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 CTAAGCCAGATG 453
DB 3 CTAAGCCAGATG 15

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 441 CTAAGCCAGATG 453
 Db 2 CTAAGCCAGATG 14
 RESULT 1336
 ABN01769
 ID ABN01769 standard; DNA; 17 BP.
 XX
 AC ABN01769;
 XX 29-MAY-2002 (first entry)
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1761.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US16981.
 XX
 PR 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234587P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 05-FEB-2001; 2001US-266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX
 PS Disclosure; SEQ ID 1761; 214pp; English.
 CC
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1 in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 441 CTAAGCCAGATG 453
 Db 2 CTAAGCCAGATG 14
 RESULT 1336
 ABN01770
 ID ABN01770 standard; DNA; 17 BP.
 XX
 AC ABN01770;
 XX 29-MAY-2002 (first entry)
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1762.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US16981.
 XX
 PR 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234587P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 05-FEB-2001; 2001US-266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX
 PS Disclosure; SEQ ID 1761; 214pp; English.
 CC
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1 in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed

CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequence.

XX SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 CTAAGCCAGATG 453
 Db 1 CTAAGCCAGATG 13

RESULT 1337
 ABT35698/c
 ID ABT35698 standard; DNA; 17 BP.

XX AC ABT35698;

XX DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 1335.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW anisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB04208.

XX PR 17-SEP-2001; 2001FR-0011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -

XX PS Disclosure; Page 189; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,

CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.

XX SQ Sequence 17 BP; 2 A; 2 C; 8 G; 5 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 395 CACACACACCTG 407
 Db 17 CACACACACCTG 5

RESULT 1338

ABT36389

ID ABT36389 standard; DNA; 17 BP.

XX AC ABT36389;

XX DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 2026.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW anisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB04208.

XX PR 17-SEP-2001; 2001FR-0011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -

XX PS Disclosure; Page 269; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the

CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 5 A; 1 C; 5 G; 6 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 TCAGAAAGTTGTT 286
DB 3 TCAGAAAGTTGTT 15

RESULT 1339

AAQ23988/c
ID AAQ23988 standard; DNA; 18 BP.

XX AC AAQ23988;
DT 26-OCT-1992 (first entry)
XX VP-1/VP-2 gene primer (4).
DE VP-1; VP-2; parvo; virus; antigen; diagnosis; ss.
KW Human parvovirus.

OS
XX JP0408985-A.
XX 23-MAR-1992.

XX 31-JUL-1990; 90JP-0202827.
XX 31-JUL-1990; 90JP-0202827.

XX (MITU) MITSUBISHI KASEI CORP.
XX WPI; 1992-147290/18.

XX Human parvovirus structural protein VP-1 and VP-2 genes - and
PT recombinant antigen useful for the diagnosis of infectious
PT erythema virus

XX Disclosure; Fig 1; 7pp; Japanese.

XX The primers represented in AAQ23985-90 are used in PCR for the
CC amplification of human parvovirus VP-1 and VP-2 gene fragments.
CC Human parvovirus VP-1 gene has the partial base sequence given in
CC AAQ23980-82. Human parvovirus VP-2 gene has the partial base sequence
CC given in AAQ23981-82. The gene can be used to prepare a recombinant
CC antigen which can be used for the diagnosis of parvovirus infection
CC by radio-immunoassay and enzyme immunoassay.

XX Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1032 CTGGCTTTCATAG 1044
DB 13 CTGGCTTTCATAG 1

RESULT 1340
AAQ90149
ID AAQ90149 standard; cDNA; 18 BP.

XX AC AAQ90149;

XX DT 21-JAN-1996 (first entry)

XX Human prostaglandin E3 receptor splice variant sense DNA primer.

XX KW Prostaglandin E3 receptor; hormone; therapy; ss.

XX OS Synthetic.

XX FN WO9514090-A1.

XX PD 26-MAY-1995.

XX PF 17-NOV-1994; 94WO-US13383.

XX PR 19-NOV-1993; 93US-0155005.

XX PA (ALLR) ALLERGAN INC.

XX PA (UYAR-) UNIV ARIZONA.

XX PI Gil DW, Regan JW;

XX DR WPI; 1995-200380/26.

XX DNA encoding human prostaglandin EP3 receptor - for use in screening
PT for agonist and antagonist compound(s) for possible pharmaceutical
PT application

XX PS Disclosure; page 27; 45pp; English.

XX CC This sense primer is common to all human EP3 clones. It was used
CC in a PCR to clone splice variants of the EP3 receptor, in
CC conjunction with antisense primers specific to the unique 3'-
CC untranslated regions of the clones.

XX SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 CGCTGACAGTCAC 185
DB 4 CGCTGACAGTCAC 16

RESULT 1341

AAV45778
ID AAV45778 standard; DNA; 18 BP.

XX AC AAV45778;

XX DT 24-DEC-1998 (first entry)

XX DE Target probe 8.

XX KW Probe; capture probe; microorganic monitoring; multiple point mutation;
XX genotyping; ss.

XX OS Synthetic.

XX PN WO9829736-A1.

XX PD 09-JUL-1998.

XX PF 31-DEC-1997; 97WO-US24098.

```
PR 31-DEC-1996; 96US-0034627.
XX (GENO-) GENOMETRIX INC.
XX Balch WJ, Eggers WD, Hogan ME, Mendoza LG;
XX WPI; 1998-388276/33.
XX
XX Reaction substrates for multiplexed micro:assay(s) between analyte
XX and binder - has probes attached to array of sites on surface,
XX useful for, e.g. diagnosis and drug screening
XX
XX Disclosure; Page 36; 100pp; English.
XX
XX Sequences AAV45771-V45786 are target probes designed and constructed to
XX bind to the capture probes (AAV45755-V45770). Each of the target probes
XX binds to only one element of the capture probe set, thus a mixture of
XX these can be added to a capture probe array. They can be used in the
XX method of the invention in the following areas: diagnosis, drug
XX screening, analysis of gene expression, cell sorting and microorganic
XX monitoring, analysis of multiple point mutations and genotyping.
XX
XX Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 other;
SQ
XX
XX Query Match 1.2%; Score 13; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 949 GTCACACGCTGGG 961
XX |||||
XX DB 3 GTCACACGCTGGG 15
XX
XX RESULT 1342
XX AAF26667
XX ID AAF26667 standard; DNA; 18 BP.
XX AC AAF26667;
XX XX
XX DT 02-APR-2001 (first entry)
XX DE Human Smad7 phosphorothioate antisense oligonucleotide SEQ ID NO:10.
XX KW Human; Smad7; antisense oligonucleotide; phosphorothioate; inhibition;
XX KW antiinflammatory; cytostatic; infection; inflammation; tumour formation;
XX KW ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1.18
XX FT /*tag= a
XX FT /note= "phosphorothioate linkages"
XX
XX US6159697-A.
XX
XX 12-DEC-2000.
XX
XX 09-JAN-2000; 2000US-0487444.
XX
XX 09-JAN-2000; 2000US-0487444.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Cowser LM;
XX
XX WPI; 2001-070108/08.
XX
XX Antisense compound capable of inhibiting the expression of human Smad7,
XX useful for preventing or delaying infection, inflammation or tumor
XX formation -
XX Claim 1; Column 40; 33pp; English.
XX PS

XX The present invention describes an antisense compound (I) of up to 30
XX nucleobases in length capable of inhibiting the expression of human
XX Smad7. (I) has antiinflammatory and cytostatic, and is a modulator of
XX Smad7 expression. (I) can be useful for inhibiting the expression of
XX human Smad7 in human cells or tissues, in vitro. (I) is commonly used
XX as a research reagent and in diagnostics for example, to elucidate the
XX function of particular genes. (I) is also useful for distinguishing
XX between functions of various members of a biological pathway and for
XX research use. (I) is also utilised for diagnostics, therapeutics,
XX prophylaxis and in kits. (I) is also useful prophylactically, e.g. to
XX prevent or delay infection, inflammation or tumour formation. AAF26667
XX to AAF26706 represent human Smad7 antisense oligonucleotides from the
XX present invention.
XX
XX Sequence 18 BP; 1 A; 12 C; 3 G; 2 T; 0 other;
SQ
XX
XX Query Match 1.2%; Score 13; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 420 CTCGGGCTGCC 432
XX |||||
XX DB 1 CTCGGGCTGCC 13
XX
XX RESULT 1343
XX ABS52682/c
XX ID ABS52682 standard; DNA; 18 BP.
XX AC ABS52682;
XX XX
XX DT 15-NOV-2002 (first entry)
XX DE mRNA display splint oligonucleotide.
XX KW Translation; ss; splint; cell-free translation system; insulin;
XX KW growth hormone; erythropoietin; ribosome display; mRNA display.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200259293-A2.
XX
XX PD 01-AUG-2002.
XX
XX PF 25-JAN-2002; 2002WO-US02344.
XX
XX PR 25-JAN-2001; 2001US-264147P.
XX
XX PA (FORB/) FORSTER A. C.
XX PA (BLAC/) BLACKLOW S C.
XX
XX PI Forster AC, Blacklow SC;
XX
XX WPI; 2002-608454/65.
XX
XX A new reconstituted cell-free translation system comprising translation
XX factors and tRNA species capable of translating exogenously added
XX mRNAs, useful for the synthesis of peptides or protein ligands or
XX catalysts, e.g. insulin -
XX
XX Disclosure; Page 15; 83pp; English.
XX
XX This invention relates to a novel reconstituted cell-free translation
XX system comprising translation factors and transfer ribonucleic acid
XX (tRNA) species which translate exogenously added messenger RNA (mRNA)
XX with highly selective incorporation at each codon to form a peptide or a
XX peptidomimetic product when the system includes one or more tRNA species
XX charged with a synthetic amino acid or amino acid analogue. The
XX translation system of the invention is useful for the synthesis of
XX peptide or protein ligands or catalysts, such as insulin, growth hormone
XX or erythropoietin, and for pure ribosome display and pure mRNA display
XX selection experiments. The translation process provides a simplified,
XX
```

CC highly purified system that offers potentially improved routes to all
 CC peptides and proteins currently synthesised by alternative routes. This
 CC overcomes the limitations of the prior art, e.g. difficulty in
 CC maintaining purified components and trace contaminants or inefficient
 CC processivity. There are several advantages associated with performing
 CC peptide and protein display in a pure system, such as an expected lack
 CC of post-translational modification of peptides, lack of proteases which
 CC often cause protein degradation problem and a lack of competition from
 CC contaminants in the selection steps. The present sequence represents
 CC a splint oligonucleotide used in the mRNA display method used in
 CC the invention.

XX Sequence 18 BP; 4 A; 2 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAA 1093
 |||||
 DB 13 ATTAAAAA 1

RESULT 1344

AAQ20008/c

ID AAQ20008 standard; DNA; 16 BP.

XX AC AAQ20008;

XX DT 01-APR-1992 (first entry)

XX DE Oligonucleotide #4 able to covalently cross-link to target DNA.

XX EX deoxyribonucleic acid; major groove; ethanocamino group;

XX KW aziridinylcytosine; cross-linking group; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 8

FT /*tag= a

FT /mod_base= OTHER

FT /note= "NAN4-ethanocytosine"

FT modified_base 14

FT /*tag= b

FT /mod_base= m5c

XX PN W09118997-A.

XX PD 12-DEC-1991.

XX PF 24-MAY-1991; 91WO-1003680.

XX PR 14-JAN-1991; 91US-0640654.

XX PR 25-MAY-1990; 90US-0529346.

XX PA (GILE-) GILEAD SCIE INC.

XX PI Matteucci MD, Krawczyk S;

XX DR WPI; 1992-007480/01.

XX FT New sequence-specific non-photo-activated crosslinking agents -
 FT bind to the major groove of duplex DNA and are esp. useful for
 FT treating latent infections e.g. HIV

XX PS Example 2; Page 21; 42pp; English.

XX CC The 3' end of this oligonucleotide carries 1,3-propanediol. The
 CC oligo is one of four oligonucleotides which were designed to
 CC specifically bind and cross-link to the duplex target sequence
 CC AAQ20004. Oligo #4 with its internal cross-linking group was less
 CC effective than the other oligonucleotides with terminal

CC cross-linking groups. See also AAQ20005-7.

XX SQ Sequence 16 BP; 0 A; 2 C; 0 G; 14 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAA 1099

|||

DB 16 AAGAAAAA 1

RESULT 1345

AAAT76488

ID AAAT76488 standard; DNA; 16 BP.

XX AC AAAT76488;

XX DT 16-SEP-1997 (first entry)

XX DE Endothelial nitric oxide antisense oligonucleotide.

XX KW Asthma; airway epithelium; adenosine free; cystic fibrosis;

XX KW chronic obstructive pulmonary disease; bronchitis; ss.

XX OS Synthetic.

XX PN W09640162-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US09306.

XX PR 07-JUN-1995; 95US-0474497.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PI Metzger WJ, Nyce JW;

XX DR WPI; 1997-051871/05.

XX PT Treatment of airway diseases such as asthma - by topically applying
 XX PT adenosine-free antisense oligonucleotide to airway epithelium of
 XX PT subject

XX PS Example 5; Page 42; 71pp; English.

XX CC A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for endothelial nitric oxide. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with
 CC hyper-reactive airways.

XX SQ Sequence 16 BP; 0 A; 6 C; 5 G; 5 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 CAGTTTCCTGGGTCC 212

|||

DB 1 CCGTTTCCTGGGTCC 16

RESULT 1346

AAAX54279

ID AAX54279 standard; DNA; 16 BP.
 AC AAX54279;
 DT 05-JUL-1999 (first entry)
 XX
 DE Endothelial nitric oxide synthase antisense oligonucleotide.
 XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; pain; cystic fibrosis;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9913886-A1.
 XX
 XX 25-MAR-1999.
 XX
 XX 17-SEP-1998; 98WO-US19419.
 XX
 XX 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 XX
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 PS Disclosure; Page 61; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAX55272-74. These multiple target
 CC oligonucleotides (specifically AAX55180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impaired
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 XX
 SQ Sequence 16 BP; 0 A; 6 C; 5 G; 5 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 197 CAGTTCTCTGGGTCC 212
 | |||||
 Db 1 CCGTTCTCTGGGTCC 16

RESULT 1347
 AAF19845
 ID AAF19845 standard; DNA; 16 BP.
 XX
 AC AAF19845;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human endothelial nitric oxide synthase polynucleotide fragment #1412.
 XX
 KW Low adenine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US08020.
 PR
 XX 06-APR-1999; 99US-0127958.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenine (A) content antisense oligonucleotides which do not
 PT trigger adenine receptors during metabolism, useful e.g. for treating
 PS cancers and respiratory obstructions -
 XX Claim 14; Page 251; 1592pp; English.
 XX
 CC The present invention describes low adenine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

XX SQ Sequence 16 BP; 0 A; 6 C; 5 G; 5 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 CAGTTTCCTGGGTCC 212
 | | | | | | | | | | | | | | | | | |
 Db 1 CCGTTTCCTGGGTCC 16

RESULT 1348
 AAA33723
 ID AAA33723 standard; DNA; 16 BP.
 AC AAA33723;
 XX
 XX 28-JUL-2000 (first entry)
 XX Low adenosine antisense oligonucleotide SEQ ID NO:1412.
 DE Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX Homo sapiens.
 OS
 XX WO200009525-A2.
 PN
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US17712.
 PF
 XX 03-AUG-1998; 98US-0095212.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Claim 18; Page 441; 1343pp; English.
 XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, cystic
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA33213 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last

CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences SEQ ID NO:11 to 1680
 CC (AAA32123 to AAA33992) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX SQ Sequence 16 BP; 0 A; 6 C; 5 G; 5 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 CAGTTTCCTGGGTCC 212
 | | | | | | | | | | | | | | | | | |
 Db 1 CCGTTTCCTGGGTCC 16

RESULT 1349
 ABL57868/c
 ID ABL57868 standard; DNA; 16 BP.
 XX
 AC ABL57868;
 XX
 XX 05-AUG-2002 (first entry)
 XX Human ABCA7 gene PCR primer ABCA7_AP.
 DE Human; ABCA7; promoter; immunomodulatory; antiinflammatory; metabolic;
 KW ATP-Binding Cassette; lipid metabolism disorder; immune response;
 KW inflammation; gene therapy; PCR; primer; ss.
 XX Homo sapiens.
 OS
 XX WO200234903-A2.
 PN
 XX 02-MAY-2002.
 PD
 XX 17-OCT-2001; 2001WO-FR03219.
 PF
 XX 24-OCT-2000; 2000FR-0013649.
 PR
 XX 28-NOV-2000; 2000US-253141P.
 XX
 XX (AVET) AVENTIS PHARMA SA.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Densfle P, Rosier M, Prades C, Arnould-Reguigne I;
 PI Osorio Fortea YJ, Duverger N, Chimini G;
 XX WPI; 2002-362799/39.
 DR
 XX New promoter of the ABCA7 gene, useful for identifying modulators of
 PT transcription and in gene therapy of e.g. disorders of lipid metabolism
 PT -
 XX Example 3; Page 98; 126pp; French.
 XX The present invention relates to ABCA7 gene promoter sequences (ABC
 CC stands for ATP-Binding Cassette), which are used to identify agents (A)
 CC that modulate transcription of nucleic acids placed under control of the
 CC promoter. (A) is potentially useful for treating or preventing defects in
 CC lipid metabolism and defects in mechanisms involved in the immune
 CC response and inflammation. The promoters can also be used in gene therapy
 CC to control expression of therapeutic genes. Analysis of the promoter
 CC sequences can be used diagnostically, particularly to identify subjects
 CC at risk of lipid metabolism disorders. The present sequence is a PCR
 CC primer for human ABCA7, used to illustrate the invention.

XX SQ Sequence 16 BP; 2 A; 4 C; 6 G; 4 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.8e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 690 GCACACCGCTTCAGG 705
 DE ||||| ||||| |||||
 DB 16 GCACACAGCTTCAGG 1

RESULT 1350
 AAQ13796

ID AAQ13796 standard; DNA; 17 BP.
 AC AAQ13796;
 XX
 XX 25-MAR-2003 (updated)
 DT 09-DEC-1991 (first entry)
 XX
 DE Probe 83-4A for cellulose synthase catalytic subunit gene.
 XX
 KW Beta-1,4 glucan synthase; Acetobacter xylinum ATCC 53582; ss.
 XX
 OS Synthetic.
 XX
 XX
 PH Key Location/Qualifiers
 FT misc_feature 6
 FT /*tag= a
 FT /label= inosine
 XX
 XX W09113988-A.
 XX
 XX 19-SEP-1991.
 PD
 XX 14-MAR-1991; 91WO-US01726.
 PF
 XX 15-MAR-1990; 90US-0494093.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Saxena IM, Lin FC, Brown RM;
 PI WPI; 1991-295642/40.
 DR
 XX Recombinant beta-1,4 glucan synthase proteins and DNA - derived
 PT from Acetobacter xylinum, for commercial prodn. of glucan
 PT polymers.
 XX
 XX Example IV; Page 74; 148pp; English.
 PS
 CC The probe is one of eight designed from a tryptic peptide obtd.
 CC from an 83 kD protein having cellulose synthase activity. Probe
 CC 83-1G hybridised with the gene, but all eight probes were found
 CC to hybridise with DNA from E. coli HB101 preventing the use of
 CC standard procedures utilising recombinant DNA libraries in E. coli.
 CC The enzyme expressed from the isolated gene can be used for the
 CC prodn. of a wide range of glucan polymer based prods.
 CC See also AAQ13789-Q13797.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 17 BP; 5 A; 2 C; 6 G; 3 T; 1 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 945 ATGAGTCAACAGCTGGG 961
 DE ||||| ||||| |||||
 DB 1 ATGAGNCAACTGATGGG 17

RESULT 1351
 AAQ20006/c
 ID AAQ20006 standard; DNA; 17 BP.
 XX
 AC AAQ20006;
 XX

DT 01-APR-1992 (first entry)
 XX
 DE Oligonucleotide #2 able to covalently cross-link to target DNA.
 XX
 KW deoxyribonucleic acid; major groove; ethanocamino group;
 KW aziridinylcytosine; cross-linking group; ss.
 XX
 OS Synthetic.
 XX
 XX
 PH Key Location/Qualifiers
 FT modified_base 17
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "N4N4-ethanocytosine"
 FT 8
 FT modified_base
 FT /*tag= b
 FT /mod_base= m5c
 FT modified_base 14
 FT /*tag= c
 FT /mod_base= m5c
 XX
 XX W09118997-A.
 EN
 XX 12-DEC-1991.
 PD
 XX 24-MAY-1991; 91WO-1003680.
 PF
 XX 14-JAN-1991; 91US-0640654.
 PR
 XX 25-MAY-1990; 90US-0529346.
 PR
 XX (GILE-) GILEAD SCIE INC.
 PA
 XX Matteucci MD, Krawczyk S;
 PI WPI; 1992-007480/01.
 DR
 XX New sequence-specific non-photo-activated crosslinking agents -
 PT bind to the major groove of duplex DNA and are esp. useful for
 PT treating latent infections e.g. HIV
 XX
 XX Example 2; Page 20; 42pp; English.
 PS
 CC The 3' end of this oligonucleotide carries 1,3-propanediol. The
 CC oligo is one of four oligonucleotides which were designed to
 CC specifically bind and cross-link to the duplex target sequence
 CC AAQ20004. Oligo #2 has the covalent cross-linking group, i.e.
 CC N4N4-ethanocytosine, at its 3' end. An assay for crosslinked triple
 CC helix showed considerable reaction with oligo #2 and with Oligo #1
 CC (see AAQ20005) which has the crosslinking group at the 5' end.
 CC The most complete reaction was seen with Oligo #3 (see AAQ20007) having
 CC N4N4-ethanocytosine at both the 5' and 3' termini. A control oligo
 CC with no cross-linking group showed no reaction. The half-life of the
 CC cross-linking reaction for Oligo #2 was ca. 1 hr (1 microm);
 CC Oligo #1 showed a rate four times slower. See also AAQ20008.
 XX
 SQ Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1084 AAAAAAAGAAAAA 1099
 DE ||||| ||||| |||||
 DB 16 AAGAAAAAGAAAAA 1

RESULT 1352
 AAQ20005/c
 ID AAQ20005 standard; DNA; 17 BP.
 XX
 AC AAQ20005;
 XX
 DT 01-APR-1992 (first entry)

```

XX Oligonucleotide #1 able to covalently cross-link to target DNA.
DE deoxyribonucleic acid; major groove; ethanamine group;
XX aziridinylcytosine; cross-linking group; ss.
KW Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "N4N4-ethanocytosine"
FT modified_base 9 /*tag= b
FT /*mod_base= m5c
FT modified_base 15 /*tag= c
FT /*mod_base= m5c
XX
XX W09118997-A.
XX
XX 12-DEC-1991.
XX
XX 24-MAY-1991; 91WO-1003680.
XX
XX 14-JAN-1991; 91US-0640654.
XX 25-MAY-1990; 90US-0529346.
XX
XX (GILE-) GILEAD SCIE INC.
XX
XX Matteucci MD, Krawczyk S;
XX
XX WPI; 1992-007480/01.
XX
XX New sequence-specific non-photo-activated crosslinking agents -
XX bind to the major groove of duplex DNA and are esp. useful for
XX treating latent infections e.g. HIV
XX
XX Example 2; Page 20; 42pp; English.
XX
XX The 3' end of this oligonucleotide carries 1,3-propanediol. The
XX oligo is one of four oligonucleotides which were designed to
XX specifically bind and cross-link to the duplex target sequence
XX AAQ20004. Oligo #1 has the covalent cross-linking group, i.e.
XX N4N4-ethanocytosine, at its 5' end. An assay for crosslinked triple
XX helix showed considerable reaction with Oligo #1 and with Oligo #2
XX (see AAQ20006) which has the crosslinking group at the 3' end.
XX The most complete reaction was seen with Oligo #3 (see AAQ20007) having
XX N4N4-ethanocytosine at both the 5' and 3' termini. A control oligo
XX with no cross-linking group showed no reaction. The half-life of the
XX cross-linking reaction for Oligo #2 was ca. 1 hr (1 microm);
XX Oligo #1 showed a rate four times slower. See also AAQ20008.
XX
XX Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1099
XX |||||
XX Db 17 AAAAAAAAAAAAAA 2
XX
XX RESULT 1353
XX AAQ26203
XX ID AAQ26203 standard; DNA; 17 BP.
XX
XX AC AAQ26203;
XX
XX 25-MAR-2003 (updated)
XX 04-JAN-1993 (first entry)
XX

```

```

XX HLA-DR beta sub-type tailed probe DRB99 hybridising region.
DE Tissue typing; identity determination; disease susceptible; ss.
XX Synthetic.
XX
XX W09210589-A1.
XX
XX 25-JUN-1992.
XX
XX 06-DEC-1991; 91WO-US09294.
XX
XX 06-DEC-1990; 90US-0623098.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Apple RJ, Begovich AB, Bugawan T, Erlich HA, Griffith RL,
XX Scharf SU;
XX
XX WPI; 1992-234644/28.
XX
XX Method for determining HLA-DR beta sub-type in DNA sample -
XX comprises amplification and hybridisation with probes and
XX primers, useful in tissue typing
XX
XX Example; Page 39; 90pp; English.
XX
XX The sequence is that of the hybridising region of tailed probe DRB99 for
XX use in a method for determining HLA-DR beta sub-type in a nucleic acid
XX sample. The method allows specific nucleic acid sequences of the second
XX exon of HLA-DR beta genes to be amplified then probed for identification
XX of polymorphic sequences. The amplified DNA is useful for typing
XX homozygous or heterozygous samples from a variety of sources and for
XX detecting allelic variants not distinguishable by serological methods.
XX The typing system can be used in a reverse dot blot format which is
XX simple and rapid to perform, produces detectable signals in minutes and
XX can be utilised in tissue typing, determination of individual identity
XX and identifying disease susceptible individuals.
XX See also AAQ26092-Q26367.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 90 TAGGACCTTCTCTTCG 105
XX |||||
XX Db 2 TAGGACCTTCTGTCCG 17
XX
XX RESULT 1354
XX AAQ75070/c
XX ID AAQ75070 standard; RNA; 17 BP.
XX
XX AC AAQ75070;
XX
XX 28-JUL-1999 (first entry)
XX
XX Mouse f1t-1 VEGF receptor hammerhead ribozyme substrate #598.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; f1t-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Mus sp.
XX
XX W09715662-A2.
XX

```

PD 01-MAY-1997.
XX 25-OCT-1996; 96WO-US17480.
XX 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
XX (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 173; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.
XX Sequence 17 BP; 0 A; 0 C; 3 G; 14 U; 0 other;
SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1099
DB ||||| ||||| |||||
16 AAAAAACAAAAACAAA 1
RESULT 1355
AAX71001/c
ID AAX71001 standard; RNA; 17 BP.
XX AC AAX71001;
XX 28-JUL-1999 (first entry)
XX Human KDR VEGF receptor hammerhead ribozyme substrate #13.
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX Homo sapiens.
XX OS
XX WO9715662-A2.
XX 01-MAY-1997.
XX 25-OCT-1996; 96WO-US17480.
XX 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
XX (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 88; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more

XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 97; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.
XX Sequence 17 BP; 5 A; 7 C; 3 G; 2 U; 0 other;
SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1020 TGTAAGCTGGGCGCTGG 1035
DB ||||| ||||| |||||
17 TGTAATGCTGAGCCTGG 2
RESULT 1356
AAX70072
ID AAX70072 standard; RNA; 17 BP.
XX AC AAX70072;
XX 28-JUL-1999 (first entry)
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1367.
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX Homo sapiens.
XX OS
XX WO9715662-A2.
XX 01-MAY-1997.
XX 25-OCT-1996; 96WO-US17480.
XX 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
XX (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 88; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more

RESULT 1359
MAX69439/C

ID AAX69439 standard; RNA; 17 BP.
 XX AAX69439;
 AC
 XX
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #734.
 XX
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 XX 01-MAY-1997.
 PD
 XX
 XX 25-OCT-1996; 96WO-US17480.
 PF
 XX 11-JAN-1996; 96US-0584040.
 PR
 XX 26-OCT-1995; 95US-0005974.
 PR
 XX (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 PI WPI; 1997-259017/23.
 XX
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PS Claim 4; Page 68; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 SQ Sequence 17 BP; 3 A; 1 C; 1 G; 12 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA 1095
 DB 16 TAGTCAAAAAA 1
 RESULT 1360
 AAX62988
 ID AAX62988 standard; RNA; 17 BP.
 XX
 AC AAX62988;
 XX
 XX 16-JUL-1999 (first entry)
 DT
 XX
 DE Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:863.
 XX
 KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
 KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
 KW modulation; gene expression; transgenic plant; cleavage; canola plant;

KW caffeine synthesis; coffee plant; nicotine production; tobacco;
 KW fruit ripening; flower pigmentation; lignin production; ss.
 XX
 OS Zea mays.
 XX
 PN WO9710328-A2.
 XX
 XX 20-MAR-1997.
 PD
 XX 12-JUL-1996; 96WO-US11689.
 PF
 XX 13-JUL-1995; 95US-0001135.
 PR
 XX (DOWC) DOWELANCO.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;
 PI Merlo PAO, Skokut TA, Young SA, Zwick MG;
 XX WPI; 1997-202224/18.
 DR
 XX Ribozyme which modulates plant gene expression - preferably
 PT modulates expression of DELTA-9 desaturase or granule bound starch
 PT synthase in maize or canola
 XX
 PS Claim 38; Page 86; 155pp; English.
 XX
 CC The present invention describes an enzymatic nucleic acid molecule (I)
 CC with RNA cleaving activity, which modulates the expression of a plant
 CC gene. Also described is a gene comprising a cDNA sequence encoding maize
 CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
 CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
 CC gene, in a plant (preferably a maize or canola plant). (I) can be used
 CC to modulate caffeine synthesis in a coffee plant, nicotine production in
 CC a tobacco plant, fruit ripening processes in an apple, tomato, pear,
 CC plum or peach plant, flower pigmentation in a rose, petunia,
 CC chrysanthemum or marigold plant or lignin production in a tobacco,
 CC aspen, poplar or pine plant.
 XX
 SQ Sequence 17 BP; 10 A; 1 C; 2 G; 4 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 9.3e+02;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1077 AACTATTAAAAA 1092
 DB 2 AUCUGUAAAAA 17
 RESULT 1361
 AAX62274
 ID AAX62274 standard; RNA; 17 BP.
 XX
 AC AAX62274;
 XX
 XX 16-JUL-1999 (first entry)
 DT
 XX
 DE Granule bound starch synthase hammerhead substrate SEQ ID NO:149.
 XX
 KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
 KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
 KW modulation; gene expression; transgenic plant; cleavage; canola plant;
 KW caffeine synthesis; coffee plant; nicotine production; tobacco;
 KW fruit ripening; flower pigmentation; lignin production; ss.
 XX
 OS Zea mays.
 XX
 PN WO9710328-A2.
 XX
 PD 20-MAR-1997.
 XX
 XX 12-JUL-1996; 96WO-US11689.
 PF

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XX 13-JUL-1995; 95US-0001135.
XX (DOWC ) DOWELANCO.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;
XX Merlo PAO, Skokut TA, Young SA, Zwick NG;
XX WPI; 1997-202224/18.
XX
XX Ribozyme which modulates plant gene expression - preferably
XX modulates expression of DELTA-9 desaturase or granule bound starch
XX synthase in maize or canola
XX
XX Claim 41; Page 74; 155pp; English.
XX
XX The present invention describes an enzymatic nucleic acid molecule (I)
XX with RNA cleaving activity, which modulates the expression of a plant
XX gene. Also described is a gene comprising a cDNA sequence encoding maize
XX Delta-9 desaturase. (I) can be used to modulate expression of a gene,
XX preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
XX gene, in a plant (preferably a maize or canola plant). (I) can be used
XX to modulate caffeine synthesis in a coffee plant, nicotine production in
XX a tobacco plant, fruit ripening processes in an apple, tomato, pear,
XX plum or peach plant, flower pigmentation in a rose, petunia,
XX chrysanthemum or marigold plant or lignin production in a tobacco,
XX aspen, poplar or pine plant.
XX
XX Sequence 17 BP; 6 A; 3 C; 5 G; 3 U; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 9.3e+02;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 777 AACAGCTGAGCGCA 792
XX |||||: |||||
XX 1 AACAGUUCGAGCGCA 16
XX
XX RESULT 1362
XX AAT93742
XX ID AAT93742 standard; DNA; 17 BP.
XX
XX AC AAT93742;
XX
XX DT 25-MAR-2003 (updated)
XX DT 06-FEB-1998 (first entry)
XX
XX DE DNA probe 1 specific for type-T cytoplasmic male sterility in Zea mays.
XX
XX TURF 2H3; maize; cytoplasm male sterility; cms; type T; cms-T;
XX open reading frame 13; probe; restriction fragment; mitochondrial DNA;
XX sterility test; ss.
XX
XX Zea mays.
XX
XX US5660983-A.
XX
XX 26-AUG-1997.
XX
XX 23-NOV-1994; 94US-0345264.
XX
XX 17-JUN-1991; 91US-0716645.
XX PR 04-DEC-1986; 86US-0937926.
XX
XX (MYCO ) MYCOGEN PLANT SCI INC.
XX (UINC-) UNIV NORTH CAROLINA STATE.
XX
XX Dewey R, Levings CS;
XX WPI; 1997-434374/40.
XX
XX
XX DNA probes specific for mitochondrial DNA associated with type-T
XX cytoplasmic male sterility - for detecting male sterility in maize
XX plants
XX
XX Claim 4; Column 23; 16pp; English.
XX
XX This DNA fragment is part of the TURF 2H3 region of Zea Mays. TURF 2H3
XX (3547 nucleotides long) is found in mitochondrial DNA, and is uniquely
XX arranged in maize affected by cytoplasm male sterility type T (cms-T).
XX The present sequence corresponds to positions 1400-1416 of TURF 2H3, and
XX is located in the middle of open reading frame 13. A synthetic
XX oligonucleotide whose sequence is complementary to the present sequence
XX has also been claimed. Both oligonucleotides can be used as probes to
XX identify a restriction fragment whose size in cms-T mitochondrial DNA is
XX different from the corresponding fragment in normal mitochondrial DNA.
XX They are useful for rapidly and specifically testing maize plants for
XX T-type cytoplasmic male sterility.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 299 CCGGGCCCTGCATGGG 314
XX |||||: |||||
XX 1 CGTGGCCCTGCATGAG 16
XX
XX Db
XX
XX RESULT 1363
XX AAV97477/C
XX ID AAV97477 standard; RNA; 17 BP.
XX
XX AC AAV97477;
XX
XX DT 17-MAR-1999 (first entry)
XX
XX DE Human EGF-R target sequence nucleotide position 2281.
XX
XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
XX hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
XX cancer; genetic drift; detection; mutation; ss.
XX
XX Homo sapiens.
XX
XX WO9833893-A2.
XX
XX 06-AUG-1998.
XX
XX 14-JAN-1998; 98WO-US00730.
XX
XX 04-DEC-1997; 97US-0985162.
XX PR 31-JAN-1997; 97US-0036476.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (UYAS-) UNIV ASTON.
XX
XX Akhtar S, Fell P, McSwiggen JA;
XX WPI; 1998-437449/37.
XX
XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
XX growth factor receptor, useful for inhibiting cell proliferation and
XX for treating cancers
XX
XX Claim 5; Page 73; 109pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules (NAMS)
XX which specifically cleave RNA derived from an epidermal growth factor
XX receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
XX represent specifically claimed target sequence from human EGF-R. AAV98044
XX to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and

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CC hairpin ribozymes respectively for human EGF-R. The NMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell.

XX Sequence 17 BP; 7 A; 6 C; 3 G; 1 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 86 TGGTTAGGACCTTCTC 101
 Db 16 TGGTTGGGAGCTTCTC 1

RESULT 1364
 AAV96673
 ID AAV96673 standard; RNA; 17 BP.
 XX AC AAV96673;
 XX DT 01-MAR-1999 (first entry)
 XX DE Potato citrate synthase target sequence position 1524.
 KW Solanidine; glucosyltransferase; potato; citrate synthase; target;
 KW hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
 KW flower formation; cleavage; solanaceous plant; ss.
 XX OS Solanum tuberosum.
 XX PN WO9832843-A2.
 XX PD 30-JUL-1998.
 XX PF 14-JAN-1998; 98WO-US00738.
 XX PR 24-NOV-1997; 97US-0979416.
 XX PR 28-JAN-1997; 97US-0036545.
 XX PR 28-JAN-1997; 97US-0036599.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX McSwiggen JA, Zwick MG;
 XX WPI; 1998-427939/36.
 XX New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid
 XX biosynthesis or regulating flowering
 XX Claim 53; Page 57; 79pp; English.

CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA-cleaving activity (e.g. ribozymes) which are capable of modulating
 CC the expression of plant genes: (i) involved in biosynthesis of
 CC alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334,
 CC and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase
 CC hammerhead and hairpin ribozymes, respectively. AAV95629 to AAV95981,
 CC and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase
 CC target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195
 CC represent potato citrate synthase hammerhead and hairpin ribozymes,
 CC respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent
 CC potato citrate synthase target sequences. Ribozymes of the present
 CC invention can be used to inhibit the synthesis of toxic alkaloids in
 CC solanaceous plants, particularly potato but also tomato, pepper,
 CC aubergine and datura or to inhibit flowering in potato, lettuce, spinach,
 CC cabbage, brussel sprouts, arugula, kale, collards, chard, beet, turnip,
 CC sweet potato and the same way that restriction endonucleases are for RNA
 CC manipulation in the same way that restriction endonucleases are for DNA,
 CC as well as to examine genetic drift and mutations in plants and to

CC detect specific RNA. The ribozymes can be targeted to specific genes or
 CC to consensus sequences within a family of related genes, and being
 CC catalytic need to be present at only very low concentrations.
 XX Sequence 17 BP; 6 A; 4 C; 1 G; 6 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 56.2%; Pred. No. 9.3e+02;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 970 CACAGTATTATATCTC 985
 Db 1 CACRAUGUAUAUCUC 16

RESULT 1365
 AAA19046
 ID AAA19046 standard; RNA; 17 BP.
 XX AC AAA19046;
 XX DT 19-JUN-2000 (first entry)
 XX DE Human TIE-2 substrate sequence SEQ ID NO:2272.
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX OS Homo sapiens.
 XX PN WO9950403-A2.
 XX PD 07-OCT-1999.
 XX PF 24-MAR-1999; 99WO-US06507.
 XX PR 27-MAR-1998; 98US-0079678.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX Claim 56; Page 133; 305pp; English.

CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,

CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC
 XX Sequence 17 BP; 5 A; 2 C; 6 G; 4 U; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 9.3e+02;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 517 TGGCATTTGGAGTCA 532
 Db : |||:::|||||
 2 UGACAUUUGGAGACA 17
 RESULT 1366
 AAA21123/C
 ID AAA21123 standard; RNA; 17 BP.
 AC AAA21123;
 XX
 XX 19-JUN-2000 (first entry)
 DT
 XX
 DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4349.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 OS Homo sapiens.
 XX
 XX WO950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX
 PF 24-MAR-1999; 99WO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI
 XX WPI; 1999-591315/50.
 DR
 XX
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors
 XX
 XX Claim 55; Page 188; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;

CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 1 A; 3 C; 0 G; 13 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1098
 Db |||||:::|||||
 16 TAAAGAAAGAAAAA 1
 RESULT 1367
 AAA22609/C
 ID AAA22609 standard; RNA; 17 BP.
 AC AAA22609;
 XX
 XX 19-JUN-2000 (first entry)
 DT
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5835.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX
 PF 24-MAR-1999; 99WO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI
 XX WPI; 1999-591315/50.
 DR
 XX
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors
 XX
 XX Claim 54; Page 231; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;

CC AAA19154 represent ribozyme sequences for Tie-2, and AAA19386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiobroma of tuberculous scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC
 CC Sequence 17 BP; 1 A; 3 C; 0 G; 13 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TAAATAAAAAAAAAA 1098
 |||||
 Db 17 TAAATAAGAGAGAAA 2

RESULT 1368
 AAA22830/c

ID AAA22830 standard; RNA; 17 BP.

XX
 AC AAA22830;

XX
 DT 19-JUN-2000 (first entry)

XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6056.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US06507.

XX 27-MAR-1998; 98US-0079678.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors

XX Claim 54; Page 245; 305pp; English.

XX The present invention describes enzymatic cleave acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl

CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA19386 to AAA19086.
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiobroma of tuberculous scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC
 CC Sequence 17 BP; 2 A; 7 C; 3 G; 5 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TGAGGCTGGAGATGG 1015
 |||||
 Db 17 TGAGGAGGAGATCG 2

RESULT 1369
 AAA22974

ID AAA22974 standard; RNA; 17 BP.

XX
 AC AAA22974;

XX
 DT 19-JUN-2000 (first entry)

XX DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6200.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US06507.

XX 27-MAR-1998; 98US-0079678.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors

XX PS Claim 54; Page 254; 305pp; English.

XX CC The present invention describes enzymatic nucleic acid molecules with

XX CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl

XX CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3

XX CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAL16775 to

XX CC AAL17167 and AAL17561 to AAL17622 represent ribozyme sequences for ARNT,

XX CC and AAL17168 to AAL17560 and AAL17623 to AAL17684 represent their

XX CC corresponding target sequences; AAL17685 to AAL18385 and AAL19087 to

XX CC AAL19154 represent ribozyme sequences for Tie-2, and AAL18386 to AAL19086

XX CC and AAL19155 to AAL19222 represent their corresponding target sequences;

XX CC AAL19223 to AAL20361 and AAL21501 to AAL21595 represent ribozyme

XX CC sequences for integrin alpha 6 subunit, and AAL20362 to AAL21500 and

XX CC AAL21596 to AAL21688 represent their corresponding target sequences;

XX CC AAL21689 to AAL22475 and AAL22476 to AAL23342 represent ribozyme sequence

XX CC for integrin subunit beta 3, and AAL22476 to AAL23262, AAL23343 to

XX CC AAL23422 represent their corresponding target sequences. The ribozymes of

XX CC the invention are used for modulating the synthesis, expression and/or

XX CC stability of an mRNA encoding angiogenic factor, especially ARNT,

XX CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are

XX CC especially used to treat cancer, diabetic retinopathy, age related

XX CC macular degeneration (ARMD), inflammation, and arthritis, as well as

XX CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,

XX CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber

XX CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,

XX CC and other syndromes and diseases related to the levels of ARNT, Tie-2,

XX CC integrin subunit alpha-6, or integrin subunit beta-3.

XX SQ Sequence 17 BP; 13 A; 1 C; 0 G; 3 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 9.3e+02;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1098

DB :|||||

2 UAAAAUUAAAAA 17

RESULT 1370

AAV92555

ID AAV92555 standard; RNA; 17 BP.

AC AAV92555;

XX 18-FEB-1999 (first entry)

DE Human A-Raf substrate position 1594.

XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;

XX target; substrate; catalyst; modulation; expression; Raf gene;

XX delivery; screening; identification; synthesis; deprotection;

XX purification; cancer; inflammation; psoriasis; non-hepatic ascites;

XX infection; genetic drift; restenosis; rheumatoid arthritis; ss.

XX Homo sapiens.

XX WO9850530-A2.

PN 12-NOV-1998.

XX 05-MAY-1998; 98WO-US09249.

XX 19-DEC-1997; 97US-0068212.

PR 09-MAY-1997; 97US-0046059.

PR 09-JUN-1997; 97US-0049002.

PR 03-JUL-1997; 97US-0051718.

PR 22-AUG-1997; 97US-0056808.

PR 02-OCT-1997; 97US-0061321.

PR 02-OCT-1997; 97US-0061324.

PR 05-NOV-1997; 97US-0064866.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;

PI Karpelsky A, Kisich K, Matulic-Adamic J, McSwiggen JA;

PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;

XX WPT; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected

PT processes - especially ribozymes that cleave Raf RNA for treating

PT cancer, restenosis, and also new ribozymes and modified nucleoside

PT triphosphates used as antiviral agents and synthons

XX Claim 177; Page 160; 259pp; English.

XX A method has been developed for the identification of a nucleic acid

CC capable of modulating a process in a biological system. The method

CC comprises: (a) introducing into the system a random library of nucleic

CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising

CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC

CC in systems where modulation has occurred and/or determining the sequence

CC of at least part of the SBDs in such systems. Nucleic acid molecules

CC with endonuclease activity and catalytic activity, from the present

CC invention, are used to modulate gene expression in plant and mammalian

CC cells and to cleave target nucleic acid, particularly for treating

CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,

CC psoriasis, non-hepatic ascites and infection. They may also be used to

CC detect genetic drift and mutations in diseased cells and to determine

CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate

CC expression of the Raf gene, are used to treat cancer, restenosis,

CC psoriasis or rheumatoid arthritis, or generally any condition associated

CC with the level of c-raf. Introduction of sugar/phosphate modifications

CC increases stability against nuclease and activity. AAV90922 to AAV93877

CC represent NACs that can be used in the method, specifically for

CC modulating the expression of a Raf gene.

XX SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 9.3e+02;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 481 GCATTCCTCAGGATCT 496

DB :|||||

1 GCAGCCCTCAGGAUCU 16

RESULT 1371

AAAF01850

ID AAF01850 standard; DNA; 17 BP.

XX AAF01850;

AC AAF01850;

XX 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #145.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;

XX interferon alpha; ss.

XX Homo sapiens.

XX WO200061729-A2.

PN 19-OCT-2000.

XX 11-APR-2000; 2000WO-US09721.

PR 12-APR-1999; 99US-0129390.

PR (RIBO-) RIBOZYME PHARM INC.

PA Blatt L, Zwick M, Pavco P, McSwiggen J;

XX WPI; 2000-647423/62.
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX Claim 37; Page 59; 164pp; English.
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 240 GCTCAGCTCTGAAGG 255
DB 1 GCTCAGCTCATGAGG 16
RESULT 1372
AAAF02013/c
ID AAFA02013 standard; DNA; 17 BP.
XX
XX AAFA02013;
AC
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #308.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX Homo sapiens.
XX WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX Claim 37; Page 63; 164pp; English.
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX

SQ Sequence 17 BP; 1 A; 11 C; 1 G; 4 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1001 GAGGCTGGAGATGGG 1016
DB 16 GAGGCTGGAGAGGGG 1
RESULT 1373
AAAF02208
ID AAFA02208 standard; DNA; 17 BP.
XX
XX AAFA02208;
AC
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #503.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX Homo sapiens.
XX WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX Claim 37; Page 67; 164pp; English.
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 1 A; 11 C; 1 G; 4 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 418 CTCTCGGGTCCCCC 433
DB 1 CTCTCGGCTACCCCC 16
RESULT 1374
AAAF02388
ID AAFA02388 standard; DNA; 17 BP.
XX
XX AAFA02388;
AC
XX
DT 16-FEB-2001 (first entry)

```

XX DE Hammerhead ribozyme substrate #683.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 37; Page 71; 164pp; English.
XX SQ Sequence 17 BP; 14 A; 0 C; 2 G; 1 T; 0 other;
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1099
Db 1 AAAAAAAAAAAAAA 16
RESULT 1375
AAFO3227/C
ID AAF03227 standard; DNA; 17 BP.
XX AC AAF03227;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #1522.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 37; Page 71; 164pp; English.
XX SQ Sequence 17 BP; 14 A; 0 C; 2 G; 1 T; 0 other;
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1099
Db 1 AAAAAAAAAAAAAA 16
RESULT 1375
AAFO3227/C
ID AAF03227 standard; DNA; 17 BP.
XX AC AAF03227;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #1522.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 37; Page 71; 164pp; English.
XX SQ Sequence 17 BP; 14 A; 0 C; 2 G; 1 T; 0 other;
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1079 CTATTAAAAA 1094
Db 16 CCATTCAAAAAA 1
RESULT 1376
AAFO6314/C
ID AAF06314 standard; DNA; 17 BP.
XX AC AAF06314;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #3111.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 127; 164pp; English.
XX SQ The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.

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PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX PS Claim 37; Page 90; 164pp; English.
XX SQ The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX SQ Sequence 17 BP; 2 A; 0 C; 4 G; 11 T; 0 other;
XX
CC Query Match 1.2%; Score 12.8; DB 1; Length 17;
CC Best Local Similarity 87.5%; Pred. No. 9.3e+02;
CC Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1079 CTATTAAAAA 1094
Db 16 CCATTCAAAAAA 1
RESULT 1376
AAFO6314/C
ID AAF06314 standard; DNA; 17 BP.
XX AC AAF06314;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #3111.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09721.
XX PR 12-APR-1999; 99US-0129390.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor
XX PT protein, interferon alpha and erythropoietin -
XX PS Claim 42; Page 127; 164pp; English.
XX SQ The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.

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XX SQ Sequence 17 BP; 3 A; 1 C; 0 G; 13 U; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1095
Db 16 TATAAAATAAAAA 1

RESULT 1377
AAA36578
ID AAA36578 standard; DNA; 17 BP.
XX AC AAA36578;
XX DT 26-JUL-2000 (first entry)
XX DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:643.
XX KW Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
XX KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
XX KW genomic classification; identification; DNA fingerprinting;
XX KW tumour characterisation; hybridisation; ss.
XX OS Homo sapiens.
XX FN WO200018960-A2.
XX PD 06-APR-2000.
XX PF 24-SEP-1999; 99WO-US22283.
XX PR 25-SEP-1998; 98US-0101757.
XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PI Landers JE, Jordan B, Housman DE, Charest A;
XX WPI; 2000-293181/25.
XX DR Detection of single nucleotide polymorphisms in genomes by preparation
XX PT and analysis of reduced complexity genomes, useful for genotyping,
XX PT fingerprinting and determining allele frequency of SNPs -
XX PS Disclosure; Page 72; 111pp; English.
XX CC A method has been developed for detecting the presence or absence of a
XX CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
XX CC method comprises preparing a reduced complexity genome (RCG) from the
XX CC genomic sample and analysing the RCG for the presence or absence of a
XX CC SNP allele. The method can be used to characterise a tumour, to generate
XX CC a genomic pattern for an individual genome or to generate a genomic
XX CC classification code for a genome. The method can be used to assess
XX CC whether a subject is at risk for developing a disease or to identify a
XX CC set of SNP alleles associated with a disease. The method can also be
XX CC used to perform linkage analysis. AAA35944 to AAA35947 represent
XX CC sequences used in the exemplification of the present invention. AAA35948
XX CC to AAA3632 represent nucleotide sequences containing SNPs.
XX SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 346 GTGCCAGCGCCCACT 361
Db 1 GTGACAGCGCCCACT 16
```

```
RESULT 1378
AAA25179/c
ID AAA25179 standard; DNA; 17 BP.
XX AC AAA25179;
XX DT 19-JUL-2000 (first entry)
XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1677.
XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX KW gene expression modification; cancer; phosphorothioate; endonuclease;
XX KW anticancer; breast cancer; endometrium cancer; ss.
XX OS Homo sapiens.
XX FN WO9954459-A2.
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-US08547.
XX PR 20-APR-1998; 98US-0082404.
XX PR 23-JUN-1998; 98US-0103636.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
XX PI Matulic-Adamic J;
XX DR WPI; 2000-013248/01.
XX PT New nucleic acids that interact, and optionally cleave, target
XX PT sequences, used to treat cancer -
XX PS Claim 77; Page 71; 148pp; English.
XX CC The present invention describes nucleic acids (A) that interact stably
XX CC with a target sequence and contain at least one phosphorodithioate
XX CC link, having endonuclease activity, (A), and more generally any
XX CC catalytic nucleic acid (A') that modulates expression of the oestrogen
XX CC receptor gene, are used to treat cancer (particularly of breast or
XX CC endometrium), in vivo or by transforming cells ex vivo and implanting
XX CC treated cells, or for other conditions associated with levels of
XX CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX CC can also be used to correlate inhibition of gene expression with
XX CC alterations in phenotype, particularly for identification of therapeutic
XX CC targets, and as research reagents (for RNA, in the same way that
XX CC restriction endonucleases are used with DNA). The combination of
XX CC modifications in (A) improves resistance to nucleases, binding affinity
XX CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX CC their corresponding target sequences. AAA26219 to AAA26271 represent
XX CC other ribozyme sequences and antisense oligonucleotides used in the
XX CC exemplification of the present invention.
XX SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAA 1099
Db 17 AAAAAA 2

RESULT 1379
AAA25181/c
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DT 19-JUL-2000 (first entry)
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1954.
DE Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
OS WO9954459-A2.
XX 28-OCT-1999.
XX 19-APR-1999; 99WO-US08547.
XX 20-APR-1998; 98US-0082404.
XX 23-JUN-1998; 98US-0103636.
XX (RIBO-) RIBOZYME PHARM INC.
PA Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer -
XX Claim 77; Page 79; 148pp; English.
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX Sequence 17 BP; 2 A; 1 C; 1 G; 13 T; 0 other;
SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAAATAAAAA 1095
DB ||| |||||
16 TATACAAAAAATAAAAA 1
RESULT 1382
ABA77753/c
ID ABA77753 standard; DNA; 17 BP.
XX AC ABA77753;
XX 24-JAN-2002 (first entry)
XX
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```
DE Retinoblastoma mutation correcting oligonucleotide SEQ ID NO: 599.
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
XX antilipemic; ss.
XX Homo sapiens.
OS WO200173002-A2.
XX 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US09761.
XX 27-MAR-2000; 2000US-192176P.
PR 27-MAR-2000; 2000US-192176P.
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX (UYDE ) UNIV DELAWARE.
PA Knies EB, Gamper HB, Rice MC;
XX WPI; 2001-639230/73.
XX Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification -
XX Claim 7; Page 80; 294pp; English.
XX The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention.
XX Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 other;
SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 992 TGGAAAGTCTGAGGCTG 1007
DB ||| |||||
16 TGGAAAGGCTGAGGTTG 1
RESULT 1383
ABA77754
ID ABA77754 standard; DNA; 17 BP.
XX AC ABA77754;
XX 24-JAN-2002 (first entry)
XX
```

XX DE Retinoblastoma mutation correcting oligonucleotide SEQ ID NO: 600.

XX XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;

XX KW retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;

XX KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;

XX KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

XX KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;

XX KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;

XX KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;

XX KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;

XX KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;

XX KW antileptic; ss.

XX OS Homo sapiens.

XX PN WO200173002-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-US09761.

XX PR 27-MAR-2000; 2000US-192176P.

XX PR 27-MAR-2000; 2000US-192179P.

XX PR 01-JUN-2000; 2000US-208538P.

XX PR 30-OCT-2000; 2000US-244983P.

XX PA (UYDE) UNIV DELAWARE.

XX XX Kmiec EB, Gamper HB, Rice MC;

XX PI WPI; 2001-639230/73.

XX DR Oligonucleotide for targeted alterations of genetic sequences and for

XX PT treating cystic fibrosis, comprises at least one mismatch and chemical

XX PT modification -

XX PS Claim 7; Page 80; 294pp; English.

XX XX The present invention provides single-stranded oligonucleotides which can

XX CC be used for the targeted alteration of genomic sequences, where the

XX CC oligonucleotide has at least one mismatch compared with the genomic

XX CC sequence to be altered. In particular, these sequences are directed at

XX CC the following genes: adenosine deaminase, p53, beta-globin,

XX CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A

XX CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus

XX CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

XX CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

XX CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and

XX CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

XX CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,

XX CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,

XX CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and

XX CC various syndromes. The present sequence is one of the gene correcting

XX CC oligonucleotides of the invention.

XX SQ Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 992 TGGAGTCTGAGGCTG 1007

Db 2 TGGAGGCTGAGGTTG 17

RESULT 1384

AAH76222/c

ID AAH76222 standard; DNA; 17 BP.

XX XX

AC AAH76222;

XX XX

DT 29-OCT-2001 (first entry)

XX XX Human prostaglandin G/H synthase-2 specific primer.

DE XX

XX KW Pyrene; gene therapy; antiinflammatory; gene expression; interleukin;

XX KW hemoxygenase-1; prostaglandin G/H synthase-2; RANTES; TNF alpha; p78;

XX KW macrophage inflammatory protein; chemokine; growth regulated protein-1;

XX KW matrix metalloproteinase-9; migration inhibitory factor-related protein;

XX KW lysozyme; GABA(A) receptor-associated protein; interferon; SCO homolog-2;

XX KW transketolase; adenosine A2a receptor; CD37 antigen properdin P factor;

XX KW G-protein; Nef-associated factor-1; signal peptidase; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200151480-A1.

XX PD 19-JUL-2001.

XX PF 11-JAN-2001; 2001WO-JP00082.

XX PR 13-JAN-2000; 2000JP-0004989.

XX PR 03-OCT-2000; 2000JP-0303711.

XX XX (TAKI) TAKARA SHUZO CO LTD.

XX PA Enoki T, Yamashita S, Nishimura K, Sagawa H, Kato I;

XX PI WPI; 2001-514436/56.

XX DR Agent for correcting gene expression regulation error comprises pyrone

XX PT compound or dihydroxy compound -

XX XX Example 4; Page 61; 93pp; Japanese.

XX XX The invention provides an agent comprising a pyrone compound or dihydroxy

XX CC compound of specified formulae given in the specification. The agent is

XX CC used for correcting gene expression regulation errors. Errors in the

XX CC following genes may be corrected: IL-6, IL-10, hemoxygenase-1,

XX CC prostaglandin G/H synthase-2, macrophage inflammatory protein-1-alpha,

XX CC RANTES, IL-1alpha, IL-1beta, TNF alpha, IL-7 receptor, macrophage

XX CC inflammatory protein-1beta, liver and activation-regulated chemokine,

XX CC macrophage-derived chemokine, macrophage inflammatory protein-2-beta,

XX CC macrophage inflammatory protein-2-alpha, growth regulated protein-1,

XX CC matrix metalloproteinase-9, migration inhibitory factor-related protein

XX CC -8, lysozyme, GABA(A) receptor-associated protein, interferon-induced 17

XX CC -kDa/15-kDa protein, interferon-inducible protein p78, SCO homolog-2,

XX CC transketolase, adenosine A2a receptor, CD37 antigen properdin P factor,

XX CC regulator of G-protein signaling-2, Nef-associated factor-1, myeloid

XX CC leukemia cell differentiation protein-1, signal peptidase complex, and

XX CC also side-effects caused by them such as inflammation. Sequences

XX CC AAH76220-76280 represent PCR primers used in the course of the

XX CC invention.

XX SQ Sequence 17 BP; 3 A; 3 C; 5 G; 6 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 257 CTTAGACAGGAGCACC 272

Db 17 CTTAAACAGGAGCATC 2

RESULT 1385

AAH95015/c

ID AAH95015 standard; RNA; 17 BP.

XX XX

AC AAH95015;

XX XX

DT 09-OCT-2001 (first entry)

XX XX Human Chk1 ribozyme substrate SEQ ID NO: 440.


```
Query Match      1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 326 AGAAGCTGTGGAGCAA 341
   ||||| ||||| |||||
Db 16 AGAAGTTCGGAGCAA 1

RESULT 1389
AAH80148
ID AAH80148 standard; cDNA; 17 BP.
XX
AC AAH80148;
XX
DT 19-SEP-2001 (first entry)
XX
DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 112.
XX
KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW disease diagnosis; ss.
XX
OS Oryctolagus cuniculus.
XX
PN US6251588-B1.
XX
PD 26-JUN-2001.
XX
PF 10-FEB-1998; 98US-0021701.
XX
PR 10-FEB-1998; 98US-0021701.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
DR WPI; 2001-424456/45.
XX
PT Predicting the potential of an oligonucleotide to hybridize to a target
PT nucleotide sequence, useful for evaluating oligonucleotide probe
PT sequences, by identifying a oligonucleotides based on the evaluation of
PT parameters -
XX
PS Example 1; Column 51; 342pp; English.
XX
CC The present invention describes a method for predicting the potential of
CC an oligonucleotide to hybridise to a (complementary) target nucleotide
CC sequence, involving identifying a subset of oligonucleotides within the
CC predetermined number of unique oligonucleotides based on the evaluation
CC of the parameter. Oligonucleotides in the subset are identified that are
CC clustered along a region of the nucleotide sequence that is hybridisable
CC to the target nucleotide sequences. This is useful for evaluating
CC oligonucleotide probe sequences. The present sequence is an
CC oligonucleotide described in the exemplification of the invention.
XX
SQ Sequence 17 BP; 1 A; 1 C; 7 G; 8 T; 0 other;

Query Match      1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 134 GTCTGCTTTGGGGCT 149
   ||||| ||||| |||||
Db 1 GTCTGTTTGGGGAT 16

RESULT 1389
AAD03856/c
ID AAD03856 standard; DNA; 17 BP.
XX
AC AAD03856;
XX

Query Match      1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 134 GTCTGCTTTGGGGCT 149
   ||||| ||||| |||||
Db 1 GTCTGTTTGGGGAT 16

RESULT 1389
AAD03856/c
ID AAD03856 standard; DNA; 17 BP.
XX
AC AAD03856;
XX
```

```
DT 02-JUL-2001 (first entry)
XX
DE PCR primer 415 used for mapping the human cell cycle checkpoint DNA.
XX
KW Human; cell cycle checkpoint; chk1; tumour; malignancy;
KW cell growth inhibitor; development deficiency; PCR primer;
KW DNA damage; kinase; ss.
XX
OS Homo sapiens.
XX
PN US6218109-B1.
XX
PD 17-APR-2001.
XX
PF 05-SEP-1997; 97US-0924183.
XX
PR 05-SEP-1997; 97US-0924183.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Elledge SJ, Sanchez Y;
XX
DR WPI; 2001-289827/30.
XX
PT New Chk1 proteins and gene sequences encoding the proteins useful as
PT probes for a portion of the chromosome associated with tumors and other
PT malignancies, growth and/or development deficiencies -
XX
PS Claim 17; Column 27; 37pp; English.
XX
CC The present sequence is PCR primer 415 used in FISH hybridisation to
CC map the human cell cycle checkpoint protein, hchk1 DNA. The
CC cell cycle checkpoints are regulatory pathways that control the order
CC and timing of cell cycle transitions, and ensure that critical events
CC such as DNA replication and chromosome segregation are completed with
CC high fidelity. The chk1 protein controls cell cycle in response to DNA
CC damage. It functions as kinase and phosphorylates the key regulators of
CC cdk tyrosine phosphorylation. The checkpoint gene sequences are used as
CC probes for a portion of the chromosome associated with tumors and other
CC malignancies, as well as growth and/or development deficiencies. The chk1
CC proteins are useful for generating specific antibodies and for inhibiting
CC growth of cells.
XX
SQ Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 other;

Query Match      1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 326 AGAAGCTGTGGAGCAA 341
   ||||| ||||| |||||
Db 16 AGAAGTTCGGAGCAA 1

RESULT 1390
ABK01170/c
ID ABK01170 standard; RNA; 17 BP.
XX
AC ABK01170;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Inozyme #440.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberszyme; zincyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
```

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04273.
 XX
 XX 11-FEB-2000; 2000US-181797P.
 XX 28-FEB-2000; 2000US-185516P.
 XX 06-MAR-2000; 2000US-187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J.
 XX (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 XX Claim 88; Page 85; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NIN
 CC motif) or an amberyzyme (cleaving RNA with an NGN triplet), a zynzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC thrombocytopaenia, and inflammatory arthropathy. The INOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is an inozyme of the invention.
 XX
 XX Sequence 17 BP; 2 A; 7 C; 2 G; 6 U; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 764 GGCAGAACTGGAGAG 779

Db
 RESULT 1391
 ID ABK01424/C
 XX ABK01424 standard; RNA; 17 BP.
 XX AC ABK01424;
 XX DT 12-MAR-2002 (first entry)
 XX DE Human NOGO Inozyme #594.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04273.
 XX
 XX 11-FEB-2000; 2000US-181797P.
 XX 28-FEB-2000; 2000US-185516P.
 XX 06-MAR-2000; 2000US-187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J.
 XX (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 XX Claim 88; Page 89; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NIN
 CC motif) or an amberyzyme (cleaving RNA with an NGN triplet), a zynzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC thrombocytopaenia, and inflammatory arthropathy. The INOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is an inozyme of the invention.
 XX
 XX Sequence 17 BP; 2 A; 7 C; 2 G; 6 U; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 764 GGCAGAACTGGAGAG 779

immunocytooma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an inozyme of the invention.

XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 667 AGCTGAGCTTACAGCA 682

Db 16 AGCTGATGGTCACAGA 1

RESULT 1392

ABK01891

ID ABK01891 standard; RNA; 17 BP.

AC ABK01891;

DT 12-MAR-2002 (first entry)

DE Human NOGO Zinzyme #213.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO2001:59103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04273.

XX 11-FEB-2000; 2000US-181797P.

PR 28-FEB-2000; 2000US-185516P.

PR 06-MAR-2000; 2000US-187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, McSwiggen J, Chowrira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury -

XX Claim 88; Page 99; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO).

XX The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGI motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is a zinzyme molecule of the invention.

SQ Sequence 17 BP; 7 A; 0 C; 6 G; 4 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 9.3e+02;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1012 ATGGGAGCTTAAGCT 1027

Db 2 AUGGGAAGUGAAGA 17

RESULT 1393

ABK01940/c

ID ABK01940 standard; RNA; 17 BP.

XX ABK01940;

XX 12-MAR-2002 (first entry)

XX Human NOGO Zinzyme #262.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
 OS Synthetic.
 XX ABK02483
 PN WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US04273.
 XX 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 100; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) pr an ambezyme (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic leukaemia, HIV (human
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targetting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid

RESULT 1394
 ABK02483
 ID ABK02483 standard; RNA; 17 BP..
 XX
 AC ABK02483;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Amberzyme #155.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; ambezyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US04273.
 XX 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 100; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) pr an ambezyme (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic leukaemia, HIV (human
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targetting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targetting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is a zinzyme molecule of the invention.
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 2 G; 7 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.3%; Pred. No. 9.3e+02;
 Matches 14; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;
 QY 764 GGCAGAACTGGAGAAG 779
 |||||
 DB 16 GGCAGAACTGGTGAAG 1

PI Gu Y, Shannon ME;
 XX WPI; 2002-697817/75.
 XX New isolated nucleic acid encoding an isoform of human pregnancy
 PT associated plasma protein E, for preventing or aborting pregnancy
 XX
 PS Example 2; Page 138; 353pp; English.
 XX
 CC This invention describes a novel isolated nucleic acid that encodes
 CC one of three new isoforms of human pregnancy associated plasma protein E,
 CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention.
 XX
 SQ Sequence 17 BP; 14 A; 0 C; 3 G; 0 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 2 AAAAAAAAAAGAGAA 17
 RESULT 1397
 ABS74959
 ID ABS74959 standard; DNA; 17 BP.
 AC ABS74959;
 XX
 XX 24-DEC-2002 (first entry)
 XX
 DE Human PAPP-Ea associated 17-mer SEQ ID 485.
 XX
 KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
 KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
 KW dysgenetic pregnancy; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002102252-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 06-APR-2001; 2001US-0827998.
 XX
 PR 26-MAY-2000; 2000US-207456P.
 XX
 PA (GUYV/) GU Y.
 PA (SHAN/) SHANNON M E.
 XX
 XX Gu Y, Shannon ME;
 XX WPI; 2002-697817/75.
 XX
 CC New isolated nucleic acid encoding an isoform of human pregnancy
 CC associated plasma protein E, for preventing or aborting pregnancy
 XX
 PS Example 2; Page 139; 353pp; English.
 XX
 CC This invention describes a novel isolated nucleic acid that encodes
 CC one of three new isoforms of human pregnancy associated plasma protein E,
 CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention.
 XX

CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention.
 XX
 SQ Sequence 17 BP; 14 A; 0 C; 2 G; 1 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 1 AAAAAAAAAAGAGAA 16
 RESULT 1398
 ABV90957/C
 ID ABV90957 standard; DNA; 17 BP.
 XX
 AC ABV90957;
 XX
 XX 23-DEC-2002 (first entry)
 XX
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1670.
 XX
 KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1239051-A2.
 XX
 PD 11-SEP-2002.
 XX
 PF 28-JAN-2002; 2002EP-0001165.
 XX
 PR 30-JAN-2001; 2001WO-US006663.
 PR 30-JAN-2001; 2001WO-US006664.
 PR 30-JAN-2001; 2001WO-US006665.
 PR 30-JAN-2001; 2001WO-US006666.
 PR 30-JAN-2001; 2001WO-US006667.
 PR 30-JAN-2001; 2001WO-US006668.
 PR 30-JAN-2001; 2001WO-US006669.
 PR 30-JAN-2001; 2001WO-US006670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 10-OCT-2001; 2001US-0328205.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 XX Shannon M;
 XX WPI; 2002-684061/74.
 XX
 CC Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
 CC POSHL-1, useful for treating disorders associated with decreased
 CC expression or activity of human POSHL1 -
 XX
 PS Example 2; SEQ ID NO 1670; 60pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (1), comprising a sequence of 730 amino
 CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an

CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention.
 CC Note: The present sequence did not form part of the printed
 CC specification, but is based on sequence information supplied to Derwent
 CC by the European Patent Office.

XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 265 GGAGCACCTTCAGAAA 280
 Db 17 GGATCACCTTCTGAAA 2

RESULT 1399
 ABV90958/c
 ID ABV90958 standard; DNA; 17 BP.

XX AC ABV90958;
 XX DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1671.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 XX KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-0001165.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001WO-US000670.

XX PR 10-OCT-2001; 2001US-0328205.

XX PA (AEOM-) AEOMICA INC.

XX PI Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
 XX POSHL-1, useful for treating disorders associated with decreased
 XX expression or activity of human POSHL1 -

XX Example 2; SEQ ID NO 1671; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

CC acids (SI, ABB93999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention.
 CC Note: The present sequence did not form part of the printed
 CC specification, but is based on sequence information supplied to Derwent
 CC by the European Patent Office.

XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 265 GGAGCACCTTCAGAAA 280
 Db 16 GGATCACCTTCTGAAA 1

RESULT 1400
 ABQ63463/c

ID ABQ63463 standard; DNA; 17 BP.

XX AC ABQ63463;

XX DT 20-AUG-2002 (first entry)

XX DE Human KTOM1a portion (ABQ63232) probe # 176.

XX KW Human; KTOM1a; kidney tumour overexpressed membrane; cytostatic;
 XX KW gene therapy; cancer; kidney; liver; bone marrow; brain; lung;
 XX KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

XX OS Homo sapiens.

XX PN WO200224750-A2.

XX PD 28-MAR-2002.

XX PF 21-SEP-2001; 2001WO-US29656.

XX PR 21-SEP-2000; 2000US-234687P.

XX PR 27-SEP-2000; 2000US-236359P.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PR 30-JAN-2001; 2001WO-US00661.

XX PR 30-JAN-2001; 2001WO-US00662.

XX PR 30-JAN-2001; 2001WO-US00663.

XX PR 30-JAN-2001; 2001WO-US00664.

XX PR 30-JAN-2001; 2001WO-US00665.

XX PR 30-JAN-2001; 2001WO-US00666.

XX PR 30-JAN-2001; 2001WO-US00667.

XX PR 30-JAN-2001; 2001WO-US00668.

XX PR 30-JAN-2001; 2001WO-US00669.

XX PR 23-MAY-2001; 2001US-0864761.

XX PR 28-AUG-2001; 2001US-315676P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhang J;

XX WPI; 2002-479509/51.


```

XX PT New human kidney tumor overexpressed membrane (KTOM1) protein and
XX PT nucleic acids encoding the protein, useful for treating subjects having
XX PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
XX PT disorder of e.g., liver or bone
XX PS Example 2; Page 180; 418pp; English.
XX CC The invention relates to a novel isolated nucleic acid encoding human
XX CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
XX CC invention has cytostatic activity. The nucleotide may have a use in gene
XX CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
XX CC monitor a disease caused by altered expression of human KTOM1.
XX CC Compositions comprising the nucleic acids, proteins or antibodies may be
XX CC used to treat subjects having defects in KTOM1 which can manifest as
XX CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
XX CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
XX CC function. The sequence represents a probe used in the invention to
XX CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX SQ Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 other;
      Query Match      1.2%; Score 12.8; DB 1; Length 17;
      Best Local Similarity 87.5%; Pred. No. 9.3e+02;
      Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 CGTGGCTCAGCTCTTG 251
Db 17 CGTGGTTCAGCTCTTG 2

RESULT 1401
ABQ63464/c
ID ABQ63464 standard; DNA; 17 BP.
XX AC ABQ63464;
XX DT 20-AUG-2002 (first entry)
XX DE Human KTOM1a portion (ABQ63232) probe # 177.
XX KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
XX KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
XX KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX OS Homo sapiens.
XX PN WO200224750-A2.
XX PD 28-MAR-2002.
XX PF 21-SEP-2001; 2001WO-US23656.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 23-MAY-2001; 2001US-0864761.
XX PR 28-AUG-2001; 2001US-315676P.
XX PA (ABOM-) ABOMICA INC.
XX PI Zhang J;

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DR WPI; 2002-479509/51.
XX PT New human kidney tumor overexpressed membrane (KTOM1) protein and
XX PT nucleic acids encoding the protein, useful for treating subjects having
XX PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
XX PT disorder of e.g., liver or bone
XX PS Example 2; Page 180; 418pp; English.
XX CC The invention relates to a novel isolated nucleic acid encoding human
XX CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
XX CC invention has cytostatic activity. The nucleotide may have a use in gene
XX CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
XX CC monitor a disease caused by altered expression of human KTOM1.
XX CC Compositions comprising the nucleic acids, proteins or antibodies may be
XX CC used to treat subjects having defects in KTOM1 which can manifest as
XX CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
XX CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
XX CC function. The sequence represents a probe used in the invention to
XX CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX SQ Sequence 17 BP; 6 A; 6 C; 3 G; 2 T; 0 other;
      Query Match      1.2%; Score 12.8; DB 1; Length 17;
      Best Local Similarity 87.5%; Pred. No. 9.3e+02;
      Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 CGTGGCTCAGCTCTTG 251
Db 16 CGTGGTTCAGCTCTTG 1

RESULT 1402
ABQ63675/c
ID ABQ63675 standard; DNA; 17 BP.
XX AC ABQ63675;
XX DT 20-AUG-2002 (first entry)
XX DE Human KTOM1a portion (ABQ63232) probe # 388.
XX KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
XX KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
XX KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX OS Homo sapiens.
XX PN WO200224750-A2.
XX PD 28-MAR-2002.
XX PF 21-SEP-2001; 2001WO-US29656.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 23-MAY-2001; 2001US-0864761.
XX PR 28-AUG-2001; 2001US-315676P.
XX PA (ABOM-) ABOMICA INC.
XX PI Zhang J;

```

XX WPI; 2002-479509/51.
 XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone -
 XX Example 2; Page 208; 418pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding human
 CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human KTOM1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in KTOM1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
 XX Sequence 17 BP; 2 A; 7 C; 5 G; 3 T; 0 other;
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 35 CTCACGGTGCAGAGG 50
 Db 17 CTCACGGTGCAGAGG 2
 RESULT 1403
 ABQ63676/c
 ID ABQ63676 standard; DNA; 17 BP.
 AC ABQ63676;
 XX 20-AUG-2002 (first entry)
 DT Human KTOM1a portion (ABQ63232) probe # 389.
 DE Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 XX Homo sapiens.
 OS WO200224750-A2.
 XX 28-MAR-2002.
 XX 21-SEP-2001; 2001WO-US29656.
 XX 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.
 XX (AEOM-) AEOMICA INC.
 PA

PI Zhang J;
 XX WPI; 2002-479509/51.
 XX New human kidney tumor overexpressed membrane (KTOM1) protein and
 PT nucleic acids encoding the protein, useful for treating subjects having
 PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
 PT disorder of e.g., liver or bone -
 XX Example 2; Page 208; 418pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding human
 CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
 CC invention has cytostatic activity. The nucleotide may have a use in gene
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
 CC monitor a disease caused by altered expression of human KTOM1.
 CC Compositions comprising the nucleic acids, proteins or antibodies may be
 CC used to treat subjects having defects in KTOM1 which can manifest as
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
 CC function. The sequence represents a probe used in the invention to
 CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
 XX Sequence 17 BP; 2 A; 7 C; 5 G; 3 T; 0 other;
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 35 CTCACGGTGCAGAGG 50
 Db 16 CTCACGGTGCAGAGG 1
 RESULT 1404
 ABQ64196/c
 ID ABQ64196 standard; DNA; 17 BP.
 AC ABQ64196;
 XX 20-AUG-2002 (first entry)
 DT Human KTOM1a portion (ABQ63232) probe # 909.
 DE Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
 XX Homo sapiens.
 OS WO200224750-A2.
 XX 28-MAR-2002.
 XX 21-SEP-2001; 2001WO-US29656.
 XX 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 28-AUG-2001; 2001US-315676P.
 XX (AEOM-) AEOMICA INC.
 PA

XX	Zhang J;
PI	WPI; 2002-479509/51.
XX	New human kidney tumor overexpressed membrane (KTOM1) protein and
XX	nucleic acids encoding the protein, useful for treating subjects having
PT	defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT	disorder of e.g., liver or bone
XX	Example 2; Page 276; 418pp; English.
PS	The invention relates to a novel isolated nucleic acid encoding human
XX	KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC	invention has cytostatic activity. The nucleotide may have a use in gene
CC	therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC	monitor a disease caused by altered expression of human KTOM1.
CC	Compositions comprising the nucleic acids, proteins or antibodies may be
CC	used to treat subjects having defects in KTOM1 which can manifest as
CC	cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC	heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC	function. The sequence represents a probe used in the invention to
CC	scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX	Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 other;
SQ	Query Match 1.2%; Score 12.8; DB 1; Length 17;
	Best Local Similarity 87.5%; Fred. NO. 9.3e+02;
	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	454 CCTTCCAGGAAGCT 469
Db	17 CCTTCCAGGTAGCT 2
RESULT 1405	
ABQ64197/C	
ID	ABQ64197 standard; DNA; 17 BP.
XX	ABQ64197;
XX	20-AUG-2002 (first entry)
DT	Human KTOM1a portion (ABQ63232) probe # 910.
DE	Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
XX	Gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW	kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
KW	Homo sapiens.
OS	WO200224750-A2.
XX	28-MAR-2002.
XX	21-SEP-2001; 2001WO-US29656.
PF	21-SEP-2000; 2000US-234687P.
XX	27-SEP-2000; 2000US-236359P.
PR	04-OCT-2000; 2000GB-0024263.
PR	30-JAN-2001; 2001WO-US00661.
PR	30-JAN-2001; 2001WO-US00662.
PR	30-JAN-2001; 2001WO-US00663.
PR	30-JAN-2001; 2001WO-US00664.
PR	30-JAN-2001; 2001WO-US00665.
PR	30-JAN-2001; 2001WO-US00666.
PR	30-JAN-2001; 2001WO-US00667.
PR	30-JAN-2001; 2001WO-US00668.
PR	30-JAN-2001; 2001WO-US00669.
PR	30-JAN-2001; 2001WO-US00670.
PR	23-MAY-2001; 2001US-0864761.
PR	28-AUG-2001; 2001US-315676P.
XX	

PT pulmonary disease (COPD), chronic bronchitis and asthma -
 PS Claim 4; Page 79; 152pp; English.
 XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 XX
 SQ Sequence 17 BP; 5 A; 8 C; 2 G; 2 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 501 GGAGATTGGCCAGTT 516
 |||||
 Db 17 GGTGATTGGCCAGGT 2

RESULT 1407
 ABK56724/c
 ID ABK56724 standard; RNA; 17 BP.
 XX
 AC ABK56724;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human CLCA1 gene enzymatic nucleic acid #1095.
 XX
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiaesthatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX
 OS Homo sapiens.
 XX
 PN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US24970.
 XX
 PR 09-AUG-2000; 2000US-224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 XX
 PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX
 DR WPI; 2002-217145/27.
 XX
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -
 XX Claim 4; Page 79; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 501 GGAGATTGGCCAGTT 516
 |||||
 Db 16 GGTGATTGGCCAGGT 1
 RESULT 1408
 ABK57217/c
 ID ABK57217 standard; RNA; 17 BP.
 XX
 AC ABK57217;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human CLCA1 gene enzymatic nucleic acid #1588.
 XX
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiaesthatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX
 OS Homo sapiens.
 XX
 PN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US24970.
 XX
 PR 09-AUG-2000; 2000US-224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 XX
 PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX
 DR WPI; 2002-217145/27.
 XX
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -
 XX Claim 4; Page 99; 152pp; English.
 XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes

CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.

XX
 SQ Sequence 17 BP; 5 A; 8 C; 2 G; 2 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 504 GATTGGCCAGTTGG 519
 |||||
 Db 16 GATTGGCCAGTTGG 1

RESULT 1409
 ABK57443/C
 ID ABK57443 standard; RNA; 17 BP.

AC ABK57443;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #1814.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

OS Homo sapiens.

PN WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US24970.

XX 09-AUG-2000; 2000US-224383P.

XX (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.

PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -

XX Claim 4; Page 113; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.

SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 499 TTGGAGATTGGCCAG 514
 |||||
 Db 16 TCGGTGATTGGCCAG 1

RESULT 1410
 ABK57770/C
 ID ABK57770 standard; RNA; 17 BP.

AC ABK57770;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #2141.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

OS Homo sapiens.

PN WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US24970.

XX 09-AUG-2000; 2000US-224383P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -

XX Claim 4; Page 135; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,

CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCAL, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCAL RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.

XX SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 504 GATTGGCCAGTTGG 519
 Db 17 GATTGGCCAGTTGG 2

RESULT 1411
 ABL92181/C
 ID ABL92181 standard; cDNA; 17 BP.

XX AC ABL92181;

XX DT 30-MAY-2002 (first entry)

XX DE Long human Tumour Endothelial Marker SEQ ID NO 347.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 XX normal endothelial marker; pan-endothelial marker; immunostimulant;
 XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 XX psoriasis; ss.

XX OS Homo sapiens.

XX PN W0200210217-A2.

XX XX 07-FEB-2002.

XX FF 01-AUG-2001; 2001WO-US24031.

XX XX 02-AUG-2000; 2000US-222599P.

XX PR 11-AUG-2000; 2000US-224360P.

XX PR 11-APR-2001; 2001US-282850P.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX DR WPI; 2002-291856/33.

XX PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -

XX PS Disclosure; Page 24; 31pp; English.

XX CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;

CC and pan-endothelial markers (PEM) ABL91903-ABL91995. The present sequence
 CC is that of an oligonucleotide marker useful to the invention.

XX SQ Sequence 17 BP; 5 A; 0 C; 3 G; 9 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAAA 1091
 Db 16 CAACTATTAAACATAA 1

RESULT 1412
 ABL91795/C
 ID ABL91795 standard; DNA; 17 BP.

XX AC ABL91795;

XX XX 29-MAY-2002 (first entry)

XX DE Human GDMPL-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1787.

XX KW Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;
 XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 XX skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN W0200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US16981.

XX PR 26-MAY-2000; 2000US-207456P.

XX PR 21-SEP-2000; 2000US-234687P.

XX PR 27-SEP-2000; 2000US-236359P.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PR 30-JAN-2001; 2001WO-US00661.

XX PR 30-JAN-2001; 2001WO-US00662.

XX PR 30-JAN-2001; 2001WO-US00663.

XX PR 30-JAN-2001; 2001WO-US00664.

XX PR 30-JAN-2001; 2001WO-US00665.

XX PR 30-JAN-2001; 2001WO-US00666.

XX PR 30-JAN-2001; 2001WO-US00667.

XX PR 30-JAN-2001; 2001WO-US00668.

XX PR 30-JAN-2001; 2001WO-US00669.

XX PR 05-FEB-2001; 2001WO-US00670.

XX XX 2001US-266860P.

XX PA (AEOM-) AECOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX DR WPI; 2002-179446/23.

XX PT New polypeptide, for raising antibodies that recognize hGDMPL-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPL-1 -

XX PS Disclosure; SEQ ID 1787; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of
 CC hGDMPL-1 can be used in gene therapy and vaccine production. The
 CC hGDMPL-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPL-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPL-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPL-1 proteins or polypeptides may

CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMLP-1 in
 CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX SQ Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 379 CGTCTCTGCTGGCGG 394
 Db 17 CCTTCTCTGTCGACG 2
 RESULT 1413
 ABN01796/c
 ID ABN01796 standard; DNA; 17 BP.
 XX AC ABN01796;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1788.
 XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US16981.
 XX PR 26-MAY-2000; 2000US-207456P.
 XX PR 21-SEP-2000; 2000US-234687P.
 XX PR 27-SEP-2000; 2000US-236359P.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PR 30-JAN-2001; 2001WO-US00661.
 XX PR 30-JAN-2001; 2001WO-US00662.
 XX PR 30-JAN-2001; 2001WO-US00663.
 XX PR 30-JAN-2001; 2001WO-US00664.
 XX PR 30-JAN-2001; 2001WO-US00665.
 XX PR 05-FEB-2001; 2001US-266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1
 XX proteins, or as specific biomolecule capture probes for

PT surface-enhanced laser desorption ionization, comprises human
 PT myosin-like protein hGDMLP-1 -
 XX Disclosure; SEQ ID 1788; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
 CC hGDMLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMLP-1 proteins, as standards in assays used to determine the
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 379 CGTCTCTGCTGGCGG 394
 Db 16 CCTTCTCTGTCGACG 1
 RESULT 1414
 ABN06603
 ID ABN06603 standard; DNA; 17 BP.
 XX AC ABN06603;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6595.
 XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US16981.
 XX PR 26-MAY-2000; 2000US-207456P.
 XX PR 21-SEP-2000; 2000US-234687P.
 XX PR 27-SEP-2000; 2000US-236359P.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PR 30-JAN-2001; 2001WO-US00661.
 XX PR 30-JAN-2001; 2001WO-US00662.
 XX PR 30-JAN-2001; 2001WO-US00663.
 XX PR 30-JAN-2001; 2001WO-US00664.
 XX PR 30-JAN-2001; 2001WO-US00665.
 XX PR 30-JAN-2001; 2001WO-US00666.
 XX PR 30-JAN-2001; 2001WO-US00667.

PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX (ABOM-) ABOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPT; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX Disclosure; SEQ ID 6595; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption/
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 other;
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 197 CAGTTTCCTGGGTTC 212
 ||| || |||||
 Db 2 CAGCTTGTGGGTTC 17
 RESULT 1415
 ABN06604
 ID ABN06604 standard; DNA; 17 BP.
 XX AC ABN06604;
 XX AC
 XX 29-MAY-2002 (first entry)
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6596.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 XX WO200192524-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX

PF 25-MAY-2001; 2001WO-US16981.
 XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024283.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX (ABOM-) ABOMICA INC.
 PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPT; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX Disclosure; SEQ ID 6596; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption/
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 other;
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 197 CAGTTTCCTGGGTTC 212
 ||| || |||||
 Db 1 CAGCTTGTGGGTTC 16
 RESULT 1416
 ABN07594
 ID ABN07594 standard; DNA; 17 BP.
 XX AC ABN07594;
 XX AC
 XX 29-MAY-2002 (first entry)
 DT

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7586.
XX DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 05-FEB-2001; 2001US-266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1.
XX PS Disclosure; SEQ ID 7586; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
XX N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 769 AACTGGAGAGAGAGTG 784
|||||
Db 2 AACTGAAGAGAGAGTG 17
|||||
RESULT 1417
ABNO7595
ID ABNO7595 standard; DNA; 17 BP.
XX AC ABNO7595;
XX XX
XX 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7587.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 05-FEB-2001; 2001US-266860P.
XX XX
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1.
XX PS Disclosure; SEQ ID 7587; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.

CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 769 AACTGGAGAGAGAGTG 784
Db 1 AACTGAAGAGAGAGTG 16

RESULT 1418
ABN08386/c
ID AEN08386 standard; DNA; 17 BP.
XX AEN08386;
AC
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8378.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WC200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX
PS Disclosure; SEQ ID 8378; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The

CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 5 A; 6 C; 5 G; 1 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 406 TGCTCCAGCAGGCTCT 421
Db 17 TGCTCCAGCTGGCTGT 2

RESULT 1419
ABN08392/c
ID AEN08392 standard; DNA; 17 BP.
XX AEN08392;
AC AEN08392;
XX
XX 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8384.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WC200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.
XX
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
XX Disclosure; SEQ ID 8384; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
XX Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 401 CACCTGCTCCAGCG 416
DB 16 CACTGCTCCAGCTG 1
RESULT 1420
ABN08663/c
ID ABN08663 standard; DNA; 17 BP.
XX
XX ABN08663;
AC
XX
XX 29-MAY-2002 (first entry)
DT
XX
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8655.
DE
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200192524-A2.
FN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US16981.
PF
XX
XX 26-MAY-2000; 2000US-207456P.
PR
XX 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.

PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
XX Disclosure; SEQ ID 8655; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 30 GGTTCCTCCAGGTGCA 45
DB 16 GCTTCCTCCAGCTGCA 1
RESULT 1421
ABK18569/c
ID ABK18569 standard; RNA; 17 BP.
XX
XX ABK18569;
AC
XX
XX 09-APR-2002 (first entry)
DT
XX
XX Human ERG G-cleaver ribozyme target sequence Seq ID No 1216.
DE
XX
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 OS Homo sapiens.
 XX OS
 XX WO2001188124-A2.
 PN
 XX
 PD 22-NOV-2001.
 XX
 XX 16-MAY-2001; 2001WO-US15866.
 XX
 XX 16-MAY-2000; 2000US-0572021.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 DR
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX
 XX Claim 4; Page 81; 149pp; English.
 PS
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 XX Sequence 17 BP; 5 A; 7 C; 2 G; 3 U; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 128 AAGGATGCTGCTTTG 143
 |||||
 17 AAGGATGCTGCGTTG 2
 Db
 RESULT 1422
 ABK18966/c
 ID ABK18966 standard; RNA; 17 BP.
 XX
 XX ABK18966;
 AC
 XX 09-APR-2002 (first entry)
 DT

XX Human ERG DNazyme target sequence Seq ID No 1613.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO2001188124-A2.
 PN
 XX
 PD 22-NOV-2001.
 XX
 XX 16-MAY-2001; 2001WO-US15866.
 XX
 XX 16-MAY-2000; 2000US-0572021.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 DR
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX
 XX Claim 4; Page 106; 149pp; English.
 PS
 XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 XX Sequence 17 BP; 4 A; 8 C; 2 G; 3 U; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 128 AAGGATGCTGCTTTG 143
 |||||
 16 AAGGATGCTGCGTTG 1
 Db

RESULT 1423
ABK19138
ID ABK19138 standard; RNA; 17 BP.
XX
AC ABK19138;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 1785.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200198124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US15866.
XX
PR 16-MAY-2000; 2000US-0572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
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PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
DR
XX
PT Novel polynucleotide which down regulates expression of Ets-related
PT gene, useful for treating cancer; diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome -
XX
PS Claim 4; Page 120; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention.
XX
SQ Sequence 17 BP; 9 A; 3 C; 4 G; 1 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 9.3e-02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 756 AAGGAGATGGCAGAAC 771
Db 1 AAAAAGAUGGCAGAAC 16
II :||:|||||
II :||:|||||
RESULT 1424
ABK26395
ID ABK26395 standard; DNA; 17 BP.
XX
AC ABK26395;
XX
DT 09-APR-2002 (first entry)
XX
DE Waxy starch production genome altering oligonucleotide #51.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW increased fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
KW Ipomoea batatas.
OS Synthetic.
OS
XX WO200192512-A2.
PN
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
XX (UYDE) UNIV DELAWARE.
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
PS Claim 7; Page 148; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),

CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention.

XX Sequence 17 BP; 7 A; 0 C; 7 G; 3 T; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 TGGAGAAATCGGAAGTG 1021

Db 1 TGGAGAAATCGGAAGTG 16

RESULT 1425

ABK26396/C

ID ABK26396 standard; DNA; 17 BP.

XX

AC ABK26396;

XX

09-APR-2002 (first entry)

XX

Waxy starch production genome altering oligonucleotide #52.

XX

Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 o-methyl modification; LNA modification; phosphorothioate linkage;
 DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 abiotic stress tolerance; improved nutritional value; hygromycin-B;
 amino acid over production; herbicide resistance; glyphosate resistance;
 imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 porphyrin herbicide resistance; triazine resistance; disease resistance;
 modified oil production; modified starch production; waxy starch;
 altered floral morphology; male-sterile plant; albino mutant;
 increased fatty acid content; reduced palmitate production; albino plant;
 increased stearate production; reduced linolenic acid production;
 photosynthetic process.

XX

Ipomoea batatas.

OS

Synthetic.

XX

WO200192512-A2.

XX

06-DEC-2001.

XX

01-JUN-2001; 2001WO-US17672.

XX

01-JUN-2000; 2000US-208538P.

PR

30-OCT-2000; 2000US-244989P.

PR

27-MAR-2001; 2000US-0818875.

XX

(UYDE) UNIV DELAWARE.

XX

Kimiec EB, Gamper HB, Rice MC, Kim J;

XX

WPI; 2002-106307/14.

XX

New oligonucleotides with modified nuclease-resistant termini, useful

for creating plants with desired phenotypes, e.g. stress tolerance,

improved nutritional value, herbicide or disease resistance, or

modified oil production

XX

Claim 7; Page 148; 220pp; English.

XX

The invention relates to an oligonucleotide for targeted alteration of a

genetic sequence, which comprises a single-stranded oligonucleotide

having a DNA domain. The DNA domain has at least one mismatch with

respect to the genetic sequence to be altered and further comprises

chemical modifications of the oligonucleotide. The chemical modifications

CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
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 CC directing repair or alteration of plant genetic information. The
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 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
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 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention.

SQ Sequence 17 BP; 3 A; 7 C; 0 G; 7 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 TGGAGAAATCGGAAGTG 1021

Db 17 TGGAGAAATCGGAAGTG 2

RESULT 1426

ABK26635/C

ID ABK26635 standard; DNA; 17 BP.

XX

AC ABK26635;

XX

09-APR-2002 (first entry)

XX

Waxy starch production genome altering oligonucleotide #291.

XX

Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 o-methyl modification; LNA modification; phosphorothioate linkage;
 DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 abiotic stress tolerance; improved nutritional value; hygromycin-B;
 amino acid over production; herbicide resistance; glyphosate resistance;
 imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 porphyrin herbicide resistance; triazine resistance; disease resistance;
 modified oil production; modified starch production; waxy starch;
 altered floral morphology; male-sterile plant; albino mutant;
 increased fatty acid content; reduced palmitate production; albino plant;
 increased stearate production; reduced linolenic acid production;
 photosynthetic process.

XX

Oryza glaberrima.

OS

Synthetic.

XX

WO200192512-A2.

XX

06-DEC-2001.

XX

01-JUN-2001; 2001WO-US17672.

XX

01-JUN-2000; 2000US-208538P.

PR

30-OCT-2000; 2000US-244989P.

PR

27-MAR-2001; 2000US-0818875.

XX

(UYDE) UNIV DELAWARE.

XX

Kimiec EB, Gamper HB, Rice MC, Kim J;

XX

WPI; 2002-106307/14.

XX

New oligonucleotides with modified nuclease-resistant termini, useful

for creating plants with desired phenotypes, e.g. stress tolerance,

```

PT improved nutritional value, herbicide or disease resistance, or
XX modified oil production
XX
PS Claim 7; Page 162; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 350 CAGCGCCACCTGTCA 365
DB 16 CGGCGCCTACCTGTCA 1
RESULT 1427
ID ABK26636 standard; DNA; 17 BP.
XX
AC ABK26636;
XX
DT 09-APR-2002 (first entry)
XX
DE Waxy starch production genome altering oligonucleotide #292.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; sulphonylurea herbicide resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW increased fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Oryza glaberrima.
OS Synthetic.
XX
XX WO200192512-A2.
XX
XX 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-US17672.
XX
XX 01-JUN-2000; 2000US-209538P.
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XX 30-OCT-2000; 2000US-244989P.
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PR 27-MAR-2001; 2001US-0818875.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Kmtec EB, Gamper HB, Rice MC, Kim J;
XX
DR WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production
XX
PS Claim 7; Page 162; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 350 CAGCGCCACCTGTCA 365
DB 2 CGGCGCCTACCTGTCA 17
RESULT 1428
AAS18428/C
ID AAS18428 standard; DNA; 17 BP.
XX
AC AAS18428;
XX
DT 12-MAR-2002 (first entry)
XX
DE PCR primer 415 used to amplify cDNA encoding human chk1.
XX
KW Human; checkpoint protein; hchk1; DNA damage; B-cell cDNA library;
KW cell cycle checkpoint pathway; inhibition of cell growth; tumour;
KW malignancy; growth deficiency; development deficiency; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX US6307015-B1.
XX
XX 23-OCT-2001.
XX
XX 12-JAN-2000; 2000US-0488364.
XX
XX 05-SEP-1997; 97US-0924183.
XX

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sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

Enemy Match

OV 514 CATTGGGATTTTCGGG 529
Best Local Similarity 87.5%; Pred. NO. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Db
1 GATCGGCAATTTGGGAG 16

ABT37161
ID ABT37161 standard; DNA; 17 BP.
XX
XX
XX ABT37161.

DT	12-JUN-2003 (first entry)	
XX		
DE	Tumour suppression related human embryonic cells	2708

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;
human fukutin; ds.

XXX
DN W02002025175-22

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

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FA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX

PI
yy
Telerman A, Amson R, Tuljinder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases

PT polypeptides, antibodies and transfected cells -

PS Disclosure: Page 360: 720pp; French.

XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence

CC given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence is compared with

CC optimal alignment, at least 80 % identity to the 17 mer sequence, a

CC the complement of any of them, or the corresponding RNA. The novel

isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 9 A; 2 C; 4 G; 2 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 110 GGTCAAGAAACGGAA 125
| | | | | | | | | |
Db 1 GATCAAGAACTGGAA 16

RESULT 1433
ABT37451/c
ID ABT37451 standard; DNA; 17 BP.

AC ABT37451;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 3088.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

XX 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001FR-0011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells -

XX Disclosure; Page 394; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid,

e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 GGCAATTCCTCAGGATC 495
| | | | | | | | | |
Db 16 GTCCTTCCTCAGGATC 1

RESULT 1434
ABT38498/c
ID ABT38498 standard; DNA; 17 BP.

AC ABT38498;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 4135.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

XX 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001FR-0011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells -

XX Disclosure; Page 517; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids,

CC Polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 3 A; 6 C; 3 G; 5 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 668 GCTGAAGTTCACAGAT 683
 ||||| |||||
 Db 17 GCTGAAGTTCACAGAT 2

RESULT 1435

ABT38748
 ID ABT38748 standard; DNA; 17 BP.

AC ABT38748;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 4385.

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001FR-0011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells

PS Disclosure; Page 546; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for

CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 5 A; 3 C; 3 G; 6 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 ACCTTCACAAAGTTGT 285

Db 2 ATCTTCACAAAGTTGT 17

RESULT 1436

ABT39374/C
 ID ABT39374 standard; DNA; 17 BP.

AC ABT39374;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 5011.

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001FR-0011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells

PS Disclosure; Page 619; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell

CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 2 G; 8 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 118 AACGGGAAGAAGGAT 133
 Db 17 AACAGGAGGAAGGAT 2
 RESULT 1437
 ID ACA06327 standard; RNA; 17 BP.
 AC ACA06327;
 AT
 DT 03-JUN-2003 (first entry)
 XX NFkB sub-unit modulating inozyme substrate #146.
 DE
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection;
 KW ss.
 OS Homo sapiens.
 XX
 XX US2002177568-A1.
 XX 28-NOV-2002.
 XX 23-MAY-2001; 2001US-0864785.
 XX 15-AUG-1994; 94US-0291932.
 XX 07-DEC-1992; 92US-0987132.
 XX 18-MAY-1994; 94US-0245466.
 XX 23-DEC-1996; 96US-0777916.
 XX (STIN/) STINCHCOMB D T.
 XX (MCSW/) MCSWIGGEN J.
 XX (DRAP/) DRAPER K G.
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 XX WPI; 2003-340953/32.
 XX Novel enzymatic nucleic acid molecules which down regulates expression
 PT of a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 3; Page 29; 72pp; English.
 XX The invention describes an enzymatic nucleic acid molecule (I) which down

CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel
 CC enzymatic nucleic acid molecule.
 XX
 SQ Sequence 17 BP; 0 A; 10 C; 4 G; 3 U; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 9.3e+02;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 420 CTCGGGTGCGCCCTG 435
 Db 2 CUCGCGUGCGCCUG 17
 RESULT 1438
 ID ACA06426 standard; RNA; 17 BP.
 AC ACA06426;
 XX
 XX 03-JUN-2003 (first entry)
 XX NFkB sub-unit modulating inozyme substrate #245.
 DE
 DE Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection;
 KW ss.
 OS Homo sapiens.
 XX
 XX US2002177568-A1.
 XX 28-NOV-2002.
 XX 23-MAY-2001; 2001US-0864785.
 XX 15-AUG-1994; 94US-0291932.
 XX 07-DEC-1992; 92US-0987132.
 XX 18-MAY-1994; 94US-0245466.
 XX 23-DEC-1996; 96US-0777916.

PA (STIN/) STINCHOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression
PT of a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases -
XX
XX Claim 3; Page 30; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a cleaving cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapies including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel
CC enzymatic nucleic acid molecule.
XX
XX Sequence 17 BP; 6 A; 4 C; 3 U; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e-02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 245 GCTCTTGAGGACTTGA 260
XX 17 GCTCTTGAGGCTCTCA 2
XX
XX RESULT 1439
XX ACA06768/c
XX ID ACA06768 standard; RNA; 17 BP.
XX
XX ACA06768;
XX
XX 03-JUN-2003 (first entry)
XX
XX NFkB sub-unit modulating inozyme substrate #587.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
XX G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
XX lung cancer; prostate cancer; colorectal cancer; brain cancer;
XX oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; head and neck cancer; ovarian cancer; melanoma;
XX lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
XX chemotherapies; paclitaxel; docetaxel; cisplatin; methotrexate;
XX cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
XX gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX transplant/graft rejection; reperfusion injury; glomerulonephritis;
XX allergic airway inflammation; inflammatory bowel disease; infection;

KW SS.
XX Homo sapiens.
XX US2002177568-A1.
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-0864785.
XX
XX 15-AUG-1994; 94US-0291932.
XX 07-DEC-1992; 92US-0987132.
XX 18-MAY-1994; 94US-0245466.
XX 23-DEC-1996; 96US-0777916.
XX
XX (STIN/) STINCHOMB D T.
XX (MCSW/) MCSWIGGEN J.
XX (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression
PT of a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases -
XX
XX Claim 3; Page 35; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a cleaving cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapies including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel
CC enzymatic nucleic acid molecule.
XX
XX Sequence 17 BP; 2 A; 10 C; 1 G; 4 U; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 9.3e-02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1001 GAGGCTGGAGATGGG 1016
XX 17 GAAGCTGGAGATGGG 2
XX
XX RESULT 1440
XX ACA07669
XX ID ACA07669 standard; RNA; 17 BP.
XX
XX ACA07669;
XX
XX 03-JUN-2003 (first entry)
XX
XX DT

DE NFKB sub-unit modulating zinzyme substrate #68.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection;
KW ss.

XX Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-0864785.

XX 15-AUG-1994; 94US-0291932.

XX 07-DEC-1992; 92US-0987132.

XX 18-MAY-1994; 94US-0245466.

XX 23-DEC-1996; 96US-0777916.

XX (STIN/) STINCHOMB D T.

XX (MCSW/) MCSWIGGEN J.

XX (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression

XX of a sequence encoding a subunit of nuclear factor kappa B useful for
XX treating cancer, inflammatory disorders and autoimmune diseases -
XX Claim 3; Page 38; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down
XX regulates expression of a sequence encoding a subunit of nuclear factor
XX kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne
XX configuration. The enzymatic nucleic acid molecule is adapted to treat
XX cancer and is useful for down-regulating REL-A activity in a cell, for
XX treating a patient having a condition associated with the level of REL-A.
XX (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
XX the presence of a divalent cation, especially Mg²⁺. The enzymatic and
XX antisense nucleic acid molecules are useful for treating breast, lung,
XX prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
XX cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
XX multidrug resistant cancer. The method involves use of other drug
XX therapies such as monoclonal antibodies, REL-A-specific inhibitors or
XX chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
XX cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
XX semcitabine or radiation therapy. The enzymatic and antisense nucleic
XX acid molecules are also useful for treating inflammatory disease such as
XX rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
XX obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
XX rejection, gene therapy applications, ischaemia/reperfusion injury
XX (central nervous system (CNS) and myocardial), glomerulonephritis,
XX sepsis, allergic airway inflammation, inflammatory bowel disease or
XX infection. This sequence represents the substrate of a novel
XX enzymatic nucleic acid molecule.

XX Sequence 17 BP; 0 A; 9 C; 4 G; 4 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 9.3e+02;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 420 CTCGGCTGCCCTG 435

DB 1 CUCGCGCUGCGCUG 16

RESULT 1441

ABX16358/c

ID ABX16358 standard; DNA; 17 BP.

XX AC ABX16358;

XX DT 08-APR-2003 (first entry)

XX Human checkpoint gene Chk1 PCR primer 415.

XX Human; checkpoint; chk1; anti-Chk1 antibody; tumour;

XX PCR; primer; ss.

XX OS Homo sapiens.

XX PN JS2002156247-A1.

XX PD 24-OCT-2002.

XX PF 12-DEC-2001; 2001US-0020038.

XX PR 12-JAN-2000; 2000US-0488364.

XX PA (ELLE/) ELLEDGE S J.

XX PA (SANC/) SANCHEZ Y.

XX PI Elledge SJ, Sanchez Y;

XX DR WPI; 2003-182651/18.

XX New anti-Chk1 antibody, that may be a monoclonal or polyclonal
XX antibody, useful for detecting a Chk1 protein that is associated with a
XX tumor -
XX Example 2; Page 15; 28pp; English.

XX The invention describes an anti-Chk1 antibody capable of specifically
XX binding to an antigenic determinant on the proteins encoded by a
XX sequence comprising 476 (3 sequences), 479, 496 or 513 amino acids.
XX A new method is used to produce the antibody, which is useful for
XX detecting a Chk1 protein that is associated with a tumour. This
XX sequence represents a primer used in mapping of human checkpoint
XX protein Chk1.

XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 325 AGAAGCTGTGGAGCAA 341

DB 16 AGAAGTCTGGAGCAA 1

RESULT 1442

ABX72106/c

ID ABX72106 standard; DNA; 17 BP.

XX AC ABX72106;

XX DT 12-MAR-2003 (first entry)

XX Human tumour endothelial marker TBM 37 DNA long tag.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;

KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX Homo sapiens.
XX WO2002083874-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US08253.
XX PR 11-APR-2001; 2001US-282850P.
XX PR 06-FEB-2002; 2002US-354262P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
XX New purified human transmembrane protein, designated as tumour
XX endothelial marker (TEM) 3, useful for detecting, diagnosing or
XX treating tumours, polycystic kidney disease, diabetic retinopathy,
XX rheumatoid arthritis or psoriasis -
XX Disclosure; Page 363; 374pp; English.
XX The present invention relates to a novel method for the isolation of
XX endothelial cells (ECs), and the identification of genes expressed in
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
XX identified in human ECs. The human EC marker proteins and the
XX polynucleotide sequences encoding them are useful for detecting,
XX diagnosing or treating tumours as well as polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are
XX also useful for inhibiting neovascularization or tumour angiogenesis,
XX for inducing an immune response to tumour endothelial cells in a
XX patient, or for identifying candidate drugs for treating tumours.
XX ABX72067-ABX72116 represent human TEM DNA tags.
XX SQ Sequence 17 BP; 5 A; 0 C; 3 G; 9 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1091
DB 16 CAACTATTAAACATAA 1
RESULT 1443
ABZ61500
ID ABZ61500 standard; RNA; 17 BP.
XX AC ABZ61500;
XX DT 21-MAR-2003 (first entry)
XX DE Human H-Ras DNase target #291.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX PD 05-DEC-2002.

KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX Homo sapiens.
XX WO2002083874-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US08253.
XX PR 11-APR-2001; 2001US-282850P.
XX PR 06-FEB-2002; 2002US-354262P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
XX New purified human transmembrane protein, designated as tumour
XX endothelial marker (TEM) 3, useful for detecting, diagnosing or
XX treating tumours, polycystic kidney disease, diabetic retinopathy,
XX rheumatoid arthritis or psoriasis -
XX Disclosure; Page 363; 374pp; English.
XX The present invention relates to a novel method for the isolation of
XX endothelial cells (ECs), and the identification of genes expressed in
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
XX identified in human ECs. The human EC marker proteins and the
XX polynucleotide sequences encoding them are useful for detecting,
XX diagnosing or treating tumours as well as polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are
XX also useful for inhibiting neovascularization or tumour angiogenesis,
XX for inducing an immune response to tumour endothelial cells in a
XX patient, or for identifying candidate drugs for treating tumours.
XX ABX72067-ABX72116 represent human TEM DNA tags.
XX SQ Sequence 17 BP; 5 A; 0 C; 3 G; 9 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1091
DB 16 CAACTATTAAACATAA 1
RESULT 1443
ABZ61500
ID ABZ61500 standard; RNA; 17 BP.
XX AC ABZ61500;
XX DT 21-MAR-2003 (first entry)
XX DE Human H-Ras DNase target #291.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX PD 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.
XX PF 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX Mcdwigggen J;
XX WPI; 2003-140484/13.
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX Claim 58; Page 116; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and
XX anti-rheumatic activity. The nucleic acid molecules are useful for
XX reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX acids are also useful for treating breast, ovarian, colorectal, lung,
XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
XX sequences for the human ribozymes of the invention.
XX SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 U; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 9.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 979 TAACTCTGAGCCCTTGG 994
DB 1 UAACUCAGCCCUCCG 16
RESULT 1444
ABZ64967/c
ID ABZ64967 standard; RNA; 17 BP.
XX AC ABZ64967;
XX DT 21-MAR-2003 (first entry)
XX DE Human HER2 DNase substrate #424.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX PD 05-DEC-2002.
XX 29-MAY-2002; 2002WO-US16840.
XX PR 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX Mcdwigggen J;
XX

DR WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

PS Claim 4; Page 141; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and

CC anti-rheumatic activity. The nucleic acid molecules are useful for

CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic

CC acids are also useful for treating breast, ovarian, colorectal, lung,

CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.

CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,

CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

CC sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 5 A; 3 C; 7 G; 2 U; 0 other;

SQ

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 474 GAACCTGGGCTTCCTC 489

DB 17 GTACTCGGCTTCCTC 2

RESULT 1445

ABZ65388

ID ABZ65388 standard; RNA; 17 BP.

AC ABZ65388;

XX 21-MAR-2003 (first entry)

DE Human HER2 DNzyme substrate #845.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;

KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

OS

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

PR 06-JUN-2001; 2001US-296249P.

PR 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

PA Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 4; Page 149; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

XX

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and

CC anti-rheumatic activity. The nucleic acid molecules are useful for

CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic

CC acids are also useful for treating breast, ovarian, colorectal, lung,

CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.

CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,

CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

CC sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 1 A; 7 C; 6 G; 3 U; 0 other;

SQ

Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 9.3e+02;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 375 CTGGCGCTCTCTCTG 390

DB 2 CUGCCGACUGUGG 17

RESULT 1446

ABZ65433/C

ID ABZ65433 standard; RNA; 17 BP.

XX 21-MAR-2003 (first entry)

DE Human HER2 DNzyme substrate #890.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;

KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

OS

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

PR 06-JUN-2001; 2001US-296249P.

PR 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

PA Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 4; Page 150; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and

CC anti-rheumatic activity. The nucleic acid molecules are useful for

CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic

CC acids are also useful for treating breast, ovarian, colorectal, lung,

CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.

CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,

CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

CC sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 5 A; 5 C; 5 G; 2 U; 0 other;

SQ

CC The present invention describes a method for constructing a cDNA tag for
 CC identifying an expressed gene. The method comprises: (a) preparation of
 CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
 CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
 CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
 CC linker Y ligated material; and (e) cleaving the amplification product.
 CC The method can be used for the construction of cDNA tags for identifying
 CC expressed genes, which is applicable in gene expression analysis, disease
 CC diagnosis and identifying target for gene therapy, including the
 CC clarification of difference in function or morphology of cells under
 CC physiological or pathological conditions. The cDNA or cells for assay can
 CC be specifically expressed, with reproducibility and accuracy in the
 CC detection of genes. The present sequence represents an expressed gene
 CC identification (EGI) cDNA tag related oligonucleotide which is used in
 CC an example from the present invention.

SQ Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1096
 |||||
 Db 14 TAAAAAATAAAAAA 1

RESULT 998
 ABQ83278/C
 ID ABQ83278 standard; DNA; 14 BP.
 AC ABQ83278;
 DT 18-JAN-2003 (first entry)
 DE EGI cDNA tag related oligonucleotide SEQ ID NO:51.
 KW cDNA tag; identification; gene expression analysis; linker;
 KW expressed gene identification; EGI; ss.
 OS Synthetic.
 FN WO200274951-A1.
 PD 26-SEP-2002.
 PF 13-MAR-2002; 2002WO-JP02338.
 PR 15-MAR-2001; 2001JP-0073959.
 PA (KURE) KUREHA CHEM IND CO LTD.
 PA (YAMA/) YAMAMOTO M.
 PA (YAMA/) YAMAMOTO N.

Yamamoto M, Yamamoto N, Hirose K, Kasai J;
 WPI; 2002-759896/82.
 Construction of cDNA tags for identifying expressed genes with specific
 linkers and recognition sequences, applicable in gene expression
 analysis, disease diagnosis and identifying target for gene therapy -
 Example 1; Page 24; 59pp; Japanese.

The present invention describes a method for constructing a cDNA tag for
 identifying an expressed gene. The method comprises: (a) preparation of
 complementary deoxyribonucleic acid; (b) producing cDNA fragment by
 cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
 fragment ligated material; (d) amplification of the linker X-cDNA tag-
 linker Y ligated material; and (e) cleaving the amplification product.
 The method can be used for the construction of cDNA tags for identifying
 expressed genes, which is applicable in gene expression analysis, disease
 diagnosis and identifying target for gene therapy, including the

CC clarification of difference in function or morphology of cells under
 CC physiological or pathological conditions. The cDNA or cells for assay can
 CC be specifically expressed, with reproducibility and accuracy in the
 CC detection of genes. The present sequence represents an expressed gene
 CC identification (EGI) cDNA tag related oligonucleotide which is used in
 CC an example from the present invention.

SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAATAAAAAA 1097
 |||||
 Db 14 AAAAAAATAAAAAA 1

RESULT 999
 ABL88471/C
 ID ABL88471 standard; DNA; 14 BP.
 AC ABL88471;
 DT 16-MAY-2002 (first entry)
 DE Oligo dt 3P1 primer 1.
 KW Pain; analgesic; gene therapy; neurological disorder;
 KW neurodegenerative disease; primer; ss.
 OS Synthetic.
 FN WO200212338-A2.
 PD 14-FEB-2002.
 PF 03-AUG-2001; 2001WO-EP09011.
 PR 03-AUG-2000; 2000DE-1037759.
 PA (CHEF) GRUENTHAL GMBH.

Gillen C, Wetzel S, Wnendt S, Weihe E, Schaefer MK;
 WPI; 2002-257469/30.
 Identifying pain-regulating compounds, useful for treating chronic pain
 and for diagnosis, by measuring binding of compounds to specific
 peptides and proteins -
 Example 1; Page 62; 213pp; German.

The invention relates to identifying pain-regulating substances (A)
 comprises (i) incubating a test substance with a cell (or preparation
 from it) that has synthesised a peptide or protein (B) and (ii) measuring
 either binding of the test substance to (B) or some functional parameter
 that is altered by this binding. The method is useful for identifying
 pain-regulating substances (A) with analgesic activity (A) along with
 nucleic acid (ABL88471-ABL88441) that encode proteins (B),
 ABB85006-ABB85037) that interact with (A); (B); vectors containing the
 nucleic acid; antibodies against (B); cells that express (B) and agents
 that bind to (B), are all useful for treating pain, particularly chronic
 pain, including use in gene therapy. The same materials can also be used
 for diagnosis, e.g. of neurological and neurodegenerative diseases. The
 present sequence is that of a PCR primer, used in examples of the
 invention.

SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1082 TTAATAAAAAAAAAA 1095
Db 14 TTAATAAAAAAAAAA 1

RESULT 1000
ABA93701/c
ID ABA93701 standard; DNA; 14 BP.
XX
AC ABA93701;
XX
DT 30-APR-2002 (first entry)
XX
DE Light responsive oligonucleotide (X1)T14.
XX
KW Light responsive; detection; single nucleotide polymorphism; SNP;
KW irradiation; ss.
XX
OS Synthetic.
XX
PN JP2001346579-A.
XX
PD 18-DEC-2001.
XX
PF 02-JUN-2000; 2000JP-0165441.
XX
PR 02-JUN-2000; 2000JP-0165441.
XX
PA (KOMI/) KOMIYAMA S.
PA (ASAN/) ASANUMA H.
XX
DR WPI; 2002-145181/19.
XX
PT Detecting single nucleotide polymorphism for expressing sensitivity
PT information of diseases and drugs, comprises using a new
PT oligonucleotide
XX
PS Example 3; Page 11; 14pp; Japanese.
XX
CC The present invention describes a method for detecting single nucleotide
CC polymorphisms (SNPs). Also described is an oligonucleotide used in the
CC detection of an SNP, prepared by binding an oligonucleotide having a
CC complementary sequence or those devoid of up to several bases with 1 or
CC more organic group(s) to be tested by light irradiation of a specific
CC wave length to vary a double strand formation property of the
CC oligonucleotide to be tested. The method is used for detecting SNPs.
CC The present sequence represents a light responsive oligonucleotide which
CC is used in an example from the present invention.
XX
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 other;
Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
Db 14 AAAAAAAAAAAAAA 1

RESULT 1001
AAD24492/c
ID AAD24492 standard; DNA; 14 BP.
XX
AC AAD24492;
XX
DT 07-MAR-2002 (first entry)
XX
DE Retinoid-regulated gene isolating poly(T) PCR primer #6.
XX
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;

```

```

KW retinoid-regulated gene; ss.
OS Unidentified.
XX
PN US6306624-B1.
XX
PD 23-OCT-2001.
XX
PF 25-JUN-1997; 97US-0882164.
XX
PR 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 2002-033254/04.
XX
PT New DNA fragments having promoter activity, useful in retinoid
PT metabolism, as well as in producing retinoic acid metabolizing
PT cytochrome P450s that are useful as targets for the treatment of
PT certain cancers -
XX
PS Disclosure; Column 13; 75pp; English.
XX
CC The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers
CC such as prostate cancer. The invention also relates to a method of
CC screening drugs for their effect on activity of RA inducible proteins.
CC The present DNA sequence is poly(T) PCR primer which is used for
CC isolating retinoid regulating genes by differential display of mRNAs.
XX
SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 other;
Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
Db 14 TTAATAAAAAAAAAA 1

RESULT 1002
AAT52134/c
ID AAT52134 standard; RNA; 15 BP.
XX
AC AAT52134;
XX
DT 25-MAR-2003 (updated)
DT 25-MAR-1997 (first entry)
XX
DE Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome;
KW AIDS; ss.

```

OS Homo sapiens.
 XX W09523225-A2.
 PN
 XX
 XX
 XX 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB00156.
 XX
 XX 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 18-MAY-1994; 94US-0245736.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 16-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozyms having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX
 XX Claim 2; Page 175; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and
 CC thereby inhibit ICAM-1 expression, making them useful for reducing
 CC transplant rejection and alleviating symptoms in patients with
 CC rheumatoid arthritis, asthma and other inflammatory disorders.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 1 A; 0 C; 0 G; 14 U; 0 other;
 XX
 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.3e-02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 15 AAAAAAAAAAAAAA 2

RESULT 1003
 AAT52140/c
 ID AAT52140 standard; RNA; 15 BP.
 XX
 AC AAT52140;
 XX
 DT 25-MAR-2003 (updated)
 XX 25-MAR-1997 (first entry)
 DE Human ICAM hammerhead ribozyme target sequence (nt. position 2912).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozyms having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX
 XX Claim 2; Page 175; 407pp; English.
 XX

CC The present sequence represents a preferred target sequence for
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC Ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and
 CC thereby inhibit ICAM-1 expression, making them useful for reducing
 CC transplant rejection and alleviating symptoms in patients with
 CC rheumatoid arthritis, asthma and other inflammatory disorders.
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 15 BP; 0 A; 1 C; 0 G; 14 U; 0 other;
 SQ Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1097

Db |||||
 14 AAAAAAAAAAAAAA 1

RESULT 1004

AAF49041/C

ID AAF49041 standard; DNA; 15 BP.

XX AC

AAF49041;

XX XX

DT 30-MAR-2001 (first entry)

XX XX

DE IGF-I oligonucleotide #1.

XX XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU00693.

XX PR 21-JUN-1999; 99US-0140345.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX Example 8; Page 60; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1097

Db |||||
 14 AAAAAAAAAAAAAA 1

RESULT 1005

AAF53330/C

ID AAF53330 standard; DNA; 15 BP.

XX AC

AAF53330;

XX XX

DT 30-MAR-2001 (first entry)

XX XX

DE IGF-I oligonucleotide #4290.

XX XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU00693.

XX PR 21-JUN-1999; 99US-0140345.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX Example 8; Page 88; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids,

CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX
 SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 TGCAGAGAGCTGCT 334
 Db 15 TGCAGAGAGCTGCT 2

RESULT 1006
 AAF53333/C
 ID AAF53333 standard; DNA; 15 BP.

XX AAF53333;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #4293.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytotoxic; dermatological; cardiac; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX WO200078341-A1.

XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU00693.
 PF
 XX 21-JUN-1999; 99US-0140345.
 PR

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -

XX Example 8; Page 88; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of

CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 3 A; 4 C; 3 G; 5 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 ACTGCAGAGAGCT 332
 Db 14 ACTGCAGAGAGCT 1

RESULT 1007
 ABK98167/C
 ID ABK98167 standard; DNA; 15 BP.

XX ABK98167;
 AC
 XX 07-OCT-2002 (first entry)
 DT

XX Triple helix forming associated oligonucleotide #37.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX Synthetic.

XX US6403302-B1.

XX 11-JUN-2002.

XX 16-DEC-1993; 93US-0168920.

XX 17-SEP-1992; 92US-0946976.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dervan PB, Beal PA;

XX WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression -

XX Example 6; Fig 20A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for
 CC forming a triple-helix comprising a double helical nucleic acid
 CC comprising first and second substantially complementary strands, and
 CC an oligonucleotide bound to a purine-rich target sequence within the
 CC double helical nucleic acid, where the oligonucleotide binds in a
 CC parallel and antiparallel orientation, respectively, to target
 CC sequences on alternate strands of the double helical nucleic acid.
 CC The method has therapeutic applications, where gene expression is
 CC controlled by selective triple-helix formation within expression
 CC regulatory sequences of a target gene. The oligonucleotides can be
 CC used to form triple-helices, and are useful to detect the presence or
 CC absence of specific sequences within genomic DNA for diagnostic and
 CC therapeutic purposes. The oligonucleotides can be selected to
 CC specifically bind to pathogenic double-stranded DNA including specific
 CC sequences required by pathogenic bacteria or viruses for replication or
 CC virulence, reducing their pathogenicity. Alternatively, the
 CC oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or
 CC viral origin. Such therapeutic oligonucleotides are capable of forming
 CC triple-helices with such sequences in cancerous cells containing the

CC activated oncogene, so preferentially killing or repressing the cancer
 CC causing cell. The present sequence represents an oligonucleotide
 CC used in the methods of the present invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;
 SQ Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 Db ||||| |||||
 15 AAAAAAAAAAAAAA 1

RESULT 1009
 ABK98168/c
 ID ABK98168 standard; DNA; 15 BP.

XX AC ABK98168;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #38.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX XX US6403302-B1.

XX PN 11-JUN-2002.

XX PD 16-DEC-1993; 93US-0168920.

XX PF 17-SEP-1992; 92US-0946976.

XX PR (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PA Dervan PB, Beal PA;

XX PI WPI; 2002-536030/57.

XX DR A triple-helix comprising a double helical nucleic acid (DHNA) and an
 XX oligonucleotide which binds in parallel and antiparallel orientation,
 XX respectively, for targeting sequences on alternate strands of DHNA to
 XX control gene expression -

XX Example 6; Fig 20A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for
 XX forming a triple-helix comprising a double helical nucleic acid
 XX comprising first and second substantially complementary strands, and
 XX an oligonucleotide bound to a purine-rich target sequence within the
 XX double helical nucleic acid, where the oligonucleotide binds in a
 XX parallel and antiparallel orientation, respectively, to target
 XX sequences on alternate strands of the double helical nucleic acid.
 XX The method has therapeutic applications, where gene expression is
 XX controlled by selective triple-helix formation within expression
 XX regulatory sequences of a target gene. The oligonucleotides can be
 XX used to form triple-helices, and are useful to detect the presence or
 XX absence of specific sequences within genomic DNA for diagnostic and
 XX therapeutic purposes. The oligonucleotides can be selected to
 XX specifically bind to pathogenic double-stranded DNA including specific
 XX sequences required by pathogenic bacteria or viruses for replication or
 XX virulence, reducing their pathogenicity. Alternatively, the
 XX oligonucleotide can be chosen to target a unique sequence of the
 XX pathogen which is not found in the genome of pathogen's host. The
 XX oligonucleotides can be used in cancer treatment by way of triple-helix
 XX suppression of specific oncogenes including those of endogenous or

CC viral origin. Such therapeutic oligonucleotides are capable of forming
 CC triple-helices with such sequences in cancerous cells containing the
 CC activated oncogene, so preferentially killing or repressing the cancer
 CC causing cell. The present sequence represents an oligonucleotide
 CC used in the methods of the present invention.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;
 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 Db ||||| |||||
 15 AAAAAAAAAAAAAA 1

RESULT 1009
 ABK98169/c
 ID ABK98169 standard; DNA; 15 BP.

XX AC ABK98169;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #39.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX XX US6403302-B1.

XX PN 11-JUN-2002.

XX PD 16-DEC-1993; 93US-0168920.

XX PF 17-SEP-1992; 92US-0946976.

XX PR (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PA Dervan PB, Beal PA;

XX PI WPI; 2002-536030/57.

XX DR A triple-helix comprising a double helical nucleic acid (DHNA) and an
 XX oligonucleotide which binds in parallel and antiparallel orientation,
 XX respectively, for targeting sequences on alternate strands of DHNA to
 XX control gene expression -

XX Example 6; Fig 20A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for
 XX forming a triple-helix comprising a double helical nucleic acid
 XX comprising first and second substantially complementary strands, and
 XX an oligonucleotide bound to a purine-rich target sequence within the
 XX double helical nucleic acid, where the oligonucleotide binds in a
 XX parallel and antiparallel orientation, respectively, to target
 XX sequences on alternate strands of the double helical nucleic acid.
 XX The method has therapeutic applications, where gene expression is
 XX controlled by selective triple-helix formation within expression
 XX regulatory sequences of a target gene. The oligonucleotides can be
 XX used to form triple-helices, and are useful to detect the presence or
 XX absence of specific sequences within genomic DNA for diagnostic and
 XX therapeutic purposes. The oligonucleotides can be selected to
 XX specifically bind to pathogenic double-stranded DNA including specific
 XX sequences required by pathogenic bacteria or viruses for replication or
 XX virulence, reducing their pathogenicity. Alternatively, the
 XX oligonucleotide can be chosen to target a unique sequence of the
 XX pathogen which is not found in the genome of pathogen's host. The

CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or
CC viral origin. Such therapeutic oligonucleotides are capable of forming
CC triple-helices with such sequences in cancerous cells containing the
CC activated oncogene, so preferentially killing or repressing the cancer
CC causing cell. The present sequence represents an oligonucleotide
CC used in the methods of the present invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 1010
ABK98186/C
ID ABK98186 standard; DNA; 15 BP.

XX AC ABK98186;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #50.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-0168920.

XX PR 17-SEP-1992; 92US-0946976.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression -

XX PS Example 7; Fig 24A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for
XX forming a triple-helix comprising a double helical nucleic acid
XX comprising first and second substantially complementary strands, and
XX an oligonucleotide bound to a purine-rich target sequence within the
XX double helical nucleic acid, where the oligonucleotide binds in a
XX parallel and antiparallel orientation, respectively, to target
XX sequences on alternate strands of the double helical nucleic acid.
XX The method has therapeutic applications, where gene expression is
XX controlled by selective triple-helix formation within expression
XX regulatory sequences of a target gene. The oligonucleotides can be
XX used to form triple-helices, and are useful to detect the presence or
XX absence of specific sequences within genomic DNA for diagnostic and
XX therapeutic purposes. The oligonucleotides can be selected to
XX specifically bind to pathogenic double-stranded DNA including specific
XX sequences required by pathogenic bacteria or viruses for replication or
XX virulence, reducing their pathogenicity. Alternatively, the

CC oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or
CC viral origin. Such therapeutic oligonucleotides are capable of forming
CC triple-helices with such sequences in cancerous cells containing the
CC activated oncogene, so preferentially killing or repressing the cancer
CC causing cell. The present sequence represents an oligonucleotide
CC used in the methods of the present invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 1011

ABK98187/C

ID ABK98187 standard; DNA; 15 BP.

XX AC ABK98187;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #51.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-0168920.

XX PR 17-SEP-1992; 92US-0946976.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression -

XX PS Example 7; Fig 24A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for
XX forming a triple-helix comprising a double helical nucleic acid
XX comprising first and second substantially complementary strands, and
XX an oligonucleotide bound to a purine-rich target sequence within the
XX double helical nucleic acid, where the oligonucleotide binds in a
XX parallel and antiparallel orientation, respectively, to target
XX sequences on alternate strands of the double helical nucleic acid.
XX The method has therapeutic applications, where gene expression is
XX controlled by selective triple-helix formation within expression
XX regulatory sequences of a target gene. The oligonucleotides can be
XX used to form triple-helices, and are useful to detect the presence or
XX absence of specific sequences within genomic DNA for diagnostic and
XX therapeutic purposes. The oligonucleotides can be selected to
XX specifically bind to pathogenic double-stranded DNA including specific

CC sequences required by pathogenic bacteria or viruses for replication or
 CC virulence, reducing their pathogenicity. Alternatively, the
 CC oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or
 CC viral origin. Such therapeutic oligonucleotides are capable of forming
 CC triple-helices with such sequences in cancerous cells containing the
 CC activated oncogene, so preferentially killing or repressing the cancer
 CC causing cell. The present sequence represents an oligonucleotide
 CC used in the methods of the present invention.

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;
 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1012
 ABX79833/c
 ID ABX79833 standard; cDNA; 15 BP.

XX AC ABX79833;

DT 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polymucleotide #158.

DE BST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

XX OS

XX PN US6472154-B1.

XX PD 29-OCT-2002.

XX PF 31-DEC-1999; 99US-0475947.

XX PR 31-DEC-1999; 99US-0475947.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX Garner HR, Wren JD, Minna JD, Fondon JW;

XX WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence,
 PT for understanding or treating genetic disease, comprises detecting
 PT tandem repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability -

XX Examples; Column 747; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples

CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 5.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1013
 AAX18365/c
 ID AAX18365 standard; DNA; 16 BP.

XX AC AAX18365;

XX DT 11-MAY-1999 (first entry)

XX DE RT-PCR primer of the invention SEQ ID 6.

XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX OS Synthetic.

XX PN JP11032765-A.

XX PD 09-FEB-1999.

XX PF 18-JUL-1997; 97JP-0208312.

XX PR 18-JUL-1997; 97JP-0208312.

XX PA (TAKI) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in
 RT-PCR

XX Disclosure; Page 10; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
 CC guanine and/or cytosine. The new nucleotides are useful as primers for
 CC RT-PCR and determination of base sequences. The new sequences allow for
 CC reproductive and highly efficient analysis of gene sequences.

XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 |||||
 Db 14 AAAAAAAAAAAAAA 1

RESULT 1014


```
AAAX18360/c
ID AAX18360 standard; DNA; 16 BP.
XX
AC AAX18360;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 1.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
FN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-0208312.
XX
PR 18-JUL-1997; 97JP-0208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in
RT-PCR
XX
PS Disclosure; Page 10; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
to sequences of at least two nucleotides of formula:
CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
CC X = a labelled compound and/or a nucleotide with voluntary sequence;
CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
CC k = natural number of 3 or over indicating the repetition of gamma, in
CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
CC guanine and/or cytosine. The new nucleotides are useful as primers for
RT-PCR and determination of base sequences. The new sequences allow for
CC reproductive and highly efficient analysis of gene sequences.
XX
SQ Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
DB 14 AAAAAAAAAAAAAA 1

RESULT 1015
AAD44145/c
ID AAD44145 standard; DNA; 16 BP.
XX
AC AAD44145;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #5 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
disease diagnosis; gene analysis; human; matrix metalloproteinase;
KW PCR; primer; ss.
XX
OS Unidentified.
XX
FN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-0163485.
XX
PR 03-OCT-1997; 97US-108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broadus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture
of DNAs into 2 or more subsets or distinguishing gene expression
PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
```

```
XX
XX 30-SEP-1998; 98US-0163485.
XX
XX 03-OCT-1997; 97US-108152P.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
XX Fillmore H, Broadus W, Gillies G;
XX
XX WPI; 2002-412824/44.
XX
XX Sequential consensus region-directed amplification for sorting mixture
of DNAs into 2 or more subsets or distinguishing gene expression
PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
amplification for sorting a mixture of DNAs into 2 or more subsets or
distinguishing gene expression patterns in 2 samples. The methods, kits
and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
more subsets or distinguishing gene expression patterns in 2 samples
e.g. for disease diagnosis and gene analysis. The present sequence is
an oligo dT PCR primer used to illustrate the method of the invention.
XX
SQ Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 1 other;

Query Match 1.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
DB 16 AAAAAAAAAAAAAA 3

RESULT 1016
AAD44147/c
ID AAD44147 standard; DNA; 16 BP.
XX
AC AAD44147;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #7 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
disease diagnosis; gene analysis; human; matrix metalloproteinase;
KW PCR; primer; ss.
XX
OS Unidentified.
XX
FN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-0163485.
XX
PR 03-OCT-1997; 97US-108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broadus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture
of DNAs into 2 or more subsets or distinguishing gene expression
PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
```

CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC oligo dt PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 1 other;
 Query Match 1.3%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 16 AAAAAAAAAAAAAA 3
 RESULT 1017
 AAD44149/C
 ID AAD44149 standard; DNA; 16 BP.
 XX
 AC AAD44149;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Oligo-dT PCR primer #9 used to illustrate the method of the invention.
 XX
 KW Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase;
 KW PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 EN US6277571-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 30-SEP-1998; 98US-0163485.
 XX
 PR 03-OCT-1997; 97US-108152P.
 XX
 PA (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 XX
 PI Fillmore H, Broadus W, Gillies G;
 XX
 DR WPI; 2002-412824/44.
 XX
 PT Sequential consensus region-directed amplification for sorting mixture
 PT of DNAs into 2 or more subsets or distinguishing gene expression
 PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
 XX
 PS Example; Fig 1C; 19pp; English.
 XX
 CC The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC oligo dt PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 1 other;
 Query Match 1.3%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 Db 16 AAAAAAAAAAAAAA 3

RESULT 1018
 AAX69798/C
 ID AAX69798 standard; RNA; 17 BP.
 XX
 AC AAX69798;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1093.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US17480.
 XX
 PR 11-JAN-1996; 96US-0584040.
 XX
 PR 26-OCT-1995; 95US-0005974.
 XX
 PA (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX
 DR WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PS Claim 4; Page 79; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 SQ Sequence 17 BP; 1 A; 1 C; 0 G; 15 U; 0 other;
 Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 17 AAAAAAAAAAAAAA 4

RESULT 1019
 AAX69803/C
 ID AAX69803 standard; RNA; 17 BP.
 XX
 AC AAX69803;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;

KW Flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX Homo sapiens.
OS
XX
XX WO9715662-A2.
PN
XX
XX PD 01-MAY-1997.
XX
XX PF 25-OCT-1996; 96WO-US17480.
XX
XX PR 11-JAN-1996; 96US-0584040.
XX
XX PR 26-OCT-1995; 95US-0005974.
XX
XX
XX PA (CHIR) CHIRON CORP.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Escobedo J, McSwiggen J, Favco P, Stinchcomb D;
XX
XX DR WPI; 1997-259017/23.
XX
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX mRNA stability - useful for treating e.g. tumour angiogenesis,
XX PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX PS Claim 4; Page 79; 218pp; English.
XX
XX CC The present invention describes nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX be treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.
XX
XX SQ Sequence 17 BP; 1 A; 2 C; 0 G; 14 U; 0 other;
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
Db 14 AAAAAAAAAAAAAA 1
RESULT 1020
ID AAA25447/c
ID AAA25447 standard; DNA; 17 BP.
XX
XX AC AAA25447;
XX
XX DT 19-JUL-2000 (first entry)
XX
XX DE
XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1945.
XX
XX KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO954459-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 19-APR-1999; 99WO-US08547.

XX
XX PR 20-APR-1998; 98US-0082404.
XX PR 23-JUN-1998; 98US-0103636.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
XX Matulic-Adamic J;
XX
XX DR WPI; 2000-013248/01.
XX
XX PT New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX
XX PS Claim 77; Page 79; 148pp; English.
XX
XX CC The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity, (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting
XX treated cells, or for other conditions associated with levels of
XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX can also be used to correlate inhibition of gene expression with
XX alterations in phenotype, particularly for identification of therapeutic
XX targets, and as research reagents (for RNA, in the same way that
XX restriction endonucleases are used with DNA). The combination of
XX modifications in (A) improves resistance to nucleases, binding affinity
XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX their corresponding target sequences. AAA26219 to AAA26271 represent
XX other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.
XX
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
Db 17 AAAAAAAAAAAAAA 4
RESULT 1021
AAH74930
ID AAH74930 standard; DNA; 18 BP.
XX
XX AC AAH74930;
XX
XX DT 29-OCT-2001 (first entry)
XX
XX DE DNA sequence of cap adaptor.
XX
XX XX Nucleotide sequence signature; nucleotide sequencing; ss.
XX
XX OS Synthetic.
XX
XX PN WO200161044-A1.
XX
XX XX PD 23-AUG-2001.
XX
XX PF 15-FEB-2001; 2001WO-US05032.
XX
XX PR 15-FEB-2000; 2000US-0182454.
XX PR 01-SEP-2000; 2000US-0654187.
XX
XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Corcoran KC, Eletr S;
XX WPI; 2001-522608/57.
XX
XX Determining nucleotide sequence signature, by obtaining optical values
XX for each nucleotide position in a group, adjusting them to get ratio of
XX final highest values near predetermined factor, generating base call -
XX
XX Disclosure; Page 19; 73pp; English.
XX
XX The specification describes a method for determining a nucleotide
XX sequence signature. The method comprises obtaining optical measurements
XX with values indicating each nucleotide in a group of nucleotide
XX positions, adjusting the values until the ratio of highest value in
XX the set to next highest values in the set is at least a predetermined
XX factor, and generating a base call for a position in the group based
XX on results after the adjustment of values. The method is used for
XX determining a signature of a nucleotide sequence, and for determining
XX a nucleotide sequence of a polynucleotide from a series of optical
XX measurements. The present sequence represents an adaptor, which is
XX used in the course of the invention.
XX
XX Sequence 18 BP; 14 A; 0 C; 3 G; 0 U; 1 other;
XX
XX
XX Query Match 1.3%; Score 14; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 6.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1097
XX |||||||||
XX 5 AAAAAAAAAAAAAA 18
XX
XX
XX RESULT 1022
XX ABL88799
XX ID ABL88799 standard; DNA; 18 BP.
XX AC ABL88799;
XX
XX 22-MAY-2002 (first entry)
XX
XX HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:21.
XX
XX Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX reverse transcriptase; binding group; ss.
XX
XX Human immunodeficiency virus type 1.
XX Synthetic.
XX
XX EPI174518-A1.
XX
XX 23-JAN-2002.
XX
XX 20-JUL-2000; 2000EP-0202611.
XX
XX 20-JUL-2000; 2000EP-0202611.
XX
XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Loukachov VV, Van Gemen B, Goudsmit J;
XX WPI; 2002-156696/21.
XX
XX Collection of binding groups for determining or typing samples,
XX especially clinical samples, has groups capable to identify essentially
XX all members of the family of nucleic acids of relatively high
XX significance -
XX
XX Disclosure; Page 12; 166pp; English.
XX
XX The present invention describes a collection of binding groups for a
XX family of nucleic acids comprising members of relative high and relative

CC low significance, where the binding groups are selected to be capable to
CC identify, alone or in combination, essentially all members of the family
CC of nucleic acids of relatively high significance. The collection of
CC binding groups is useful for typing of nucleic acid in a clinical sample,
CC by contacting the nucleic acid with the collection and determining
CC whether one or more binding groups bound to the nucleic acid of the
CC sample. This method is useful for determining whether the sample
CC comprises at least a part of a member of relatively high significance of
CC a family of nucleic acids. The collection of binding groups is useful for
CC diagnosing the severity of a disease caused by a pathogen containing a
CC member of a family of nucleic acids. ABL88799 to ABL89321 represent
CC oligonucleotide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 18 BP; 7 A; 2 C; 7 G; 2 T; 0 other;
XX
XX Query Match 1.3%; Score 14; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 6.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 766 CAGAACTGGAGAG 779
XX |||||||||
XX 4 CAGAACTGGAGAG 17
XX
XX
XX RESULT 1023
XX ABL88821
XX ID ABL88821 standard; DNA; 18 BP.
XX AC ABL88821;
XX
XX 22-MAY-2002 (first entry)
XX
XX HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:43.
XX
XX Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX reverse transcriptase; binding group; ss.
XX
XX Human immunodeficiency virus type 1.
XX Synthetic.
XX
XX EPI174518-A1.
XX
XX 23-JAN-2002.
XX
XX 20-JUL-2000; 2000EP-0202611.
XX
XX 20-JUL-2000; 2000EP-0202611.
XX
XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Loukachov VV, Van Gemen B, Goudsmit J;
XX WPI; 2002-156696/21.
XX
XX Collection of binding groups for determining or typing samples,
XX especially clinical samples, has groups capable to identify essentially
XX all members of the family of nucleic acids of relatively high
XX significance -
XX
XX Disclosure; Page 17; 166pp; English.
XX
XX The present invention describes a collection of binding groups for a
XX family of nucleic acids comprising members of relative high and relative
XX low significance, where the binding groups are selected to be capable to
XX identify, alone or in combination, essentially all members of the family
XX of nucleic acids of relatively high significance. The collection of
XX binding groups is useful for typing of nucleic acid in a clinical sample,
XX by contacting the nucleic acid with the collection and determining
XX whether one or more binding groups bound to the nucleic acid of the
XX sample. This method is useful for determining whether the sample
XX comprises at least a part of a member of relatively high significance of
XX a family of nucleic acids. The collection of binding groups is useful for

```
CC diagnosing the severity of a disease caused by a pathogen containing a
CC member of a family of nucleic acids. ABL8779 to ABL89321 represent
CC oligonucleotide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 18 BP; 7 A; 3 C; 7 G; 1 T; 0 other;

Query Match          1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 CAGAACTGGAGAG 779
DB 4 CAGAACTGGAGAG 17

RESULT 1024
ABA82759
ID ABA82759 standard; DNA; 18 BP.
XX
XX
AC ABA82759;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human protective DNA sequence CNI-00739 fragment #32.
XX
XX Human; protective sequence; cell death; cancer; autoimmune disease;
KW neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;
KW ds.
XX
XX Homo sapiens.
XX
PN WO200176457-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11663.
XX
PR 11-APR-2000; 2000US-0547735.
XX
PA (COGE-) COGENT NEUROSCIENCE INC.
XX
PI Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC, Barney S;
PI P-PSDB; ABB44672.
DR WPI; 2002-025874/03.
XX
XX New protective sequences and their products, useful for diagnosing and
PT treating diseases involving cell death, including neurological
PT disorders e.g. stroke and for identifying modulators of expression of
PT the protective sequences -
XX
PS Claim 2; Fig 7; 283pp; English.
XX
CC The present invention relates to protective sequence proteins
CC (ABB44624-ABB44830) and their coding sequences (ABA82701-ABA82937).
CC The sequences, when introduced into a cell either predisposed to undergo
CC cell death or in the process of undergoing cell death, prevent, delay or
CC rescue the cell from death, hence, these sequences are named "protective
CC sequences". The sequences are useful for treating and/or ameliorating
CC cancer, autoimmune diseases and neurological disorders e.g. stroke.
CC Further examples of diseases which may be treated by the present
CC invention are given in the specification.
XX
XX
SQ Sequence 18 BP; 6 A; 1 C; 7 G; 4 T; 0 other;

Query Match          1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1000 TGAGGCTGGAGAA 1013
DB 2 TGAGGCTGGAGAA 15
```

```
RESULT 1025
ABT33769/C
ID ABT33769 standard; DNA; 19 BP.
XX
XX
AC ABT33769;
XX
DT 29-MAY-2003 (first entry)
XX
DE Ribozyme substrate target sequence SEQ ID No 120.
XX
XX Cytostatic; gene therapy; apoptosis; cancer growth inhibition;
KW drug screening; ss.
XX
XX Homo sapiens.
XX
PN WO200292840-A2.
XX
PD 21-NOV-2002.
XX
PF 14-MAY-2002; 2002WO-US15198.
XX
PR 14-MAY-2001; 2001US-290927P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Kelly B, Habita C, Robbins J, Barber J;
XX WPI; 2003-129308/12.
XX
XX New isolated nucleic acid molecule useful for regulating apoptosis
PT induction in cells, for inhibiting the growth of cancer in subjects,
PT and for drug screening -
XX
XX Example 3; Page 43; 153pp; English.
XX
CC The invention relates to a novel isolated molecule comprising bases 2-8
CC or 13-16 of 2 16 base pair sequences, or comprising a 1731 base pair
CC sequence, all given in the specification or at least 95 % identity with
CC the 1731 bp sequence. The nucleic acid molecule is useful in regulating
CC apoptosis in cells and in drug screening. The method is useful in
CC facilitating the induction of apoptosis in cells, in identifying an agent
CC that can facilitate the induction of apoptosis in cells, and in
CC inhibiting the growth of a cancer. This polynucleotide sequence
CC represents a ribozyme substrate target sequence relating to the
CC invention.
XX
SQ Sequence 19 BP; 2 A; 4 C; 4 G; 7 T; 2 other;

Query Match          1.3%; Score 14; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 6.6e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 354 GCCAACCTGTGACAGAG 371
DB 18 SYCAACCTGTGACAGAG 1

RESULT 1026
AAQ75194
ID AAQ75194 standard; cDNA; 20 BP.
XX
XX
AC AAQ75194;
XX
DT 25-MAR-2003 (updated)
DT 23-AUG-1995 (first entry)
XX
DE ALL-1 exon 3 nested PCR primer 3.2c.
XX
XX Acute lymphoblastic leukaemia; acute nonlymphoblastic leukaemia;
KW chromosomal translocation; rearrangement; abnormality; detection;
KW ALL-1; direct tandem duplication; ss.
```

OS Synthetic.
 XX WO9426930-A1.
 XX 24-NOV-1994.
 XX 22-APR-1994; 94WO-US04496.
 XX 14-MAY-1993; 93US-0062443.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Canaani E, Croce C;
 XX WPI; 1995-006818/01.
 XX New acute lymphocytic leukaemia gene prods. - used for the
 PT diagnosis and treatment of leukaemias, partic. acute
 PT lymphoblastic or nonlymphoblastic leukaemia
 XX Example 6; Page 58; 207pp; English.
 XX The ALL-1 gene rearrangement was studied in 3 adult patients with
 CC acute myeloid leukaemia and who lacked cytogenetic evidence of
 CC 11q23 translocations. Oligonucleotide primers 3.1c and 5.3 (see
 CC AAQ75191 and AAQ75192) were used in a first PCR amplification, followed
 CC by nested PCR using the primers 6.1 and 3.2c (AAQ75193 and AAQ75194).
 CC A single rearranged ALL-1 band was seen for each patient. Each
 CC clone begins and ends with a portion of ALL-1 exon 5; the 5'-3'
 CC order of ALL-1 exons within each clone was 5-6-2-3-4-5. This novel
 CC exon structure indicates that the ALL-1 rearrangement in each
 CC patient is the result of direct tandem duplication of a portion of
 CC the ALL-1 gene.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 other;
 SQ Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 677 CACAGATGGATCTG 690
 DB |||||
 2 CACAGATGGATCTG 15
 RESULT 1027
 AAT48516
 ID AAT48516 standard; DNA; 20 BP.
 XX AC AAT48516;
 XX 08-APR-1997 (first entry)
 XX Human ALL-1 gene exon 3-derived primer, used for leukaemia diagnosis.
 XX ALL; acute lymphoblastic leukaemia; acute myeloid leukaemia; AML;
 KW primer; probe; PCR; polymerase chain reaction; detection; diagnosis;
 KW prognosis; chromosome 11q23; solid tumour; gastric carcinoma;
 KW translocation; cancer; neoplasia; ss.
 XX Homo sapiens.
 OS US5567586-A.
 XX 22-OCT-1996.
 XX 18-MAY-1995; 95US-0446926.
 XX 18-MAY-1995; 95US-0446926.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX

XX Croce CM;
 XX WPI; 1996-484992/48.
 XX Detection of ALL-1 gene rearrangement or mutation in solid tumour -
 PT using ALL-1-specific probe or primer
 XX Example 1; Column 13; 10pp; English.
 XX AAT48513-T48518 are PCR primers used for the isolation of the ALL-1
 CC gene from total cDNA from the human gastric carcinoma cell line
 CC Mgc80-3 and subsequent subcloning of the gene into the TA vector
 CC (Invitrogen). Where all retrieved sequences could be sequenced and
 CC analysed for ALL-1 gene rearrangements. ALL-1 gene rearrangement
 CC results in a variety of solid tumours and is also responsible for
 CC acute lymphoblastic leukaemia (ALL) and acute myeloid leukaemia (AML).
 CC The ALL-1 gene is located at chromosome 11 band q23, in leukaemias
 CC with translocations involving 11q23, the ALL-1 gene fuses with one
 CC of many different genes, or (in the case of AML) self fusion resulting
 CC in a partially duplicated gene and a transcript with an in-frame
 CC fusion of either exon 6 or exon 8 with exon 2. The primers (which
 CC may also be used as probes) are useful for the diagnosis and
 CC prognosis of human solid tumours and leukaemias, as mentioned.
 XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 other;
 SQ Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 677 CACAGATGGATCTG 690
 DB |||||
 2 CACAGATGGATCTG 15
 RESULT 1028
 AAT73291/C
 ID AAT73291 standard; DNA; 20 BP.
 XX AC AAT73291;
 XX 12-DEC-1997 (first entry)
 XX Primer 1 for pUC19 DNA amplification.
 XX primer; PCR; polymerase chain reaction; sequencing; walking;
 KW complementary extension reaction; low redundancy; universal primer; ss.
 XX Synthetic.
 XX EP767240-A2.
 XX 09-APR-1997.
 XX 17-SEP-1996; 96EP-0114907.
 XX 30-JAN-1996; 96JP-0013634.
 XX 18-SEP-1995; 95JP-0238141.
 XX (HITA) HITACHI LTD.
 XX Kambara H, Okano K;
 XX WPI; 1997-205424/19.
 XX Efficient sequencing of long DNA by fragment walking - with
 PT simultaneous sequencing of restriction enzyme fragment and adjacent
 PT region of intact DNA, avoids the need for cloning and requires fewer
 PT primers
 XX Example 1; Page 11; 50pp; English.
 XX

CC A method for DNA analysis based on a complementary extension reaction
 CC using a DNA polymerase, comprises a combination of fragment walking and
 CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
 CC restriction enzyme and the targeted DNA sequence can be determined
 CC directly from the digested DNA fragments. By exploring the overlapping
 CC sequence of the determined base sequence, the overall base sequence of a
 CC lengthy DNA can be determined with low redundancy without cloning or
 CC subcloning. In addition, the method can be done with commercially
 CC available universal primers or with fewer primers than required in
 CC existing methods. AAT73291-92 are primers used in determination of the
 CC pUC19 sequence. Primer extension was carried out using 16 primers
 CC AAT73293.

XX Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 DB 14 AAAAAAAAAAAAAA 1

RESULT 1029
 AAT73292/c
 ID AAT73292 standard; DNA; 20 BP.
 XX
 AC AAT73292;
 XX
 DT 12-DEC-1997 (first entry)
 DE
 DE Primer 2 for pUC19 DNA amplification.
 XX
 KW primer; PCR; polymerase chain reaction; sequencing; walking;
 KW complementary extension reaction; low redundancy; universal primer; ss.
 XX
 OS Synthetic.
 PN EP767240-A2.
 XX
 XX EP767240-A2.
 PD
 PD 09-APR-1997.
 XX
 PF 17-SEP-1996; 96EP-0114907.
 XX
 PR 30-JAN-1996; 96JP-0013634.
 PR 18-SEP-1995; 95JP-0238141.
 XX
 PA (HITA) HITACHI LTD.
 XX
 PI Kambara H, Okano K;
 XX
 DR WPI; 1997-205424/19.
 XX
 PT Efficient sequencing of long DNA by fragment walking - with
 PT simultaneous sequencing of restriction enzyme fragment and adjacent
 PT region of intact DNA, avoids the need for cloning and requires fewer
 PT primers
 XX
 PS Example 1; Page 11; 50pp; English.

CC A method for DNA analysis based on a complementary extension reaction
 CC using a DNA polymerase, comprises a combination of fragment walking and
 CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
 CC restriction enzyme and the targeted DNA sequence can be determined
 CC directly from the digested DNA fragments. By exploring the overlapping
 CC sequence of the determined base sequence, the overall base sequence of a
 CC lengthy DNA can be determined with low redundancy without cloning or
 CC subcloning. In addition, the method can be done with commercially
 CC available universal primers or with fewer primers than required in
 CC existing methods. AAT73291-92 are primers used in determination of the
 CC pUC19 sequence. Primer extension was carried out using 16 primers
 CC AAT73293.

XX Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 DB 14 AAAAAAAAAAAAAA 1

RESULT 1030
 AAT45308/c
 ID AAT45308 standard; DNA; 20 BP.
 XX
 AC AAT45308;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-AUG-1997 (first entry)
 XX
 DE Oligonucleotide probe for dengue 1 fever virus.
 XX
 KW Probe; identification; dengue 1 fever; virus; detection;
 KW flavivirus; ss.
 XX
 OS Synthetic.
 XX
 PN RU2057811-Cl.
 XX
 PD 10-APR-1996.
 XX
 PF 17-DEC-1990; 90SU-4892388.
 XX
 PR 17-DEC-1990; 90SU-4892388.
 XX
 PA (OMNA=) OMSK NAT INFLAMMATION INFECTIONS RES INST.
 XX
 PI Drokina DA, Zlobin VI;
 XX
 DR WPI; 1997-019519/02.
 XX
 PT Set of 11 oligo-nucleotide probes for identification of flaviviruses
 PT - comprising probes specific for tick, Japanese, Murray Valley and
 PT St. Louis encephalitis, yellow fever, dengue, and West Nile
 PT viruses
 XX
 PS Claim 1; Columns 7-8; 4pp; Russian.

CC The present sequence, a probe for the identification of dengue 1
 CC fever virus, is a member of a probe set for the detection
 CC of flaviviruses. The probe set gives increased accuracy in
 CC identification of flaviviruses because of the use of highly
 CC specific probes.
 CC Use of the probe set for the identification of flaviviruses
 CC involved the synthesis of deoxyoligonucleotides, study of their
 CC specificity, immobilisation of RNA on nitrocellulose filters,
 CC labelling with 32P and hybridisation. After hybridisation the
 CC radioactivity was measured with a scintillation counter, and
 CC signals 2 to 3 fold higher than the background considered
 CC positive. The probe set was used to test 50 strains of 16 types
 CC of flavivirus.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 CCAACAGCAGGAT 570
 |||||

Db 14 CCAACAGCAGGGAT 1

RESULT 1031
 AAX96705
 ID AAX96705 standard; DNA; 20 BP.
 AC AAX96705;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 KW vaccine; neutralising epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB01890.
 XX
 PR 04-NOV-1998; 98US-0107078.
 PR 21-NOV-1997; 97FR-0014673.
 XX
 PA (GEST) GENSET.
 PI Griffais R;
 PI
 XX
 DR WPI; 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae
 PS Page 1847; Disclosure; 1912pp; English.
 XX
 CC AAX91991-X97517 represent PCR primers used to amplify open reading
 CC frames and other nucleic acid sequences from the genome of
 CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
 CC disease such as pneumonia and bronchitis and is thought to be a
 CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 CC by the open reading frames of the C. pneumoniae genome (see AAX34584-
 CC AAX35879) can be used in immunogenic compositions as vaccines. Vectors
 CC containing C. pneumoniae nucleotides sequences can also be used as
 CC immunogenic compositions, especially where the vector directs the
 CC expression of a neutralising epitope of C. pneumoniae.
 XX
 SQ Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 other;
 Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAAACGGGAGAGAA 129
 |||||
 Db 1 GAAACGGGAGAGAA 14

RESULT 1032
 AAA09108
 ID AAA09108 standard; DNA; 20 BP.
 AC AAA09108;
 XX
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE 5' RACE primer CHI-1B for 5' chi-conotoxin (chi-MrIA) gene.
 XX
 KW 5' RACE; primer; chi-conotoxin; chi-MrIA; cone snail; inhibitor;

KW amine transporter; neuronal; noradrenaline transporter; antiarrhythmic;
 KW urinary tract disorder; analgesic; cardiant; antidepressant;
 KW anxiolytic; anti-inflammatory; ss.
 OS Conus marmoreus.
 XX
 PN WO200020444-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-AU00844.
 XX
 PR 02-OCT-1998; 98AU-0006274.
 XX
 PA (UQUU) UNIV QUEENSLAND.
 XX
 PI Lewis RJ, Alewood PF, Sharpe IA;
 XX
 DR WPI; 2000-303738/26.
 XX
 PT Isolated, synthetic or recombinant chi-conotoxin peptide capable of
 PT inhibiting neuronal amine transporter used for treatment or prophylaxis
 PT of urinary or cardiovascular conditions, mood disorders, or
 PT treatment/control of pain/inflammation
 XX
 PS Example 7; Page 30; 47pp; English.
 XX
 CC Primer CHI-1B was designed from the mature chi-MrIA peptide sequence
 CC (AAY92229), a novel conotoxin. CHI-1B was used with AP1 (AAA09109) to
 CC amplify the 5' region of the chi-MrIA gene from Conus marmoreus. The
 CC peptide is an inhibitor of the neuronal amine transporters, especially
 CC the neuronal noradrenaline transporter. Inhibitors of noradrenaline
 CC re-uptake which have a negligible anti-cholinergic effect are
 CC particularly useful in the treatment of lower urinary tract disorders.
 CC Chi-MrIA (0.1 nM-1 micro M) inhibited the accumulation of radiolabeled
 CC noradrenaline in a concentration-dependent manner, with a log IC-50
 CC value of -8.17 plus or minus 0.0275 (n = 4). The concentration of
 CC chi-MrIA required to inhibit the accumulation by 50 percent was found to
 CC be approximately 7 nM. This concentration is approximately one order of
 CC magnitude lower than that needed for desipramine to produce the same
 CC effect. The peptides are useful for the treatment or prophylaxis of
 CC urinary or cardiovascular conditions or diseases (arrhythmia or coronary
 CC heart failure) or mood disorders (depression, anxiety or cravings), or
 CC the treatment or control of pain or inflammation (chronic pain,
 CC neuropathic pain or inflammatory pain).
 XX
 SQ Sequence 20 BP; 4 A; 2 C; 3 G; 4 T; 7 other;
 Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 64.7%; Pred. No. 6.9e+02;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 364 GGGTGGCAGAGTTATA 980
 |||||
 Db 4 GGGTGGCAGAGTTATA 20

RESULT 1033
 AAD11996/c
 ID AAD11996 standard; DNA; 20 BP.
 AC AAD11996;
 XX
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human FPIB antisense oligonucleotide (ISIS# 107805).
 XX
 KW Human; FPIB; protein phosphatase 1B inhibitor; antisense; gene therapy;
 KW infection; inflammation; tumour; prophylaxis; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT modified_base 1..5
 FT /note= "Phosphorothioate backbone"
 FT /tag= b
 FT /mod_base= OTHER
 FT modified_base 16..20
 FT /note= "Methoxyethyl residues"
 FT /tag= c
 FT /mod_base= OTHER
 FT modified_base 2..3
 FT /note= "Methoxyethyl residues"
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 8
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 10..11
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 13
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 19
 FT /tag= h
 FT /mod_base= m5c
 FT
 FT US6261840-B1.
 FT
 FT 17-JUL-2001.
 FT
 FT 18-JAN-2000; 2000US-0487368.
 FT
 FT 18-JAN-2000; 2000US-0487368.
 FT
 FT (ISIS-) ISIS PHARM INC.
 FT
 FT Cowsett LM, Wyatt J;
 FT
 FT WPI; 2001-432181/46.
 FT
 FT New antisense compounds capable of modulating expression of human
 FT protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment
 FT of diseases associated with expression of protein phosphatase -
 FT
 FT Claim 1; Column 43-44; 71pp; English.
 FT
 FT The invention is directed to antisense compounds, particularly
 FT oligonucleotides which are targeted to a DNA encoding protein
 FT phosphatase 1B (PTP1B) to modulate its expression. The antisense
 FT compounds are useful for diagnosis, prophylaxis and treatment of
 FT diseases associated with the expression of PTP1B, to prevent or
 FT delay infection, inflammation and tumour formation and as a
 FT research reagent. The PTP1B DNA is useful in gene therapy.
 FT The present sequence is an antisense oligonucleotide with a
 FT phosphorothioate backbone. This oligo is targeted to human
 FT PTP1B to inhibit its expression.
 FT
 FT Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 other;
 FT
 FT Query Match 1.3%; Score 14; DB 1; Length 20;
 FT Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 FT Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FT
 FT QY 698 CTTCCAGGTGCCCA 711
 FT
 FT Db 17 CTTCCAGGTGCCCA 4
 FT
 FT RESULT 1034
 FT AAF99302/c

ID AAF99302 standard; DNA; 20 BP.
 XX
 AC AAF99302;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #418.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200122972-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US26383.
 XX
 PR 25-SEP-1999; 99US-0156113.
 XX
 PR 27-SEP-1999; 99US-0156135.
 XX
 PR 23-AUG-2000; 2000US-0227436.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 DR WPI; 2001-273485/28.
 XX
 PT Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and IG nucleic acids -
 XX
 PS Claim 101; Page 46; 338pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. coxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells.
 CC Note: the present sequence may have a phosphorothioate backbone.
 XX
 SQ Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 other;
 XX
 Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1084 AAAAAAAAAAAAAA 1097
 XX
 Db 20 AAAAAAAAAAAAAA 7
 XX
 RESULT 1035
 XX ABS77947/c
 XX ID ABS77947 standard; DNA; 20 BP.
 XX
 AC ABS77947;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #431.
 XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
 KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
 KW macular degeneration; corneal graft rejection; neovascular glaucoma;
 KW retrolental fibroplasia; rubrosis; Osler-Weber Syndrome;
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
 KW haemophilic joint; angiofibroma; wound granulation;
 KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
 OS Synthetic.
 XX WO200253141-A2.
 PN 11-JUL-2002.
 XX 14-DEC-2001; 2001WO-US48458.
 XX 14-DEC-2000; 2000US-255534P.
 PR (COLE-) COLEY PHARM GROUP INC.
 PA Bratzler RL;
 PI WPI; 2002-566690/60.
 XX Inhibiting angiogenesis in a subject, involves administering at least
 PT one antiangiogenic nucleic acid molecule to the subject -
 XX Claim 2; Page 27; 276pp; English.
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule.
 CC Also included is a kit comprising a first container housing the
 CC antiangiogenic nucleic acids, and instructions for administering them to
 CC a subject having a condition characterised by unwanted angiogenesis.
 CC The method is useful for inhibiting angiogenesis associated with solid
 CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
 CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
 CC macular degeneration, corneal graft rejection, neovascular glaucoma,
 CC retrolental fibroplasia, rubrosis, Osler-Weber Syndrome, myocardial
 CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
 CC joints, angiofibroma, wound granulation, intestinal adhesions,
 CC atherosclerosis, scleroderma and hypertrophic scars. The present
 CC sequence is an antiangiogenic nucleic acid of the invention.
 XX Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 other;
 SQ Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 DB 20 AAAAAAAAAAAAAA 7
 RESULT 1036
 ABK85071/c
 ID ABK85071 standard; DNA; 20 BP.
 XX AC ABK85071;
 XX 13-AUG-2002 (first entry)
 XX Human PTP1B antisense oligonucleotide ISIS 107805.
 XX Antisense; protein phosphatase 1B; PTP1B; ss; probe; human;
 KW type 2 diabetes; obesity; ovarian cancer; chronic myeloid leukaemia;
 KW hyperproliferative disease; antidiabetic; anorectic; cytostatic;
 KW blood glucose; gene therapy.
 XX Homo sapiens.
 OS

PN US2002055479-A1.
 XX 09-MAY-2002.
 XX 14-MAY-2001; 2001US-0854883.
 XX 18-JAN-2000; 2000US-0487368.
 XX 31-JUL-2000; 2000US-0629644.
 XX (COWS/) COWSERT L M.
 PA (WYATT/) WYATT J.
 PA (FREI/) FREIER S M.
 PA (MONI/) MONIA B P.
 PA (BUTL/) BUTLER M M.
 PA (MCKA/) MCKAY R.
 XX Cowsert LM, Wyatt J, Freier SM, Monia BP, Butler MM, McKay R;
 PI WPI; 2002-462914/49.
 XX Compound for inhibiting the expression of protein phosphatase 1B
 PT (PTP1B) and for treating diabetes, cancer, or obesity, comprises an
 PT antisense oligonucleotide targeted to nucleic acid encoding PTP1B -
 XX Claim 3; Page 23; 133pp; English.
 XX The invention relates to a compound of 8-50 nucleobases in length
 CC targeted to a nucleic acid encoding protein phosphatase 1B (PTP1B), where
 CC the compound specifically hybridises with and inhibits the expression of
 CC PTP1B (e.g. an antisense oligonucleotide). Also included are (1) a
 CC compound of 8-50 nucleobases in length which specifically hybridises with
 CC an 8 nucleobase portion of an active site on a nucleic acid encoding
 CC PTP1B; (2) inhibiting the expression of PTP1B in cells or tissues
 CC comprising contacting the cells or tissues with the compound; treating an
 CC animal having or suspected of having a disease or condition associated
 CC with PTP1B comprising administering the compound; (4) decreasing blood
 CC sugar levels in an animal comprising administering the compound;
 CC (5) preventing or delaying the onset of a disease or condition
 CC associated with PTP1B in an animal comprising administering the compound;
 CC and (6) preventing or delaying the onset of an increase in blood glucose
 CC levels in an animal comprising administering the compound. The compound
 CC is used to inhibit the expression of PTP1B in cells or tissues, to treat
 CC or prevent or delay the onset of a disease or condition associated with
 CC PTP1B, such as type 2 diabetes, obesity, cancer (especially ovarian
 CC cancer, chronic myeloid leukaemia and hyperproliferative diseases
 CC in an animal having or suspected of having the disease or condition,
 CC and for decreasing blood sugar levels or preventing or delaying the
 CC onset of an increase in blood glucose levels in an animal. The compound
 CC is also used in diagnostics, therapeutics, prophylaxis, and in research
 CC reagents and kits. The present sequence is an antisense compound of the
 CC invention targeting human PTP1B.
 XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 other;
 SQ Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 698 CTTGAGGTGCCCCA 711
 DB 17 CTTGAGGTGCCCCA 4
 RESULT 1037
 ABK37240/c
 ID ABK37240 standard; DNA; 20 BP.
 XX AC ABK37240;
 XX 08-MAY-2002 (first entry)
 XX Human PTP1B mRNA level inhibition antisense DNA #37.
 XX

Human; mouse; rat; protein tyrosine phosphatase 1B; PTP1B; ss; adipose; liver; kidney; metabolic disease; type 2 diabetes; obesity; cancer; hyperproliferative condition; blood serum; blood plasma; antidiabetic; blood glucose level; cytostatic; anorectic; antisense gene therapy; PTP1B mRNA level inhibition.

OS Homo sapiens.
 XX WO200210378-A2.
 XX 07-FEB-2002.
 XX 30-JUL-2001; 2001WO-US23874.
 XX 31-JUL-2000; 2000US-0629644.
 XX (ISIS-) ISIS PHARM INC.
 XX Cowsett LM, Wyatt J, Freier SM, Monia BP, Butler MM, McKay R;
 XX WPI; 2002-180079/23.
 XX Novel antisense compound useful for treating type 2 diabetes, cancer
 XX and obesity, is targeted to nucleic acid encoding human protein
 XX phosphatase 1B, and hybridises and inhibits PTP1B expression -
 XX Claim 3; Page 68; 142pp; English.

CC The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding protein phosphatase 1B (PTP1B), which specifically hybridises
 CC with and inhibits the expression of PTP1B. The compounds of the invention
 CC are useful for inhibiting the expression of PTP1B in liver, kidney or
 CC adipose cells or tissues and for treating an animal, preferably human,
 CC having a disease or condition associated with PTP1B, including metabolic
 CC diseases or conditions, e.g. type 2 diabetes and obesity, or
 CC hyperproliferative conditions such as cancer. The sequences are also
 CC useful for decreasing blood (serum or plasma) glucose levels in an animal
 CC e.g. a diabetic human or rodent, for preventing or delaying the onset of
 CC a disease or condition associated with PTP1B, and for preventing or
 CC delaying the onset of an increase in blood glucose levels. This sequence
 CC represents a PTP1B mRNA level inhibition antisense oligonucleotide of the
 CC invention.

XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 other;
 SQ

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 698 CTTGAGGTGCCCA 711
 |||||
 Db 17 CTTGAGGTGCCCA 4

RESULT 1038
 ABL194254
 ID ABL194254 standard; DNA; 20 BP.
 XX AC ABL194254;
 XX 16-FEB-2002 (first entry)
 XX Capture oligonucleotide zip ID#1341 oligo #9.
 XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 XX environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX WO200179548-A2.
 FN

XX 25-OCT-2001.
 PD 04-APR-2001; 2001WO-US10958.
 XX 14-APR-2000; 2000US-197271P.
 XX (CORR) CORNELL RES FOUND INC.
 XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX WPI; 2002-034366/04.
 DR Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch -
 XX Example 5; Fig 29; 300pp; English.

CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (1) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABL194254 to
 CC ABL197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.

XX Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 other;
 SQ

Query Match 1.3%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 AACTTGGTGCCAGC 353
 |||||
 Db 3 AACTTGGTGCCAGC 16

RESULT 1039
 ABL39308/c
 ID ABL39308 standard; DNA; 20 BP.
 XX AC ABL39308;
 XX 16-APR-2002 (first entry)
 XX Immunoestimulatory nucleic acid SEQ ID NO: 737.
 XX Antibody-induced cell lysis; cancer; immunoestimulatory; CD20;
 XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX modified_base 1..20
 XX /*tag= a
 XX /mod_base= OTHER

FT XX /note= "phosphorothioate backbone"

FN XX WO200197843-A2.

PD XX 27-DEC-2001.

XX XX

PF XX 22-JUN-2001; 2001WO-US20154.

XX XX

PR XX 22-JUN-2000; 2000US-213346P.

XX XX

PA XX (IOWA) UNIV IOWA RES FOUND.

XX XX

PI XX Weiner G, Hartmann G;

DR XX WPI; 2002-154611/20.

XX XX

PT XX Treating or preventing cancer, such as basal cell carcinoma, comprises

PT XX administering immunostimulatory nucleic acids that induce expression of

PT XX cell surface antigens and antibodies to a subject having or at risk of

PT XX developing cancer -

XX XX

PS XX Disclosure; Page 283; 312pp; English.

CC XX

CC XX The present invention relates to methods for treating or preventing

CC XX cancer, involving administering to a subject having or at risk of

CC XX developing cancer immunostimulatory nucleic acids that induce expression

CC XX of cell surface antigens and antibodies. The methods are useful for

CC XX treating or preventing cancer such as basal cell carcinoma, bladder

CC XX cancer, bone cancer, brain and central nervous system (CNS) cancer,

CC XX breast cancer, cervical cancer, colon and rectum cancer, connective

CC XX tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx

CC XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,

CC XX non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian

CC XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC XX cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC XX present sequence is an immunostimulatory oligonucleotide described in

CC XX the exemplification of the invention.

XX XX

SQ XX Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097

DB 20 AAAAAAAAAAAAAA 7

RESULT 1040

AAQ13914

ID AAQ13914 standard; DNA; 17 BP.

XX AC

XX AAQ13914;

XX AC

XX 25-MAR-2003 (updated)

DT 05-NOV-1991 (first entry)

XX XX

XX Probe YZ30 to N-ras codon 61.

DE XX

XX ras; point mutation; oncogenesis; PCR; tumour; ss.

XX XX

XX Synthetic.

OS XX

XX WO9112343-A.

PN XX

XX 22-AUG-1991.

PD XX

XX 07-FEB-1991; 91WO-US00858.

PF XX

XX 07-FEB-1990; 90US-0477260.

PR XX

XX (CETU) CETUS CORP.

PA XX

XX Mccormick FP, Lyons JF;

PI XX WPI; 1991-267154/36.

DR XX

XX XX

PT XX Method for detection of point mutation(s) in nucleic acid

PT XX segments - where segments encode GTP binding protein or sub-unit

PT XX and method involves amplification followed by sequence-specific

PT XX probe hybridisation

XX XX

PS XX Example; Page 57; 69pp; English.

XX XX

CC XX This probe corresponds to the sequence around codon 61 of the ras

CC XX p21 gene. It is one of 63 probes which are of use in detecting

CC XX point mutations in nucleic acid sequences encoding ras proteins,

CC XX specifically at positions 12, 13 and 61, three potentially oncogenic

CC XX sites. See AAQ13900-Q13962.

CC XX (Updated on 25-MAR-2003 to correct PI field.)

XX XX

SQ XX Sequence 17 BP; 7 A; 1 C; 7 G; 2 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 6.4e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 769 AACTGGGAGAGAGTGT 785

DB 1 AGCTGGAGAGAGAGT 17

RESULT 1041

AAQ20635

ID AAQ20635 standard; DNA; 17 BP.

XX AC

XX AAQ20635;

XX XX

DT 10-APR-1992 (first entry)

XX XX

DE XX Detection probe for detecting DNA corresp. to HIV-1 gag region.

XX XX

KW XX Capture probe; sandwich hybridisation assay;

KW XX human immunodeficiency virus; AIDS; ss.

XX XX

OS XX Synthetic.

XX XX

PN XX WO9119812-A.

XX XX

PD XX 26-DEC-1991.

XX XX

XX 11-JUN-1991; 91WO-FR00468.

PF XX

XX 11-JUN-1990; 90FR-0007249.

PR XX

XX (INMR) BIO MERIEUX.

PA XX

XX Cros P, Allibert P, Mallet F, Mabilat C, Mandrand B;

PI XX

XX WPI; 1992-024428/03.

DR XX

XX XX

PT XX Sandwich hybridisation of single strand nucleic acid - using

PT XX short immobilised capture probe and detection probe with

PT XX non-radioactive label, for diagnosing e.g. human papilloma virus

PT XX or HIV

XX XX

PS XX Claim 42; Page 39; 51pp; French.

XX XX

CC XX Target DNA corresponding to HIV-1 gag region is detected using a

CC XX capture probe (AAQ20634) fixed passively to a solid hydrophobic support

CC XX together with this detection probe labelled with a

CC XX non-radioactive marker. The capture and detection probes are able to

CC XX hybridise to non-overlapping segments of the target sequence.

CC XX See AAQ20389-Q20420 and AAQ20630-Q20663.

XX XX

```
SQ Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1001 GAGGCTGGAGAAATGGGA 1017
DB 1 GAAGCTGCAGAAATGGGA 17

RESULT 1042
AAQ20637
ID AAQ20637 standard; DNA; 17 BP.
XX
AC AAQ20637;
XX
DT 10-APR-1992 (first entry)
XX
DE Detection probe for detecting DNA corresp. to HIV-2 gag region.
KW Capture probe; sandwich hybridisation assay;
KW human immunodeficiency virus; AIDS; ss.
XX
OS Synthetic.
XX
PN WO9119812-A.
XX
PD 26-DEC-1991.
XX
PF 11-JUN-1991; 91WO-FR00468.
XX
PR 11-JUN-1990; 90FR-0007249.
XX
PA (INMR) BIO MERIEUX.
PI Cros P, Allibert P, Mallet F, Mabilat C, Mandrand B;
XX
DR WPI; 1992-024428/03.
XX
PT Sandwich hybridisation of single strand nucleic acid - using
PT short immobilised capture probe and detection probe with
PT non-radioactive label, for diagnosing e.g. human papilloma virus
or HIV
XX
PS Claim 44; Page 40; 5lpp; French.
XX
CC Target DNA corresponding to HIV-2 gag region is detected using a
CC capture probe (see AAQ20636) fixed passively to a solid hydrophobic
CC support together with this detection probe labelled with a
CC non-radioactive marker. The capture and detection probes are able to
CC hybridise to non-overlapping segments of the target sequence.
CC See AAQ20389-Q20420 and AAQ20630-Q20663.
XX
SQ Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1001 GAGGCTGGAGAAATGGGA 1017
DB 1 GAAGCTGCAGAAATGGGA 17

RESULT 1043
AAAX75069/c
ID AAAX75068 standard; RNA; 17 BP.
XX
AC AAAX75068;
XX
DT 28-JUL-1999 (first entry)
XX

SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 U; 0 other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AACACAAAACAAAAAA 1

RESULT 1044
AAAX75069/c
ID AAAX75069 standard; RNA; 17 BP.
XX
AC AAAX75069;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse f1t-1 VEGF receptor hammerhead ribozyme substrate #597.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; f1t-1;
KW f1k-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 173; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (f1t-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (f1k-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAAX7275 to AAAX7572 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 U; 0 other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AACACAAAACAAAAAA 1

RESULT 1044
AAAX75069/c
ID AAAX75069 standard; RNA; 17 BP.
XX
AC AAAX75069;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse f1t-1 VEGF receptor hammerhead ribozyme substrate #597.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; f1t-1;
KW f1k-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN WO9715662-A2.
```

PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX WPI; 1997-259017/23.
 DR
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PT Claim 4; Page 79; 218pp; English.
 PS
 XX
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 XX Sequence 17 BP; 2 A; 2 C; 0 G; 13 U; 0 Other;
 SQ
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps
 QY 1082 TTATAAAAAAAAAAAAAA 1098
 DB 17 TTGGAAAAAAAAAAAAAA 1
 RESULT 1046
 AAX62272
 ID AAX62272 standard; RNA; 17 BP.
 AC AAX62272;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Granule bound starch synthase hammerhead substrate SEQ ID NO:147.
 XX
 KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
 KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
 KW modulation; gene expression; transgenic plant; cleavage; canola plant;
 KW caffeine synthesis; coffee plant; nicotine production; tobacco;
 KW fruit ripening; flower pigmentation; lignin production; ss.
 XX
 OS Zea mays.
 XX
 PF WO9710328-A2.
 PN
 PD 20-MAR-1997.
 PP
 PF 12-JUL-1996; 96WO-US11689.
 XX
 PF 13-JUL-1995; 95US-0001135.
 PR
 XX (DWC) DOWELANCO.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;
 PI Merlo PAO, Skokut TA, Young SA, Zwick MG;
 DR
 DR WPI; 1997-202224/18.
 XX
 PT Ribozyme which modulates plant gene expression - preferably
 PT modulates expression of DELTA-9 desaturase or granule bound starch
 PT synthase in maize or canola
 XX
 PS Claim 41; Page 74; 155pp; English.
 XX
 CC The present invention describes an enzymatic nucleic acid molecule (I)

CC with RNA cleaving activity, which modulates the expression of a plant
 CC gene. Also described is a gene comprising a cDNA sequence encoding maize
 CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
 CC preferably delta-9 desaturase or a granule bound starch synthase (GBSS)
 CC gene, in a plant (preferably a maize or canola plant). (I) can be used
 CC to modulate caffeine synthesis in a coffee plant, nicotine production in
 CC a tobacco plant, fruit ripening processes in an apple, tomato, pear,
 CC plum or peach plant, flower pigmentation in a rose, petunia,
 CC chrysanthemum or marigold plant or lignin production in a tobacco,
 CC aspen, poplar or pine plant.
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 U; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 6.4e+02;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 776 GAAGAAGTGTGAGCGCA 792
 Db 1 GAAGAAGTGTGAGCGCA 17
 RESULT 1047
 AAA22975
 ID AAA22975 standard; RNA; 17 BP.
 AC AAA22975;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6201.
 DE
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; anti-inflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US06507.
 XX
 PR 27-MAR-1998; 98US-0079678.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or
 PT stability of an mRNA encoding an angiogenic factors -
 XX
 PS Claim 54; Page 254; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme

CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
 CC for integrin subunit beta 3, and AAA2476 to AAA23262, AAA23343 to
 CC AAA2422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberculous scleritis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX
 SQ Sequence 17 BP; 14 A; 0 C; 0 G; 3 U; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 6.4e+02;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1099
 Db 1 UAAAAAUAATAAAAAA 17
 RESULT 1048
 AAF03226/C
 ID AAF03226 standard; DNA; 17 BP.
 XX
 AC AAF03226;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1521.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US09721.
 XX
 PR 12-APR-1999; 99US-0129390.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 DR
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX
 PS Claim 37; Page 90; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX
 SQ Sequence 17 BP; 2 A; 0 C; 3 G; 12 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1079 CTATTAAAAA 1095
 DB 17 CCATTCAAAAAA 1

RESULT 1049
 AAF06239/c
 ID AAF06239 standard; DNA; 17 BP.
 XX
 AC AAF06239;
 XX
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #3036.
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 OS Homo sapiens.
 XX WO200061729-A2.
 PN 19-OCT-2000.
 PD
 XX
 PF 11-APR-2000; 2000WO-US09721.
 XX
 PR 12-APR-1999; 99US-0129390.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX
 PS Claim 42; Page 125; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the IR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX
 SI Sequence 17 BP; 2 A; 10 C; 2 G; 3 U; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1003 GGCTGGAGATGGAG 1019
 DB 17 GGCTGGAGATGGAG 1

RESULT 1050
 AAF06240/c
 ID AAF06240 standard; DNA; 17 BP.
 XX
 AC AAF06240;
 XX
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #3037.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX WO200061729-A2.
 PN 19-OCT-2000.
 PD
 XX
 PF 11-APR-2000; 2000WO-US09721.
 XX
 PR 12-APR-1999; 99US-0129390.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX
 PS Claim 42; Page 125; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the IR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX
 SI Sequence 17 BP; 2 A; 9 C; 2 G; 4 U; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1002 AGGCTGGAGATGGAA 1018
 DB 17 AGGCTGGAGATGGCA 1

RESULT 1051
 AAA25180/c
 ID AAA25180 standard; DNA; 17 BP.
 XX
 AC AAA25180;
 XX
 DT 19-JUL-2000 (first entry)
 DE
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1678.
 KW Oestrogen receptor; C-rat; K-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US08547.
 XX
 PR 20-APR-1998; 98US-0082404.
 PR 23-JUN-1998; 98US-0103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.


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XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX
XX Claim 77; Page 71; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting
XX treated cells, or for other conditions associated with levels of
XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX can also be used to correlate inhibition of gene expression with
XX alterations in phenotype, particularly for identification of therapeutic
XX targets, and as research reagents (for RNA, in the same way that
XX restriction endonucleases are used with DNA). The combination of
XX modifications in (A) improves resistance to nucleases, binding affinity
XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX their corresponding target sequences. AAA26219 to AAA26271 represent
XX other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 6.4e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1100
XX ||||| ||||| |||||
XX Db 17 AAAAAATAAAACAAAA 1
XX
XX RESULT 1052
XX AAA25445/C
XX ID AAA25445 standard; DNA; 17 BP.
XX AC AAA25445;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1943.
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08547.
XX
XX 20-APR-1998; 98US-0082404.
XX
XX 23-JUN-1998; 98US-0103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;

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PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX
XX Claim 77; Page 79; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting
XX treated cells, or for other conditions associated with levels of
XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX can also be used to correlate inhibition of gene expression with
XX alterations in phenotype, particularly for identification of therapeutic
XX targets, and as research reagents (for RNA, in the same way that
XX restriction endonucleases are used with DNA). The combination of
XX modifications in (A) improves resistance to nucleases, binding affinity
XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX their corresponding target sequences. AAA26219 to AAA26271 represent
XX other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 6.4e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1100
XX ||||| ||||| |||||
XX Db 17 AAAAAATAAAACAAAA 1
XX
XX RESULT 1053
XX AAA25446/C
XX ID AAA25446 standard; DNA; 17 BP.
XX AC AAA25446;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1944.
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08547.
XX
XX 20-APR-1998; 98US-0082404.
XX
XX 23-JUN-1998; 98US-0103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;

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XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer -

XX Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, in vivo or by transforming cells ex vivo and implanting
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
DB |||||

RESULT 1054
AAA25455/C

ID AAA25455 standard; DNA; 17 BP.

AC AAA25455;

XX 19-JUL-2000 (first entry)

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1953.
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

XX WO9954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US08547.

XX 20-APR-1998; 98US-0082404.

XX 23-JUN-1998; 98US-0103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX

PT New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -

XX Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, in vivo or by transforming cells ex vivo and implanting
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.

XX Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1096
DB |||||

RESULT 1055
AAA25555

ID AAA25555 standard; DNA; 17 BP.

AC AAA25555;

XX 19-JUL-2000 (first entry)

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2053.
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

XX WO9954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US08547.

XX 20-APR-1998; 98US-0082404.

XX 23-JUN-1998; 98US-0103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer -

PT sequences, used to treat cancer -
 PS Claim 77; Page 83; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 17 BP; 13 A; 1 C; 0 G; 3 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1081 ATTAAAAAATAAAAAA 1097
 DB 1 ATTAAAAAATAAAAAA 17
 RESULT 1056
 ABA78137
 ID ABA78137 standard; DNA; 17 BP.
 AC ABA78137;
 XX
 XX 24-JAN-2002 (first entry)
 DT
 XX
 DE BRCAl mutation correcting oligonucleotide SEQ ID NO: 983.
 XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antitickling; antianaemic; haemostatic;
 KW antileptic; ss.
 XX Homo sapiens.
 OS
 XX WO200173002-A2.
 PN
 XX 04-OCT-2001.
 PD
 XX 27-MAR-2001; 2001WO-US09761.
 PF
 XX 27-MAR-2000; 2000US-192176P.
 PR
 XX 27-MAR-2000; 2000US-192179P.
 PR
 XX 01-JUN-2000; 2000US-208538P.
 PR
 XX 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.
 PA
 XX Kmiec EB, Gamper HB, Rice MC;
 PI

XX
 DR WPI; 2001-639230/73.
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 XX modification -
 PS Claim 7; Page 103; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin, 2A
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX
 SQ Sequence 17 BP; 11 A; 1 C; 2 G; 3 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1079 CTATTAAAAAATAAAA 1095
 DB 1 CTATTAAAAAATAAAA 17
 RESULT 1057
 ABA78138/c
 ID ABA78138 standard; DNA; 17 BP.
 XX
 AC ABA78138;
 XX
 XX 24-JAN-2002 (first entry)
 DT
 XX
 DE BRCAl mutation correcting oligonucleotide SEQ ID NO: 984.
 XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antitickling; antianaemic; haemostatic;
 KW antileptic; ss.
 XX Homo sapiens.
 OS
 XX WO200173002-A2.
 PN
 XX 04-OCT-2001.
 PD
 XX 27-MAR-2001; 2001WO-US09761.
 PF
 XX 27-MAR-2000; 2000US-192176P.
 PR
 XX 27-MAR-2000; 2000US-192179P.
 PR
 XX 01-JUN-2000; 2000US-208538P.
 PR
 XX 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.
 PA
 XX

PI Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 PS Claim 7; Page 103; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 2 C; 1 G; 11 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1079 CTATTAAAAAAGAAA 1095
 Db 17 CTATTAAAAAAGAAA 1
 RESULT 1058
 AAS11599/c
 ID AAS11599 standard; DNA; 17 BP.
 AC AAS11599;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Porcine reproductive and respiratory virus, PCR primer Euro1.
 DE
 DE PRRSV infection; vaccine; immunogen; antibody; ss; PCR primer;
 KW Euro1.
 KW
 OS Porcine reproductive and respiratory virus.
 XX
 XX WO200159077-A1.
 XX
 XX 16-AUG-2001.
 XX
 XX 08-FEB-2001; 2001WO-US04351.
 XX
 XX 08-FEB-2000; 2000US-0181041.
 XX 30-MAR-2000; 2000US-0193220.
 XX 24-MAY-2000; 2000US-0206624.
 XX 29-JUN-2000; 2000US-0215373.
 XX 05-JAN-2001; 2001US-0260041.
 XX
 XX (MINU) UNIV MINNESOTA.
 XX (COLL) COLLINS J E.
 XX (FAAB) FAABERG K S.
 XX (ROSS) ROSSOW K D.
 XX
 XX Collins JE, Faaberg KS, Rossow KD;
 PI WPI; 2001-514657/56.
 XX
 DR

XX Isolated porcine reproductive and respiratory syndrome virus useful for
 PT production of antibodies, comprises RNA polynucleotide with specified
 PT sequence -
 XX
 PS Disclosure; Page 28; 74pp; English.
 XX
 CC The invention relates to an isolated porcine reproductive and respiratory
 CC syndrome virus (PRRSV) (deposited with ATCC, not stated) or comprising an
 CC RNA polynucleotide from PRRSV and the polypeptides encoded by it.
 CC An antibody that binds to a European-like PRRSV is useful for detecting a
 CC PRRSV in a porcine subject, by contacting a virus particle with the
 CC antibody under conditions to form a complex with a virus particle, and
 CC detecting the complex, where the presence of the complex indicates the
 CC presence of PRRSV, or by providing a biological sample from a porcine
 CC subject, adding the antibody to the sample under conditions to form a
 CC complex with a virus particle in the sample and detecting the complex,
 CC where the presence of the complex indicates the presence of PRRSV.
 CC The virus particle is obtained from a biological sample comprising lung
 CC tissue. The antibody, a composition comprising an inactivated or
 CC attenuated PRRSV or a PRRSV polypeptide is useful for treating a porcine
 CC subject at risk of infection with a PRRSV or displaying symptoms of a
 CC PRRSV infection, by administering the antibody or composition to the
 CC animal, where the antibody is an neutralising antibody. The virus,
 CC polynucleotide or protein is useful for producing the antibodies.
 CC The present sequence is a PCR primer used to distinguish between
 CC a European-like and a non European-like PRRSV.
 XX
 SQ Sequence 17 BP; 2 A; 3 C; 6 G; 6 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 260 AGACGAGGAGCCTTCA 276
 Db 17 AGACGAGGAGCCTTCA 1
 RESULT 1059
 AAH95016/c
 ID AAH95016 standard; RNA; 17 BP.
 AC AAH95016;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human Chk1 ribozyme substrate SEQ ID NO: 441.
 DE
 DE Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 KW RNA cleavage; cancer; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO200157206-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 02-FEB-2001; 2001WO-US03504.
 XX
 XX 03-FEB-2000; 2000US-0179983.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (FATT) FATTAYE A R.
 XX
 XX Fattaey AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 PI WPI; 2001-496922/54.
 XX
 XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 PT molecules, which downregulates expression of a checkpoint kinase-1
 PT gene, useful for treating colorectal, lung, breast or prostate cancers
 PT

XX PS Claim 4; Page 61; 115pp; English.

XX CC The present invention provides nucleic acid molecules capable of

XX CC downregulating the expression of the human checkpoint kinase-1 (Chk1)

XX CC gene. These may be antisense or ribozyme sequences, and are useful in the

XX CC treatment of diseases associated with conditions affected by Chk1 levels,

XX CC including cancer. The present sequence is an oligonucleotide described in

XX CC the exemplification of the invention.

XX SQ Sequence 17 BP; 3 A; 5 C; 3 G; 6 U; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 6.4e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 326 AGAAGCTGTGAGCAAC 342

DB 17 AGAAGTCTGAGCAAC 1

RESULT 1060

AAH80147

ID AAH80147 standard; cDNA; 17 BP.

XX AC AAH80147;

XX DT 19-SEP-2001 (first entry)

XX OS Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 111.

XX DE Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;

XX KW disease diagnosis; ss.

XX OS Oryctolagus cuniculus.

XX PN US6251588-B1.

XX PD 26-JUN-2001.

XX PF 10-FEB-1998; 98US-0021701.

XX PR 10-FEB-1998; 98US-0021701.

XX PA (AGIL-) AGILENT TECHNOLOGIES INC.

XX PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;

XX DR WPI; 2001-424456/45.

XX PT Predicting the potential of an oligonucleotide to hybridize to a target

XX PT nucleotide sequence, useful for evaluating oligonucleotide probe

XX PT parameters -

XX PS Example 1; Column 49; 342pp; English.

XX CC The present invention describes a method for predicting the potential of

XX CC an oligonucleotide to hybridize to a (complementary) target nucleotide

XX CC sequence, involving identifying a subset of oligonucleotides within the

XX CC predetermined number of unique oligonucleotides based on the evaluation

XX CC of the parameter. Oligonucleotides in the subset are identified that are

XX CC clustered along a region of the nucleotide sequence that is hybridisable

XX CC to the target nucleotide sequence. This is useful for evaluating

XX CC oligonucleotide probe sequences. The present sequence is an

XX CC oligonucleotide described in the exemplification of the invention.

XX SQ Sequence 17 BP; 1 A; 1 C; 7 G; 8 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 6.4e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 133 TGCTGCTTTGGGGCT 149

DB 1 TGCTGCTTTGGGGAT 17

RESULT 1061

ABK02484

ID ABK02484 standard; RNA; 17 BP.

XX AC ABK02484;

XX DT 12-MAR-2002 (first entry)

XX DE Human NOGO Amberzyme #156.

XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

XX KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

XX KW DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;

XX KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

XX KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

XX KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

XX KW inflammatory arthropathy; central nervous system injury;

XX KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

XX KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

XX KW Parkinson's disease; ataxia; Huntington's disease;

XX KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200159103-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04273.

XX PR 11-FEB-2000; 2000US-181797P.

XX PR 28-FEB-2000; 2000US-185516P.

XX PR 06-MAR-2000; 2000US-187128P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (CHOW/) CHOWRIRA B M.

XX PI Blatt L, McSwiggen J, Chowrira BM;

XX DR WPI; 2001-607195/69.

XX PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX PT constructs, which down regulate expression of a CD20 gene or neurite

XX PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,

XX PT and central nervous system injury -

XX PS Claim 88; Page 134; 200pp; English.

XX CC The invention relates to a nucleic acid molecule which down regulates

XX CC expression of a CD20 gene and a nucleic acid molecule which down

XX CC regulates expression of a neurite growth inhibitor gene (NOGO).

XX CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

XX CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

XX CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN

XX CC motif) or an amberyne (cleaving RNA with an NGN triplet), a zinzyme

XX CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used

XX CC to cleave RNA of CD20 in the presence of a divalent cation that is

XX CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce

XX CC CD20 activity of the cell and treat a patient having a condition

XX CC associated with the level of CD20. The treatment may further comprise the

XX CC use of one or more therapies. In particular, the CD20 targeting

XX CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell

XX CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky

XX CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human

CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-tar-getting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-tar-getting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is an amberzyme molecule of the invention.
 XX Sequence 17 BP; 7 A; 0 C; 7 G; 3 U; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 6.4e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1008 GAGATGGGAGTGTAA 1024
 |||||:|||||:|||||
 Db 1 GAGUAGGGAGAGUGAAA 17

RESULT 1062
 ABS74958
 ID ABS74958 standard; DNA; 17 BP.
 AC ABS74958;
 XX ABS74958;
 XX 24-DEC-2002 (first entry)
 XX Human PAPP-Ea associated 17-mer SEQ ID 484.
 XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
 KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
 KW dyngenetic pregnancy; primer; ss.
 XX Homo sapiens.

OS US2002102252-A1.
 FN 01-AUG-2002.
 PD 06-APR-2001; 2001US-0827998.
 PF 26-MAY-2000; 2000US-207456P.
 PR (GUY/) GU Y.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Shannon ME;
 XX WPI; 2002-697817/75.
 XX New isolated nucleic acid encoding an isoform of human pregnancy
 PT associated plasma protein E, for preventing or aborting pregnancy -
 PS Example 2; Page 138; 353pp; English.

XX This invention describes a novel isolated nucleic acid that encodes
 CC one of three new isoforms of human pregnancy associated plasma protein E,
 CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC dyngenetic pregnancies. The nucleic acids are used as probes to assess
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the

CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dyngenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention.
 XX Sequence 17 BP; 15 A; 0 C; 2 G; 0 U; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAA 1100
 |||||:|||||:|||||
 Db 1 AAAAAAAAAAGAGAGAAA 17

RESULT 1063
 ABT06038/C
 ID ABT06038 standard; DNA; 17 BP.
 AC ABT06038;
 XX ABT06038;
 XX 28-OCT-2002 (first entry)
 XX Human IgM heavy chain gene related PCR primer SEQ ID No 52.
 XX Single Primer Amplification; nested oligonucleotide extension reaction;
 KW hairpin; SPA; library; PCR; primer; ss.
 XX Homo sapiens.

OS WO200248401-A2.
 FN 20-JUN-2002.
 PD 10-DEC-2001; 2001WO-US47727.
 PF 11-DEC-2000; 2000US-254669P.
 PR 19-SEP-2001; 2001US-323400P.
 XX (ALEX-) ALEXION PHARM INC.
 XX Bowdish KS, Barbas-frederickson S, Lin Y, Mcwhirter J, Maruyama T;
 XX WPI; 2002-500537/53.
 XX Amplifying nucleic acid by synthesizing template nucleic acid
 PT containing a predetermined sequence and hairpin structure and using the
 PT template for target amplification by Single Primer Amplification -
 XX Example 3; Page 22; 54pp; English.

XX The invention relates to a method for amplifying a nucleic acid using
 CC Single Primer Amplification (SPA). The method comprises synthesising a
 CC template nucleic acid containing a predetermined sequence and hairpin
 CC structure with the nested oligonucleotide extension reaction. The method
 CC is useful for amplifying a nucleic acid, preferably for amplifying a
 CC family of related nucleic acid sequences to build a complex library of
 CC polypeptides encoded by the sequences. The engineered nucleic acid strand
 CC is useful for amplifying a nucleic acid strand by providing a nucleic
 CC acid with a predetermined sequence engineered onto its first end, a
 CC sequence complementary to the predetermined sequence and a hairpin
 CC structure between them and contacting the engineered nucleic acid strand
 CC with a primer containing at least a portion of the predetermined
 CC sequence. This process is done in the presence of a polymerase and
 CC nucleotides under conditions suitable for polymerisation to produce a
 CC complementary nucleic acid strand. The method of the invention is useful
 CC for producing large amounts of a target nucleic acid sequence and for
 CC amplifying simultaneously more than one different target nucleic acid
 CC sequence located on the same or different nucleic acid molecules. This
 CC polynucleotide sequence represents a PCR primer of the invention.

XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 GGTTCCTCCAGTGCAG 46
 DB 17 GGATCCTCCAGTGCAG 1

RESULT 1064
 AEN08387/c
 ID AEN08387 standard; DNA; 17 BP.
 XX
 AC AEN08387;
 DT 29-MAY-2002 (first entry)
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8379.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US16981.
 XX
 PR 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 05-FEB-2001; 2001WO-US00670.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 PS Disclosure; SEQ ID 8379; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1 can be used in gene therapy and vaccine production. The hGDMPLP-1 nucleic acids can be used as probes to detect, characterize and quantify hGDMPLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMPLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMPLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMPLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption

CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 405 CTGCTCCAGTGCCTCT 421
 DB 17 CTGCTCCAGTGCCTGT 1

RESULT 1065
 AEN08389/c
 ID AEN08389 standard; DNA; 17 BP.
 XX
 AC AEN08389;
 DT 29-MAY-2002 (first entry)
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8381.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US16981.
 PR 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 05-FEB-2001; 2001WO-US00670.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 PS Disclosure; SEQ ID 8381; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 86.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 403 CCCTGCTCCAGCAGGCT 419
Db 17 CTCGTCTCCAGCTGGCT 1

RESULT 1066
ABN08390/c
ID ABN08390 standard; DNA; 17 BP.
XX AC ABN08390;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8382.
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 27-SEP-2000; 2000US-234687P.
XX PR 04-OCT-2000; 2000US-236359P.
XX PR 30-JAN-2001; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 30-JAN-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.

XX (ABOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMLP-1
XX proteins, or as specific biomolecule capture probes for
XX surface-enhanced laser desorption ionization, comprises human
XX myosin-like protein hGDMLP-1 -
XX Disclosure; SEQ ID 8382; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
XX hGDMLP-1 can be used in gene therapy and vaccine production. The
XX hGDMLP-1 nucleic acids can be used as probes to detect, characterise
XX and quantify hGDMLP-1 nucleic acids in samples, as amplification
XX substrates, to provide initial substrates for the recombinant engineering
XX of hGDMLP-1 protein variants having desired phenotypic improvements, and
XX for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
XX be used as immunogens to raise antibodies that specifically recognise
XX hGDMLP-1 proteins, as standards in assays used to determine the
XX biomolecule capture probes for surface-enhanced laser desorption
XX ionisation, as therapeutic supplement in patients having specific
XX deficiency in hGDMLP-1 production, and in vaccines or for replacement
XX therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
XX diagnosing a disorder associated with the expression of hGDMLP-1, in
XX particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
XX chromosome 22. The present sequence represents an oligomer used in the
XX screening of the hGDMLP-1 sequence in the exemplification of the present
XX invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 86.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 402 ACCCTGCTCCAGCAGGC 418
Db 17 ACTCTGCTCCAGCTGGC 1

RESULT 1067
ABN08391/c
ID ABN08391 standard; DNA; 17 BP.
XX AC ABN08391;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8383.
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 05-FEB-2001; 2001US-266860P.
XX (ABOM-) ABOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 8383; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;
SQ
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 401 CACCTGCTCCAGGAGG 417
Db 17 CACTGCTCCAGTGG 1
RESULT 1068
ID ABN08662/c
ID ABN08662 standard; DNA; 17 BP.
XX AC ABN08662;
XX 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8654.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US16981.
XX 26-MAY-2000; 2000US-207456P.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX 30-JAN-2001; 2001WO-US00661.
XX 30-JAN-2001; 2001WO-US00662.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00666.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 05-FEB-2001; 2001US-266860P.
XX (ABOM-) ABOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 8654; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;
SQ
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 30 GCTTCTCCAGTGCAG 46
Db 17 GCTTCTCCAGTGCAG 1


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ID ABZ65528 standard; RNA; 17 BP.
XX
AC ABZ65528;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNazyme substrate #985.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16940.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 4; Page 152; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ65520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 U; 0 other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1083 TAAAAAATAAAAAA 1099
Db 17 TAAAAAATAAAAAA 1
RESULT 1072
AAT60989/c
ID AAT60989 standard; DNA; 18 BP.
XX
AC AAT60989;
XX
DT 28-OCT-1997 (first entry)
XX
DE Primer for lacI.
XX
KW Preparation; construction; plasmid; pSGE705; pBR; globin;
KW replication origin; tetracycline resistance; di-alpha; di-beta;
KW tac promoter; lacI; polymerase chain reaction; PCR; primer;
ABZ65528 standard; RNA; 17 BP.
amplification; ss.
XX
OS Synthetic.
XX
PN WO9704110-A1.
XX
PD 06-FEB-1997.
XX
PF 12-JUL-1996; 96WO-US11600.
XX
PR 14-JUL-1995; 95US-0001179.
XX
PA (SOMA-) SOMATOGEN INC.
XX
PI Glascock CB, Weickert MJ;
XX
DR WPI; 1997-132648/12.
XX
PT Prokaryotic cell contg. plasmid including regulatable expression
PT unit - for heterologous protein, and chromosomal gene encoding
PT regulator of this unit controlled by strong promoter, provides tight
PT control of expression
XX
PS Example 16; Page 39; 60pp; English.
XX
CC The present sequence was used in the preparation of the plasmid
CC pSGE705, which has the pBR origin of replication, tetracycline
CC resistance gene, the di-alpha and di-beta globin genes, tac promoter
CC and lacI.
XX
SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 other;
Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 336 GAGCAACTGGTGCCAG 352
Db 17 GATCACTGGTGCCAG 1
RESULT 1073
AAV29451
ID AAV29451 standard; DNA; 18 BP.
XX
AC AAV29451;
XX
DT 31-JUL-1998 (first entry)
XX
DE Calcium ion channel alpha subunit exon 38 specific forward primer.
XX
KW Calcium ion channel alpha subunit; human; episodic ataxia type 2;
KW familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN Homo sapiens.
XX
PD EP834561-A1.
XX
PF 08-APR-1998.
XX
PR 27-SEP-1996; 96EP-0202707.
XX
PR 27-SEP-1996; 96EP-0202707.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Ferrazi MD, Frants RR, Ophoff RA, Terwindt GM;
XX
DR WPI; 1998-195461/18.
XX
PT New human nucleic acid associated with migraine and episodic ataxia
```

library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of defining a set of oligonucleotides (ONs) that modulate the expression of a tNA sequence via binding of the ONs with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONs with the tNA according to defined criteria; and (2) a method of defining a set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences that are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAZ52701 to AAZ52706, represent sequences used in the exemplification of the present invention.

XX Sequence 18 BP; 12 A; 2 C; 2 G; 2 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 935 GTTTGTTTATGATGTC 951
DB 18 GTTTGTTTATGATGTC 2

RESULT 1075
AAZ06604/C
ID AAZ06604 standard; DNA; 18 BP.
XX AAZ06604;
AC AAZ06604;
XX 23-NOV-1999 (first entry)
DT ELK-1 expression modulator #44.
DE

Human ELK-1; p62TCF; Ets domain transcription factor protein; apoptosis; expression inhibition; infection; inflammation; tumour formation; diagnosis; phosphorothioate; antisense compound; ss.
Synthetic.

Key modified_base 1..18 Location/Qualifiers
FT /*tag= a Internucleoside phosphorothioate linkages"
FT modified_base 1..4
FT /*tag= b
FT /*tag= "Optionally 2-methoxyethyl (2'-MOE) nucleosides except cytosine residues which are 5-methylcytosine"
FT modified_base 15..18
FT /*tag= c
FT /*tag= "Optionally 2-methoxyethyl (2'-MOE) nucleosides except cytosine residues which are 5-methylcytosine"

US5948680-A.
XX 07-SEP-1999.
XX 17-DEC-1998; 98US-0213767.
XX 17-DEC-1998; 98US-0213767.
XX (ISIS-) ISIS PHARM INC.
XX Baker BF, Cowsett LM;
XX WPI; 1999-517959/43.
DR

type 2 - useful for diagnosis and development of specific treatments
XX Disclosure; Page 10; 157pp; English.

This primer is used for the PCR amplification of an exon of the human calcium ion channel alpha 1 subunit. The channel is related to familial hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is derived from, related to or associated with a gene present in humans on chromosome 19p13.1-13.2. The encoding nucleic acid can be used to localise or identify genes related to episodic neurological disorders, specifically migraine, FHM or EA-2, but also epilepsy. It can also be used to distinguish between alleles of the corresponding gene. Cells and animals containing recombinant expression vectors comprising the nucleic acid can be useful in study, development and treatment of migraine, FHM, EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and natural or synthetic antibodies against the proteins can be used to diagnose FHM, EA-2, migraine and other neurological conditions associated with cation channel dysfunction.

XX Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 307 TGCATGGGAAGACTGC 323
DB 2 TGCCTGGGAAGACTGC 18

RESULT 1074
AAZ41089/C
ID AAZ41089 standard; DNA; 18 BP.
XX AAZ41089;
AC AAZ41089;
XX 26-JAN-2000 (first entry)
DT Human ELK-1 phosphorothioate antisense oligonucleotide SEQ ID NO:241.

Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence-based technology; antisense drug discovery; target validation; ss.

Synthetic.
OS Homo sapiens.
XX WO9953101-A1.
XX 21-OCT-1999.
XX 13-APR-1999; 99WO-US08269.
XX 13-APR-1998; 98US-0081483.
XX 28-APR-1998; 98US-0067638.
XX (ISIS-) ISIS PHARM INC.
XX Cowsett LM, Baker BF, McNeil J, Freier SM, Sasnor HM, Brooks DG; Ohashi C, Wyatt JR, Borchers AH, Vickers TA;
XX WPI; 1999-620446/53.

Identifying compounds which modulate expression of nucleic acids, used to provide compounds having defined physical, chemical or bioactive properties, e.g. antisense activity
XX Example 24; Page 105; 264pp; English.

A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tNA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a

XX Antisense compound useful for diagnosis, treatment and prevention of
PT disease associated with ELK-1 expression
XX
XX Claim 3; Column 39; 31pp; English.
XX
XX Sequences AA206571-206607 are antisense polynucleotides targeted to a
CC nucleic acid molecule encoding human ELK-1 (also known as p22TCF). ELK-1
CC is a member of the ternary complex factor subfamily of Bts-domain
CC transcription factor proteins. The polynucleotides inhibit the
CC expression of human ELK-1, and this sequence targets the 3' untranslated
CC region of the ELK-1 RNA. Sequences AA206571-206607 all cause at least 30%
CC inhibition of ELK-1 expression. The antisense sequences can be used to
CC inhibit the expression of human ELK-1 in human cells or tissues in vitro.
CC ELK-1 uses a bipartite recognition mechanism mediated by both protein-DNA
CC and protein-protein interactions to regulate genes by direct and indirect
CC DNA binding and has been shown to control various signal transduction
CC pathways and other cell functions including apoptosis. This means that
CC antisense compounds inhibiting expression of ELK-1 can be used to treat
CC diseases associated with its expression in animals, particularly humans
CC and to prevent or delay infection, inflammation or tumour formation. The
CC compounds can also be used for diagnosis, as research reagents and in
CC kits.
XX
XX Sequence 18 BP; 12 A; 2 C; 2 G; 2 T; 0 other;
SQ
Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 935 GTTTGTTTATGATC 951
DB 18 GTTTGTTTATATC 2

RESULT 1076
AA257824
ID AA257824 standard; DNA; 18 BP.
XX
XX AA257824;
AC
XX
XX 11-APR-2000 (first entry)
DE HSV-2 VP16 gene reverse PCR primer.
XX
XX Fine array transcript mapping; FAT mapping; FATMap;
KW HSV-2; differential expression; VP16; PCR primer; ss.
XX
XX Herpes simplex virus type 2.
OS
XX WO9967422-A1.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US13813.
PF
XX
XX 24-JUN-1998; 98US-0090464.
PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA
XX
XX Leary JJ, Tal-Singer R;
PI
XX
XX WPI; 2000-147217/13.
DR
XX
XX Novel analytical method designated Fine Array Transcript Mapping, a
PT useful for detecting and measuring RNA molecules transcribed from a
PT genome, differential expression, and sequence mapping -
XX
XX Example 1; Page 16; 53pp; English.
PS
XX This sequence represents a reverse PCR primer targeted at the VP16
CC gene of herpes simplex virus type 2 (HSV-2) SB5 (ATCC VR 2546).
CC It was used for semi-quantitative PCR analysis of SB5 cDNA. PCR

CC using the VP16 primer pair generated a 192 bp product, and allowed
CC detection of 1 HSV copy from 45 cycles (or 100 copies from 35
CC cycles). The invention provides a novel genetic analysis method
CC termed Fine Array Transcript Mapping (FAT Mapping) for detecting
CC and measuring RNA molecules transcribed from a genome, differential
CC expression, and mapping of the 5' sequence of a transcript. FAT
CC mapping involves probing a test grid containing an array of 100s to
CC 1000s of overlapping genomic clones or DNA fragments with probes
CC consisting of labeled cDNAs representing the RNA transcripts from
CC test populations. The system allows quantitative measurements
CC of the expression of rare transcripts, and enables the analysis of
CC 100s of genes within a genomic sequence in a single run. The
CC method can be used to measure the differential expression of
CC transcripts between 2 or more different viral, tissue or cell
CC populations which share a common genomic sequence, or to determine
CC whether a particular open reading frame is expressed under certain
CC conditions. The FATMap technique has been applied to the HSV-2
CC genome.
XX
XX Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 other;
SQ
Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 920 CAGCGGAGCTTTCAGGT 936
DB 1 CAGCGGAGGTTTCAGGT 17

RESULT 1077
AAH27102
ID AAH27102 standard; DNA; 18 BP.
XX
XX AAH27102;
AC
XX
XX 06-AUG-2001 (first entry)
DT
XX
XX Heltest4 cleavage fragment.
DE
XX
XX Cleavage structure; target sequence detection; flap endonuclease;
KW PEN; Heltest4; ss.
XX
XX Synthetic.
OS
XX WO200132922-A2.
PN
XX 10-MAY-2001.
PD
XX
XX 27-OCT-2000; 2000WO-US29663.
PF
XX
XX 29-OCT-1999; 99US-0430692.
PR
XX (STRA-) STRATAGENE.
PA
XX
XX Sorge JA;
PI
XX
XX WPI; 2001-328805/34.
DR
XX
XX The labelling of nucleic acids for their detection and quantification
PT comprises the formation of a cleavage structure and its cleavage with a
PT five' exonuclease-1 or flap endonuclease-1 -
XX
XX Example 3; Page 22; 81pp; English.
PS
XX
XX This invention relates to a method for generating a signal indicative of
CC the presence of a target nucleic acid sequence in a sample. The method
CC comprises the formation of a cleavage structure through the incubation of
CC a sample comprising a target nucleic acid sequence and a nucleic acid
CC polymerase and cleaving the cleavage structure with a 5' exonuclease-1 or
CC flap endonuclease (FEN) to generate the signal. The method is used for
CC the detection and quantification of a target nucleic acid sequence. The
CC present sequence represents a fragment of oligonucleotide Heltest4, which

CC is used in an assay to evaluate the activity of a PEN endonuclease. This
CC sequence is the fragment of Heitest4 which is cleaved off by PEN.

XX Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
|||||
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1078
AAFI7432
ID AAFI7432 standard; DNA; 18 BP.
XX AAFI7432;
XX 09-MAR-2001 (first entry)
XX L1 cleavage site related sequence #22.
XX Retrotransposon; genetic defect; cystic fibrosis; ds.
XX Unidentified.
XX OS
XX PN US6150160-A.
XX PD 21-NOV-2000.
XX PF 28-APR-1997; 97US-0847844.
XX PR 16-NOV-1995; 95US-0006831.
XX PR 15-NOV-1996; 96US-0749805.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Moran JV, Dombroski BA, Kazanian HH, Boeke JD;
XX WPI; 2001-060015/07.
XX DR
XX PT DNAC comprising a promoter P and an L1 cassette sequence having a core
XX PT retrotransposon element, useful for random insertion of a heterologous
XX PT or homologous DNA sequence into a cell genome and for correcting
XX PT genetic defects -
XX PS Disclosure; Fig 14; 87pp; English.

CC The present invention relates to DNA for a promoter and an L1
CC cassette sequence having a core retrotransposon element. The invention
CC is useful for random insertion of a heterologous or homologous DNA
CC sequence into a cell genome, and for correction of a genetic defect
CC in the cell into which the insertion is made. Genetic defects which
CC may be corrected includes cystic fibrosis, mutations in the
CC dystrophin gene, genetic defects associated with blood clotting and
CC other genetic defects.

XX Sequence 18 BP; 11 A; 1 C; 2 G; 4 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 1079 CTATTAAAAA 1095
|||||
DB 2 CTATTAAAAA 18

RESULT 1079
ABZ72124

ID ABZ72124 standard; DNA; 18 BP.

AC ABZ72124;

XX 03-APR-2003 (first entry)

XX Gene 216 SSCP detection primer SEQ ID NO 96.

DE Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
XX antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
KW obesity; inflammatory bowel disease; primer; ss.

XX Synthetic.

XX WO200178894-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US12245.

XX 13-APR-2000; 2000US-0548797.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Keith T;

XX WPI; 2001-639428/73.

XX Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
XX proteins they encode, useful for the prevention, diagnosis and
XX treatment of asthma, obesity and inflammatory bowel disease -

XX Example 10; Page 149; 520pp; English.

XX The invention relates to isolated genes (Gene 216) from human chromosome
XX 20p13-p12 and the proteins they encode. The nucleic acids and proteins
XX may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate Gene 216 expression. For example, the
XX nucleic acids (or vectors) and proteins may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of Gene 216 by expressing
XX inactive proteins or to supplement the patients own production of Gene
XX 216 proteins. Additionally, the nucleic acids may be used to produce the
XX secreted Gene 216 protein, by inserting the nucleic acids into a host
XX cell and culturing the cell to express the protein. The nucleic acids
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar nucleic acid
XX sequences in samples and therefore which patients may be in need of
XX restorative therapy. The Gene 216 protein may also be used as antigens in
XX the production of antibodies against Gene 216 and in assays to identify
XX modulators of Gene 216 expression and activity. The anti-Gene 216
XX antibodies and antagonists may also be used to down regulate expression
XX and activity. The anti-Gene 216 antibodies may also be used as diagnostic
XX agents for detecting the presence of Gene 216 proteins in samples (e.g.
XX by enzyme linked immunosorbant assay or ELISA). Disorders that may be
XX prevented, diagnosed and/or treated by the above methods include, for
XX example asthma, obesity and inflammatory bowel disease. The present
XX invention is that of a Gene 216 related primer used in examples of the
XX sequence is that of a Gene 216 related primer used in the physical mapping of the gene
XX (ABZ72067-ABZ72088), polymorphism identification using single strand
XX conformational polymorphism (SSCP) analysis (ABZ72091-ABZ72184),
XX sequencing (ABZ72185-ABZ72268) and genotyping (ABZ72317-ABZ72362).

XX Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 CCAGGTGCAGAGCGG 53
|||||
DB 2 CCAGGTGCAGAGCGAG 18

XX	FEN 1 nuclease cleavage product.
DE	ss; nucleic acid detection; FEN nuclease.
XX	Synthetic.
KW	WO200244326-A2.
OS	06-JUN-2002.
PN	26-NOV-2001; 2001WO-US44215.
XX	30-NOV-2000; 2000US-0728574.
PD	(STRA-) STRATAGENE.
PF	Sorge JA, Whalen AM;
PR	WPI; 2002-508503/54.
XX	Detecting/measuring target nucleic acid, by forming cleavage structure
XX	by incubating target nucleic acid with probe having binding moiety,
PT	cleaving structure to release nucleic acid and detecting released
PT	fragments -
PS	Disclosure; Page 38; 157pp; English.
CC	This invention relates to a novel method for detecting/measuring a
CC	target nucleic acid. The method comprises forming a cleavage structure
CC	by incubating the target sequence with a probe comprising a binding
CC	moiety and a secondary structure that changes upon binding of the probe
CC	to the target, cleaving the cleavage structure to release a nucleic
CC	acid fragment, and detecting and/or measuring the fragment captured by
CC	binding of the binding moiety to a capture element on a solid support.
CC	The method of the invention is useful for detecting or measuring a
CC	target nucleic acid and are useful for generating a signal indicative of
CC	the presence of the target nucleic acid in a sample. Another method of
CC	the invention is useful for simultaneously forming a cleavage structure,
CC	amplifying the target nucleic acid in a sample and cleaving the cleavage
CC	structure. The method does not require multiple steps, subsequent
CC	amplification process, and allows for concurrent amplification and
CC	detection of target nucleic acid in a sample. The present sequence
CC	represents a cleavage product generated by FEN 1 nuclease shown
CC	in an example of the method of the invention.
XX	Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 other;
SQ	
Query Match	1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity	88.2%; Pred. No. 6.7e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1084 AAAAAAAAAAAAAAAA 1100
Db	1 AATAAATAAATAAATAA 17
RESULT 1082	
ABL541126	
ID	ABL541126 standard; DNA; 18 BP.
XX	AC ABL541126;
XX	DT 12-JUL-2002 (first entry)
XX	Cleavage product of FEN nuclease template Heltest4.
DE	FEN; endonuclease; nuclease; template; Heltest4;
KW	nucleic acid detection; ss.
XX	Synthetic.
OS	US6350580-B1.
PN	

XX	Generating a signal indicating presence of a target nucleic acid, for
XX	use in a polymerase chain reaction, comprises incubating target nucleic
XX	acid with a probe to form a cleavage structure that is cleaved with
XX	nuclease -
XX	Example 6; Page 37; 62pp; English.
XX	The present sequence represents the cleavage product of an oligonucleotide
XX	used to test FEN nuclease activity. FEN nucleases are used in the course
XX	of the invention. The specification describes a method for generating a
XX	signal indicative of the presence of a target nucleic acid sequence in a
XX	sample. The method comprises forming a cleavage structure comprising
XX	a duplex and single-stranded nucleic acid, by incubating the target nucleic
XX	acid sequence with a probe having a secondary structure that changes upon
XX	binding of the probe to the target nucleic acid sequence, and cleaving
XX	the cleavable structure with a nuclease to release a nucleic acid
XX	fragment. The method is useful for generating a signal indicative of
XX	the presence of target nucleic acid sequence in a sample. It is useful
XX	in a polymerase chain reaction (PCR)-based assay or non-PCR based assay
XX	for detecting naturally occurring target nucleic acid sequences in a
XX	solution including RNA and DNA that is isolated and purified from cells,
XX	tissues, single cell organisms, bacteria or viruses, and for detecting
XX	synthetic targets in solution, including RNA or DNA oligonucleotides, and
XX	peptide nucleic acids.
XX	Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 other;
SQ	
Query Match	1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity	88.2%; Pred. No. 6.7e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1084 AAAAAAAAAAAAAAAA 1100
Db	1 AATAAATAAATAAATAA 17
RESULT 1081	
ABK87302	
ID	ABK87302 standard; DNA; 18 BP.
XX	AC ABK87302;
XX	DT 24-SEP-2002 (first entry)

XX PD 26-FEB-2002.
 XX PR 11-OCT-2000; 2000US-0686179.
 XX PF 11-OCT-2000; 2000US-0686179.
 XX PR 11-OCT-2000; 2000US-0686179.
 XX PF (STRA-) STRATAGENE.
 XX PA Sarge JA;
 XX PI WPI; 2002-380832/41.
 XX DR
 XX PT Detecting a target nucleic acid in a polymerase chain reaction process
 XX PT comprises forming a cleavage structure by incubating with a probe
 XX PT having secondary structure that changes upon binding and cleaving with
 XX PT a nuclease to release a fragment -
 XX PS
 XX PS Example 6; Column 66; 62pp; English.
 XX CC The present sequence is the 18-nucleotide cleavage product of FEN
 XX CC nuclease template 1 oligonucleotide, Heltest4 (see ABU54126), which
 XX CC was used in a method for determining FEN endonuclease activity.
 XX CC Heltest4 binds to M13 to produce a complementary double-stranded
 XX CC domain and a non-complementary 5' overhang. This duplex forms
 XX CC template 2. Template 3 has an additional primer, FENAS (see
 XX CC ABU54127), bound to M13 and is directly adjacent to Heltest4. In
 XX CC the presence of template 3, FENAS binds the free 5' terminus of
 XX CC Heltest4, migrates to the junction and cleaves Heltest4 to produce
 XX CC the present 18-nucleotide fragment. FEN nuclease is preferred for
 XX CC use in the method of the invention, which relates to generating a
 XX CC signal to detect the presence of a target nucleic acid in a sample.
 XX CC In this method, a nucleic acid is treated with a probe that has a
 XX CC secondary structure which changes upon binding of the probe to a
 XX CC target nucleic acid sequence, and a nuclease. The invention also
 XX CC provides a process for detecting or measuring a nucleic acid that
 XX CC allows for concurrent amplification, cleavage and detection of a
 XX CC target nucleic acid sequence in a sample.
 XX SQ Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 6.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1100
 DB 1 AAAAAAAAAAAAAA 17
 RESULT 1083
 ID ABA91529 standard; DNA; 18 BP.
 XX AC ABA91529;
 XX DT 23-APR-2002 (first entry)
 XX DE
 XX DE DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.
 XX DE DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT misc_RNA 8..9
 XX FT /*tag= a
 XX FT /label= RNA
 XX PN WO200206531-A2.
 XX XX 24-JAN-2002.

PF 12-JUL-2001; 2001WO-US221166.
 XX 14-JUL-2000; 2000US-0616761.
 PR 30-MAR-2001; 2001US-0823647.
 XX (GENE-) APPLIED GENE TECHNOLOGIES INC.
 XX PA Dattagupta N;
 XX PI WPI; 2002-171819/22.
 XX DR
 XX PT Probes for detecting target nucleotide sequence in sample, has sequence
 XX PT that forms hairpin structure having a double-stranded segment and
 XX PT single-stranded loop collectively forming region complementary to
 XX PT target sequence -
 XX PS
 XX PS Example 4; Page 49; 72pp; English.
 XX CC The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
 XX CC AGT02013. This is one of a set of oligonucleotides (see
 XX CC ABA91527-30) used to assess the minimum number of ribonucleotides
 XX CC in DNA-RNA chimeric oligonucleotides required for RNase H cleavage.
 XX CC Each oligonucleotide of the set had a different number of
 XX CC ribonucleotides, 2 in the present case. The oligonucleotides were
 XX CC mixed with target DNA oligonucleotide AGT02009 (see ABA91531) and
 XX CC incubated with RNase H (5 U/ml) at 37 degrees C for 30 minutes.
 XX CC The results showed that 4 ribonucleotides were the minimum number
 XX CC for RNA cleavage. The invention provides probes for nucleic acid
 XX CC hybridisation. The probes form a hairpin structure comprising a
 XX CC double-stranded stem and a single-stranded loop, and are capable of
 XX CC both intramolecular and intermolecular hybridisation. The
 XX CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid
 XX CC that is resistant to RNase H cleavage. When the probe hybridises
 XX CC with a target DNA, the RNA strand in the DNA:RNA duplex becomes
 XX CC sensitive to RNase H treatment and can be removed. Arrays and
 XX CC methods for nucleic acid hybridisation using the probes are provided.
 XX SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 6.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAATTAATAA 1
 RESULT 1084
 ID ABZ76952 standard; DNA; 18 BP.
 XX AC ABZ76952;
 XX DT 07-MAY-2003 (first entry)
 XX DE
 XX DE Bovine DGAT BAC-DNA sequencing primer #25.
 XX DE Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14;
 XX DE bovine; milk; meat marbling; low fat; polymorphic; SNP;
 XX DE single nucleotide polymorphism; PCR primer; ss.
 XX OS Bos taurus.
 XX OS Synthetic.
 XX PN WO2003004630-A2.
 XX XX 16-JAN-2003.
 XX XX 05-JUL-2002; 2002WO-EP07520.
 XX XX 06-JUL-2001; 2001EP-0116412.
 XX PR 13-MAY-2002; 2002US-379412P.

XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
 XX Fries H, Winter A;
 XX WPI; 2003-239205/23.
 XX New nucleic acid molecule comprising a sequence of an allele of a
 PT polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for
 PT testing a mammal for its predisposition for fat content of milk and for
 PT meat marbling -
 XX
 PS Example 1; Page 35; 91pp; English.
 XX The present invention describes a nucleic acid molecule (NA) (I) encoding
 CC a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or
 CC indicative for low fat content of milk and to low meat marbling
 CC (intramuscular fat content). Human DGAT is located to chromosome 8, and
 CC bovine DGAT is located to chromosome 14. (I) is useful for testing a
 CC mammal for its predisposition for fat content of milk and/or its
 CC predisposition for meat marbling. The method comprises analysing the
 CC gene encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
 CC polymorphisms (SNPs)) which are connected with the predisposition. The
 CC nucleotide polymorphisms are located in the coding region of the DGAT
 CC gene and result in substitution, deletion and/or addition of an amino
 CC acid sequence of the polypeptide which is encoded by the gene. The
 CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT
 CC gene a guanine and a cytosine residue, at position 3343 a cytosine or
 CC guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
 CC thymine, which correlate with a predisposition for low fat content of
 CC milk and low meat marbling. The nucleic acid molecule has at the position
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine
 CC residues which correlate with a predisposition for high content of milk
 CC and high meat marbling. The nucleotide polymorphisms are located in a
 CC region which is responsible for the regulation of the expression of the
 CC product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to
 CC ABP96046 represent sequences used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 2 A; 9 C; 3 G; 4 T; 0 other;
 SQ Query Match 1.3%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred.No. 6.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 633 CAGTCCCGCTCCCTGCA 649
 DB 1 CAGTCTGTCTCCCTCCA 17
 RESULT 1085
 ABZ77008
 ID ABZ77008 standard; DNA; 18 BP.
 XX AC ABZ77008;
 XX 07-MAY-2003 (first entry)
 XX Bovine DGAT PCR primer #44.
 DE Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14;
 KW bovine; milk; meat marbling; low fat; polymorphic; SNP;
 KW single nucleotide polymorphism; PCR primer; ss.
 XX Bos taurus.
 OS Synthetic.
 XX WO2003004630-A2.
 PN 16-JAN-2003.
 PD 05-JUL-2002; 2002WO-EF07520.
 XX

PR 06-JUL-2001; 2001EP-0116412.
 PR 13-MAY-2002; 2002US-379412P.
 XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
 XX Fries H, Winter A;
 XX WPI; 2003-239205/23.
 XX New nucleic acid molecule comprising a sequence of an allele of a
 PT polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for
 PT testing a mammal for its predisposition for fat content of milk and for
 PT meat marbling -
 XX
 PS Example 1; Page 36; 91pp; English.
 XX The present invention describes a nucleic acid molecule (NA) (I) encoding
 CC a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or
 CC indicative for low fat content of milk and to low meat marbling
 CC (intramuscular fat content). Human DGAT is located to chromosome 8, and
 CC bovine DGAT is located to chromosome 14. (I) is useful for testing a
 CC mammal for its predisposition for fat content of milk and/or its
 CC predisposition for meat marbling. The method comprises analysing the
 CC gene encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
 CC polymorphisms (SNPs)) which are connected with the predisposition. The
 CC nucleotide polymorphisms are located in the coding region of the DGAT
 CC gene and result in substitution, deletion and/or addition of an amino
 CC acid sequence of the polypeptide which is encoded by the gene. The
 CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT
 CC gene a guanine and a cytosine residue, at position 3343 a cytosine or
 CC guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
 CC thymine, which correlate with a predisposition for low fat content of
 CC milk and low meat marbling. The nucleic acid molecule has at the position
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine
 CC residues which correlate with a predisposition for high content of milk
 CC and high meat marbling. The nucleotide polymorphisms are located in a
 CC region which is responsible for the regulation of the expression of the
 CC product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to
 CC ABP96046 represent sequences used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 2 A; 9 C; 3 G; 4 T; 0 other;
 SQ Query Match 1.3%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred.No. 6.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 633 CAGTCCCGCTCCCTGCA 649
 DB 1 CAGTCTGTCTCCCTCCA 17
 RESULT 1086
 ABZ74977
 ID ABZ74977 standard; DNA; 18 BP.
 XX AC ABZ74977;
 XX 25-MAR-2003 (first entry)
 XX Human gene 216 polymorphism detection PCR primer #34.
 DE Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;
 KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism;
 KW SNP; gene therapy; respiratory disease; asthma; obesity; PCR;
 KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;
 KW adult respiratory distress syndrome; inflammatory bowel syndrome.
 XX Homo sapiens.
 OS WO200283077-A2.
 PN 24-OCT-2002.
 XX

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XX PF 15-APR-2002; 2002WO-US12063.
XX PR 13-APR-2001; 2001US-0834597.
XX PR 13-APR-2001; 2001WO-US12245.
XX PA (SCHE ) SCHERING CORP.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Keith T, Little RD, Van Berdewegh P, Dupuis J, Del Mastro RG;
XX PI Simon J, Allen K, Pandit S;
XX DR WPI; 2003-092960/08.
XX FT New isolated gene 216 nucleic acids, useful for diagnosing, preventing
XX FT or treating a disorder, such as asthma, bronchial hyper-responsiveness,
XX FT chronic obstructive pulmonary disease, obesity or inflammatory bowel
XX FT syndrome -
XX PS Example 10; Page 155; 650pp; English.
XX CC This invention relates to a novel isolated nucleic acid, gene 216,
XX CC identified from human chromosome 20p13-p12. The invention also discloses
XX CC regions of the 216 gene that contain single nucleotide polymorphisms
XX CC (SNP's) which may be used as markers for disease susceptibility or
XX CC severity. The nucleotides of the invention may have antiasthmatic,
XX CC antiinflammatory or anorectic activities and may be used in gene
XX CC therapy. The nucleic acids, antibodies or its fragments are useful for
XX CC diagnosing, preventing or treating a disorder, such as respiratory
XX CC diseases (e.g. asthma, bronchial hyper-responsiveness, chronic
XX CC obstructive pulmonary disease or adult respiratory distress syndrome),
XX CC obesity, or inflammatory bowel syndrome. The nucleic acids are also
XX CC useful for identifying increased susceptibility of a subject to the
XX CC disorders mentioned. The nucleic acids can also be used as primers and
XX CC templates for the recombinant production of disorder-associated
XX CC peptides or polypeptides, for chromosome and gene mapping, or for
XX CC tissue distribution studies. The present sequence represents a gene
XX CC 216 specific PCR primer used in the scope of the invention.
XX SQ Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 CCAGGTGCACAGGCGG 53
DB 2 CCAGGTGCACAGAGCAG 18

RESULT 1087
AAQ20028/c
ID AAQ20028 standard; DNA; 19 BP.
XX AC AAQ20028;
XX DT 01-APR-1992 (first entry)
XX DE Cross-linking oligomer 114 for targeting HUMILIB.
XX KW deoxyribonucleic acid; major groove; ethan amino group; IL-1;
XX KW aziridinylcytosine; cross-linking group; o-xyloso linking group;
XX KW human interleukin-1 beta; inverted polarity region; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "N-methyl-8-oxo-2'-deoxyadenine"
XX FT modified_base 4 /*tag= b

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FT /*mod_base= OTHER
FT /*note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 14...19
FT /*tag= c
FT /*label= inverted_polarity_region
FT /*note= "see comments"
FT 14
FT /*tag= d
FT /*mod_base= OTHER
FT /*note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 18
FT /*tag= e
FT /*mod_base= OTHER
FT /*note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 19
FT /*tag= f
FT /*mod_base= OTHER
FT /*note= "N4N4-ethanocytosine"
XX XX
XX PN W09118997-A.
XX PD 12-DEC-1991.
XX PF 24-MAY-1991; 91WO-1003680.
XX PR 14-JAN-1991; 91US-0640654.
XX PR 25-MAY-1990; 90US-0529346.
XX PA (GILE-) GILEAD SCIE INC.
XX PI Matteucci MD, Krawczyk S;
XX DR WPI; 1992-007480/01.
XX FT New sequence-specific non-photo-activated crosslinking agents -
XX FT bind to the major groove of duplex DNA and are esp. useful for
XX FT treating latent infections e.g. HIV
XX PS Example 4; Page 25; 42pp; English.
XX CC This oligomer contains an inverted polarity region formed from an
XX CC o-xyloso dimer synthon. Residues 13 and 14 are linked via an
XX CC o-xyloso group (i.e. nucleotides that have xylose sugar linked via
XX CC the o-xyloso ring). The sequence is designed to target the Human
XX CC interleukin-1 beta gene beginning at nucleotide 7378 and will
XX CC covalently cross-link to it via the N4N4-ethanocytosine group.
XX CC See also AAQ20026-Q20030.
XX SQ Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TAAAAA AAAAAAAAAA 1099
DB 18 TAAAT AAAAAAAAAAATAA 2

RESULT 1088
AAQ20029/c
ID AAQ20029 standard; DNA; 19 BP.
XX AC AAQ20029;
XX DT 01-APR-1992 (first entry)
XX DE Cross-linking oligomer 115 for targeting HUMILIB.
XX KW deoxyribonucleic acid; major groove; ethan amino group; IL-1;
XX KW aziridinylcytosine; cross-linking group; o-xyloso linking group;
XX KW human interleukin-1 beta; inverted polarity region; ss.
XX

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OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT modified_base 4 /*tag= b
FT /mod_base= OTHER
FT modified_base 14 /*tag= c
FT /mod_base= OTHER
FT modified_base 14 /*tag= d
FT /mod_base= OTHER
FT modified_base 18 /*tag= e
FT /mod_base= OTHER
FT modified_base 19 /*tag= f
FT /mod_base= OTHER
XX WO9118997-A.
XX 12-DEC-1991.
XX 24-MAY-1991; 91WO-1003680.
XX 14-JAN-1991; 91US-0640654.
XX 23-MAY-1990; 90US-0529346.
XX (GILE-) GILEAD SCIE INC.
XX Matteucci MD, Krawczyk S;
XX WPI; 1992-007480/01.
XX
XX New sequence-specific non-photo-activated crosslinking agents -
XX bind to the major groove of duplex DNA and are esp. useful for
XX treating latent infections e.g. HIV
XX
XX Example 4; Page 25; 42pp; English.
XX
XX This oligomer contains an inverted polarity region formed from an
XX o-xyloso dimer synthon. Residues 13 and 14 are linked via an
XX o-xyloso group (i.e. nucleotides that have xylose sugar linked via
XX the o-xyloso ring). The sequence is designed to target the Human
XX interleukin-1 beta gene beginning at nucleotide 7378 and will
XX covalently cross-link to it via the N4N4-ethanocytosine groups.
XX See also AAQ20026-Q20030.
XX
XX Sequence 19 BP; 3 A; 2 C; 0 G; 14 T; 0 other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 19;
XX Best Local Similarity 86.2%; Pred. No. 7.1e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1083 TAAAAAATAAAAAA 1099
XX ||||| |||||
XX Db 18 TAAATATAAAAAATAA 2
XX
XX RESULT 1089
XX AAQ30374/c
XX ID AAQ30374 standard; DNA; 19 BP.
XX
XX AC AAQ30374;

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XX 25-MAR-2003 (updated)
XX 07-DEC-1992 (first entry)
XX
XX Oligomer HUM beta 114 for forming triplex with IL-1 target duplex.
XX
XX Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
XX HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT modified_base 4 /*tag= b
FT /mod_base= m5c
FT modified_base 14 /*tag= c
FT /mod_base= m5c
FT modified_base 18 /*tag= d
FT /mod_base= m5c
FT modified_base 19 /*tag= e
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT 14..20
FT /*tag= f
FT /label= inverted polarity_region
FT /note= "see comments"
FT 13..14
FT /*tag= g
FT /note= "o-xyloso dimer synthon linkage"
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US08811.
XX
XX 23-NOV-1990; 90US-0617907.
XX 18-JAN-1991; 91US-0643382.
XX 08-APR-1991; 91US-0683420.
XX 17-APR-1991; 91US-0686544.
XX 17-APR-1991; 91US-0686546.
XX 17-APR-1991; 91US-0686547.
XX 27-SEP-1991; 91US-0766733.
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with
XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,
XX hepatitis, herpes, malignancy and inflammation
XX
XX Claim 12; Page 70; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at
XX physiological pH with a purine rich target sequence by coupling
XX into the major groove of the duplex. The specific target sequence
XX of this oligomer is the human interleukin -1 beta gene beginning at
XX nucleotide 7378 contg. a purine rich sequence concd. on one strand
XX of the duplex. The oligomer, and others like it are useful in
XX diagnosis and therapy of diseases characterised by specific DNA
XX duplex targets, e.g. HPV; HER; HIV; hepatitis B, herpes, malignant
XX tumours and inflammation. The triple helices form under mild conditions
XX thus assays may be carried out without subjecting the test specimen to

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CC harsh conditions. The oligomer contains an inverted polarity region
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
 CC (nucleotides have the 3' positions of xylose sugars linked via the
 CC o-xyloso ring). Two nucleotides are coupled through a xylose residue
 CC to form the dimer synthon. This additional modification may render
 CC the oligomer stable to nuclease activity. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems.
 CC See also AAQ25452-25501 and AAQ30226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX

SQ Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
 Query Match 1.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1099
 DB 18 TAAATAAAAAAATAA 2

RESULT 1090
 AAQ30375/c
 ID AAQ30375 standard; DNA; 19 BP.

XX AC AAQ30375;
 XX 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)

XX Oligomer HUM beta 115 for forming triplex with IL-1 target duplex.
 XX Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
 KW HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
 XX
 XX Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 FT modified_base 4
 FT /*tag= b
 FT /mod_base= m5C
 FT modified_base 14
 FT /*tag= c
 FT /mod_base= m5C
 FT modified_base 18
 FT /*tag= d
 FT /mod_base= m5C
 FT modified_base 19
 FT /*tag= e
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 FT misc_feature 14..20
 FT /*tag= f
 FT /label= inverted polarity_region
 FT /note= "see comments"
 FT misc_feature 13..14
 FT /*tag= g
 FT /note= "O-xyloso dimer synthon linkage"

XX WO9209705-A1.
 PN 11-JUN-1992.
 XX 25-NOV-1991; 91WO-US08811.
 XX 23-NOV-1990; 90US-0617907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0686544.

PR 17-APR-1991; 91US-0686546.
 PR 17-APR-1991; 91US-0686547.
 PR 27-SEP-1991; 91US-0766733.
 XX
 XX (GILE-) GILEAD SCI INC.
 XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
 XX WPI; 1992-217083/26.
 XX
 XX New oligomers contg. modified bases - which form a triplex with
 FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 FT hepatitis, herpes, malignancy and inflammation
 XX
 XX Claim 12; Page 70; 77pp; English.

CC The synthetic oligomer is capable of forming a triplex at
 CC physiological pH with a purine rich target sequence by coupling
 CC into the major groove of the duplex. The specific target sequence
 CC of this oligomer is the human interleukin -1 beta gene beginning at
 CC nucleotide 7378 contg. a purine rich sequence concd. on one strand
 CC of the duplex. The oligomer, and others like it are useful in
 CC diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV; HER; HIV; hepatitis B, herpes, malignant
 CC tumours and inflammation. The triple helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions. The oligomer contains an inverted polarity region
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
 CC (nucleotides have the 3' positions of xylose sugars linked via the
 CC o-xyloso ring). Two nucleotides are coupled through a xylose residue
 CC to form the dimer synthon. This additional modification may render
 CC the oligomer stable to nuclease activity. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems.
 CC See also AAQ25452-25501 and AAQ30226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 19 BP; 3 A; 2 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1099
 DB 18 TAAATAAAAAAATAA 2

RESULT 1091
 AAT65904/c
 ID AAT65904 standard; DNA; 19 BP.

XX AC AAT65904;
 XX 25-MAR-2003 (updated)
 DT 18-JUN-1997 (first entry)

XX Primer #1 to amplify repeat sequence marker Mfd54.
 XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.

XX Synthetic.
 XX US5582979-A.
 XX 10-DEC-1996.
 XX 04-APR-1994; 94US-0222177.
 XX 05-SEP-1991; 91US-0754351.
 PR 21-APR-1989; 89US-0341562.

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PR 04-APR-1994; 94US-0222177.
XX (MARS-) MARSHFIELD CLINIC.
XX Weber JL;
XX WPI; 1997-042299/04.
DR Detection of polymorphic genetic markers of the form
PT (dc-da)n(dg-dt)n - using novel nucleic acid mols. as primers
XX
XX Disclosure; Column 11-12; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing,
CC human genetic analysis, such as linkage analysis of genetic disease,
CC commercial animal or plant breeding or pedigree analysis. Clones
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-da).(dG-dT)
CC probe. Over 100 repeat blocks were isolated. The primers
CC AAT65798-T66047 were used to PCR amplify the inserts from the isolated
CC clones containing the repeat sequences. The primers AAT65904-5 were used
CC to amplify the repeat sequence marker clone Mid54.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 19 BP; 4 A; 4 C; 7 G; 4 T; 0 other;
SQ
    Query Match 1.3%; Score 13.8; DB 1; Length 19;
    Best Local Similarity 88.2%; Pred. No. 7.1e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 350 CAGCGCCAACTGTCAG 366
DB 17 CAGCCTCACTGTCAG 1

RESULT 1092
AAZ72847
ID AAZ72847 standard; DNA; 19 BP.
AC AAZ72847;
XX
XX 10-SEP-2001 (first entry)
XX Human biallelic marker upstream amplification primer SEQ ID NO:7203.
DE
DE Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -

PR 04-APR-1994; 94US-0222177.
XX (MARS-) MARSHFIELD CLINIC.
XX Weber JL;
XX WPI; 1997-042299/04.
DR Detection of polymorphic genetic markers of the form
PT (dc-da)n(dg-dt)n - using novel nucleic acid mols. as primers
XX
XX Disclosure; Column 11-12; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing,
CC human genetic analysis, such as linkage analysis of genetic disease,
CC commercial animal or plant breeding or pedigree analysis. Clones
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-da).(dG-dT)
CC probe. Over 100 repeat blocks were isolated. The primers
CC AAT65798-T66047 were used to PCR amplify the inserts from the isolated
CC clones containing the repeat sequences. The primers AAT65904-5 were used
CC to amplify the repeat sequence marker clone Mid54.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 19 BP; 4 A; 4 C; 7 G; 4 T; 0 other;
SQ
    Query Match 1.3%; Score 13.8; DB 1; Length 19;
    Best Local Similarity 88.2%; Pred. No. 7.1e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 767 AGAAGTGGAGAGAGT 783
DB 1 AGAAGTGGAGAGAGT 17

RESULT 1093
AAZ76004
ID AAZ76004 standard; DNA; 19 BP.
XX
XX AAZ76004;
AC
XX
XX 10-SEP-2001 (first entry)
XX Human biallelic marker downstream amplification primer SEQ ID NO:10360.
DE
DE Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -

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CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.

XX Sequence 19 BP; 6 A; 9 C; 0 G; 4 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CCATCTCAACACGCGCT 632
 Db 1 CCATCTCAACACCTACT 17

RESULT 1094
 AAA95378/C
 ID AAA95378 standard; DNA; 19 BP.

XX AAA95378;

XX 12-FEB-2001 (first entry)

DE Rat Smo coding sequence PCR primer #1.

XX Rat; Nurrl; tyrosine hydroxylase; catecholamine-related disease;
 KW Parkinson's disease; manic depression; schizophrenia; PCR primer; ss.

OS Rattus norvegicus.

XX WO200058451-A1.

PD 05-OCT-2000.

XX 21-MAR-2000; 2000WO-US07544.

XX 26-MAR-1999; 99US-0277078.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

PI Sakurada K, Palmer T, Gage FH;

XX WPI; 2000-656165/63.

XX Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase
 PT expression useful for treating catecholamine-related diseases such as
 PT Parkinson's disease, manic depression and schizophrenia -

PS Example 1; Page 20; 68pp; English.

XX The present invention describes the rat Nurrl coding and protein
 CC sequences. The Nurrl protein is involved in the induction of tyrosine
 CC hydroxylase expression in adult rat-derived hippocampal progenitor cells.
 CC The Nurrl gene and protein can be used in the treatment of
 CC catecholamine-related diseases such as Parkinson's disease, manic
 CC depression and schizophrenia. They can also be used to induce tyrosine
 CC hydroxylase expression and identify tyrosine hydroxylase related
 CC deficiencies, which are linked to the same diseases. The present sequence
 CC is a PCR primer used in a method to differentiate adult neural progenitor
 CC cells.

XX Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 954 CAGCTGGCAGGGTGGC 970
 Db 17 CAGATGAGCAGGGTGGC 1

RESULT 1095
 AAA84710/C
 ID AAA84710 standard; DNA; 19 BP.

XX AAA84710;

XX 04-DEC-2000 (first entry)

XX Cyclin E ribozyme binding site #243.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

PD 08-JUN-2000.

XX 06-DEC-1999; 99WO-US28772.

XX 04-DEC-1998; 98US-0110954.

XX (IMMU-) IMMUSOL INC.

PI Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -

XX Disclosure; Page 81; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.

XX Sequence 19 BP; 5 A; 0 C; 3 G; 11 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAAAA 1092
 Db 18 CAATTATTAAAAAAA 2

RESULT 1096
 AAZ94157/C
 ID AAZ94157 standard; DNA; 19 BP.

XX AAZ94157;

XX 19-JUN-2000 (first entry)

XX Human PEMT2 PCR primer.

KW	Phosphatidylethanolamine N-methyltransferase-2; PENT2; human;
KW	liver cancer; hepatoma; antitumour; antiproliferative;
KW	therapy; diagnosis; PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200014198-A2.
XX	
XX	16-MAR-2000.
XX	
PF	13-AUG-1999; 99WO-US18463.
XX	
XX	02-SEP-1998; 98US-0146218.
PR	
XX	(RESE) RESEARCH CORP TECHNOLOGIES INC.
PA	
XX	
PI	Vance DE, Walkey CJ, Cui Z;
XX	
DR	WPI; 2000-256956/22.
XX	
PT	Isolated nucleic acid molecule encoding phosphatidylethanolamine
PT	N-methyltransferase protein used to treat phosphatidylethanolamine
PT	N-methyltransferase-associated disorders such as liver cancer -
XX	
XX	Example 8; Page 57; 11pp; English.
CC	
CC	The present sequence is that of a primer used in the PCR
CC	amplification of the open reading frame of a cDNA clone (see
CC	AAZ94150) encoding human phosphatidylethanolamine N-methyltransferase
CC	(PENT-2, see AAY79199). The PCR product was subcloned into
CC	mammalian expression vector pCI, and PENT-2 was expressed in
CC	rat hepatoma McArdle-RH7777 cells. The invention relates to
CC	novel human PENT2 polynucleotides and protein (see AAY79199), and
CC	to methods of using them in the treatment and diagnosis of liver
CC	disorders, such as liver cancer.
XX	
SQ	Sequence 19 BP; 2 A; 7 C; 7 G; 3 T; 0 other;
	Query Match 1.3%; Score 13.8; DB 1; Length 19;
	Best Local Similarity 88.2%; Pred. No. 7.1e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gap
QY	552 GTAGCCCAACAGCAGGG 568
Db	18 GTAGCCCAACAGCAGGG 2
RESULT 1097	
AAH45473	
ID	AAH45473 standard; DNA; 19 BP.
XX	
AC	AAH45473;
XX	
DT	07-SEP-2001 (first entry)
XX	
DE	PCR primer Shh-U2 specific for human secreted sonic hedgehog cDNA.
XX	
KW	Sporadic basal cell carcinoma; BCC; detection; Gli3; skin cancer;
KW	transcription factor; PCR primer; human; ss; sonic hedgehog; shh.
XX	
OS	Homo sapiens.
XX	
PN	US6238876-B1.
XX	
PD	29-MAY-2001.
XX	
PF	22-JUN-1998; 98US-0102491.
XX	
PR	20-JUN-1997; 97US-0050286.
XX	
PA	(UYNV) UNIV NEW YORK STATE.
XX	
PI	Altaba ARI;
PI	

XX	WPI; 2001-366473/38.
XX	Detecting the onset or presence of skin cancer, particularly sporadic
XX	basal cell carcinoma, comprises measuring the level of Gli1 in the
XX	sample -
XX	Disclosure; Column 8; 2lpp; English.
XX	This invention relates to a method of detecting the onset or presence of
XX	sporadic basal cell carcinoma (BCC) in an animal. The method involves
XX	measuring the level of Gli1 in a sample of skin. Gli1 levels above basal
XX	or normal indicate the presence or onset of sporadic basal cell
XX	carcinoma. Gli1 is a zinc finger transcription factor down stream of
XX	secreted sonic hedgehog (shh) activation in a cascade of cytoplasmic
XX	signal transduction. Gli1 in turn can induce Shh expression in an
XX	auto regulatory manner. There are links between ectopic expression of the
XX	Gli1 gene and the development or onset of BCC. The method is useful for
XX	detecting the onset or presence of sporadic basal cell carcinoma,
XX	particularly in detecting skin cancer. The present sequence represents a
XX	PCR primer specific for human Shh cDNA. The primer is used in the method
XX	of the invention.
XX	Sequence 19 BP; 7 A; 6 C; 3 G; 3 T; 0 other;
XX	Query Match 1.3%; Score 13.8; DB 1; Length 19;
XX	Best Local Similarity 88.2%; Pred. No. 7.1e+02;
XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	462 GAAGAGCTCCAGAACT 478
Db	
	1 GAAGATCTCCAGAACT 17
RESULT 1098	
AAH59872/c	
ID	AAH59872 standard; DNA; 19 BP.
XX	AAH59872;
XX	10-SEP-2001 (first entry)
XX	Cyclin E ribozyme binding site SEQ ID NO:2296.
XX	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX	recognition site; target; ribozyme binding site; eye disease; vulnery;
XX	proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX	cytokine; inflammation; cell-cycle dependent kinase; cyclin; WMP;
XX	matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX	antiproliferic; dermatological; antiseborrheic; antidiabetic; virucide;
XX	antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
XX	atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX	basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX	sickle cell retinopathy; ss.
XX	Homo sapiens.
OS	Synthetic.
XX	WO200130362-A2.
XX	03-MAY-2001.
XX	26-OCT-2000; 2000WO-US29500.
XX	26-OCT-1999; 99US-0161532.
XX	(IMMU-) IMMUSOL INC.
XX	Robbins JM, Tritz R;
XX	WPI; 2001-300427/31.
XX	Treating proliferative skin or eye diseases and scarring using

PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX
 PS Example 1; Page 239; 408pp; English.
 XX
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, anti-aging,
 CC ophthalmological, vulnerary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAU57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 19 BP; 5 A; 0 C; 3 G; 11 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACATATTAATAAAAAA 1092
 |||||
 Db 18 CAATTAATTAATAAAAAA 2

RESULT 1099

AAAF76084
 ID AAF76084 standard; DNA; 19 BP.

AC AAF76084;

DT 22-MAY-2001 (first entry)

DE Maize MADS-box gene ZmMADS2 PCR primer, SEQ ID NO:28.

XX Maize MADS box gene; ZmMADS2; pollen-specific expression;
 KW pollen development; function; transgenic plant; male sterility;
 KW hybrid seed production; PCR primer; ss.

XX Zea mays.

XX WC200112799-A2.

PD 22-FEB-2001.

XX 16-AUG-2000; 2000WO-EF08002.

XX 18-AUG-1999; 99EP-0116268.

PA (SUED-) SUEDEWESTDEUTSCHE SAATZUCHT.

XX Loerz H, Dresselhaus T, Schreiber D, Heuer S;

XX WPI; 2001-211214/21.

XX Novel nucleic acid molecule useful for cloning and expressing a pollen
 PT specific sequence in a plant -

XX Example 1; Page 32; 66pp; English.

XX The invention relates to regulatory elements (AAF76059-AAF76067) from

CC the maize MADS box gene ZmMADS2 (AAF76068) which are capable of directing
 CC expression in a pollen-specific manner. The ZmMADS2 protein (AAB73333)
 CC is expressed particularly in mature pollen after dehiscence, indicating
 CC that it has an essential role in pollen development and function, in
 CC particular in pollen tube growth. The invention also relates to vectors
 CC and host cells comprising the ZmMADS2 regulatory or genomic sequence, and
 CC their use in the generation of transgenic plants. The ZmMADS2 regulatory
 CC sequences are useful for cloning and expressing a pollen-specific or
 CC pollen-abundant gene in a plant, and may also be used to drive the
 CC expression of a gene of interest in a pollen-specific or pollen-preferred
 CC manner. The ZmMADS2 regulatory sequences are useful for isolating related
 CC regulatory sequences of other plant species which confer pollen or group
 CC specificity to genes of interest operably linked to them. The regulatory
 CC sequences are useful in plant breeding, especially for the production of
 CC hybrid seed. In particular, they may be used to drive the pollen-specific
 CC expression of heterologous genes which confer nuclear or cytoplasmic male
 CC sterility in transgenic plants (e.g., cereals). Sequences AAF76081-
 CC AAF76084 represent PCR primers used in the isolation of cDNA encoding
 CC ZmMADS2 (AAF76058).

XX
 SQ Sequence 19 BP; 1 A; 8 C; 3 G; 7 T; 0 other;

Query Match 1.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 CGCGGCTAGTTCCTCC 38

Db 2 CTCGGCTAGTTCCTCC 18

RESULT 1100

AAAF76471

ID AAF76471 standard; DNA; 19 BP.

AC AAF76471;

DT 11-MAY-2001 (first entry)

DE Maize ZmMADS2 coding sequence PCR primer SEQ ID NO: 28.

XX Male sterile plant; maize; hybrid breeding; pollen tube; ZmMADS2;
 KW grain; cereal; corn; PCR primer; ss.

XX Zea mays.

XX WC200112798-A2.

XX 22-FEB-2001.

XX 16-AUG-2000; 2000WO-EF08001.

XX 18-AUG-1999; 99EP-0116267.

XX (SUED-) SUEDEWESTDEUTSCHE SAATZUCHT.

XX Loerz H, Dresselhaus T, Schreiber D, Heuer S;

XX WPI; 2001-211213/21.

XX Novel nucleic acid molecule, ZmMADS2 derived from pollen of Zea mays
 PT useful for cloning and expressing a pollen specific sequence in a plant
 PT and for producing male sterile plants -

XX Example 1; Page 74; 76pp; English.

XX The present invention provides the protein and coding sequences of the
 CC Zea mays ZmMADS2 protein, which is specifically expressed in pollen. The
 CC sequences can be used to produce male sterile plants, as ZmMADS2 is
 CC essential for pollen tube growth. These are useful in hybrid breeding,
 CC particularly of corn, cereal and grain. The present sequence is a PCR
 CC primer for the ZmMADS2 coding sequence.


```
SQ Sequence 19 BP; 1 A; 8 C; 3 G; 7 T; 0 other;
Query Match      1.3%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 CGCGGCTAGGTTCTCTCC 38
   |||||
DB 2 CTCGGCTAGCTTCTCTCC 18

RESULT 1101
ABN88132/C
ID ABN88132 standard; DNA; 19 BP.
XX
AC ABN88132;
XX
DT 12-AUG-2002 (first entry)
XX
DE Caenorhabditis elegans related dSERN1 upstream primer.
XX
KW Caenorhabditis elegans; C. elegans; reproduction; development;
KW antineurite; nematode; plant protectant; gene therapy; infection;
KW calabar swelling; lymphatic filariasis; elephantiasis; onchocercoma;
KW primer; ss.
XX
OS Caenorhabditis elegans.
OS Synthetic.
XX
XX WO200238600-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-EPI3038.
XX
PR 09-NOV-2000; 2000US-246721P.
XX
PA (CENI-) CENIX BIOSCIENCE GMBH.
XX
PI Echeverri C, Goenczy P, Hyman A, Coulson A, Jones S, Oegema K;
PI Kirkham M;
XX
XX WPI; 2002-471547/50.
XX
PT New Caenorhabditis elegans genes required for viability, growth or
PT reproduction of nematodes, useful for diagnosing or treating e.g.
PT onchocercoma or elephantiasis in humans or animals, or plant diseases
PT caused by e.g. Heterodera
XX
PS Example 2; Page 28; 35pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I),
CC which encodes a polypeptide (II) required for the viability and/or growth
CC and/or reproduction of nematodes (Caenorhabditis elegans), or its
CC fragment (I) and (II) have nematocidal and plant protectant activities,
CC and can be used in gene therapy. (I) is useful for producing (II)
CC required for the viability, growth and/or reproduction of nematodes.
CC Nucleic acids, probes, polypeptides, fusion proteins and antibodies from
CC the present invention are also useful in a screening assay for
CC interacting drugs that inhibit, stimulate or affect worm growth,
CC viability or reproduction. They are useful for diagnosing or treating
CC human or animal diseases associated with the infection or presence of
CC nematode worms, e.g. Wucheria bancrofti, Brugia malayi, Loa loa or
CC Onchocerca volvulus. These diseases include calabar swellings, lymphatic
CC filariasis (elephantiasis) or onchocercoma. The nucleic acids, probes,
CC polypeptides, fusion proteins and antibodies are also useful for
CC diagnosing or treating plant diseases associated with the infection or
CC presence of nematode worms. Furthermore, the nucleic acid and amino
CC acid sequences are useful for developing computational models, structural
CC models or other models for evaluating drug binding and efficacy. The
CC present sequence represents a primer which is used in an example from
CC the present invention in RNAi experiments.
XX

SQ Sequence 19 BP; 0 A; 5 C; 3 G; 11 T; 0 other;
Query Match      1.3%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 GAAACGGGAAGGAAGGA 132
   |||||
DB 19 GAAACAGCAGGAAGGA 3

RESULT 1102
ABL45877
ID ABL45877 standard; DNA; 15 BP.
XX
AC ABL45877;
XX
DT 26-APR-2002 (first entry)
XX
DE Human EDG6 gene allele specific primer SEQ ID NO: 71.
XX
KW Human; endothelial differentiation, G-protein coupled receptor 6;
KW EDG6; haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
KW cytosolic; antiinflammatory; gene therapy; SNP;
KW single nucleotide polymorphism; primer; ss.
XX
OS Homo sapiens.
OS
XX WO200206446-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US22523.
XX
PR 17-JUL-2000; 2000US-218727P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PI Kliem SE, Koshy B;
XX
XX WPI; 2002-171804/22.
XX
PT New genetic variants of endothelial differentiation, G-protein coupled
PT receptor-6 gene for studying expression, function of the gene and
PT expressing EDG6 protein for use in screening drugs to treat cancer,
PT inflammation
XX
PS Claim 16; Page 14; 11pp; English.
XX
CC The present invention provides the gene, protein and cDNA sequences of
CC the human endothelial differentiation, G-protein coupled receptor 6
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
CC within the sequences. The sequences can be used in the identification of
CC the haplotype of an individual, and in the treatment of cancer,
CC angiogenesis and inflammation. The present sequence is an allele specific
CC primer for the EDG6 gene, which is found on chromosome 19p13.3.
XX
SQ Sequence 15 BP; 1 A; 4 C; 7 G; 2 T; 1 other;
Query Match      1.2%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.1e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 233 GGCCGTGGCTCAGC 246
   |||||
DB 1 GGCCGTGGCTCAGS 14

RESULT 1103
AAD25198
ID AAD25198 standard; DNA; 15 BP.
XX
AC AAD25198;
```

XX 12-MAR-2002 (first entry)

XX Human homeo box D3 (HOXD3) gene polymorphism detecting ASO primer #15.

XX Human; homeo box D3; HOXD3; polymorphism; developmental disorder;

XX haplotype; HT; allele-specific oligonucleotide; ASO; tumour; therapy;

XX drug screening; cytostatic; primer; ss.

XX Homo sapiens.

XX WO200190127-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US16982.

XX 25-MAY-2000; 2000US-207076P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Kazemi A, Koshy B, Kumar AM;

XX WPI; 2002-075363/10.

XX New genetic variants of Homeo Box D3 for studying expression and

XX function of the protein, and for screening drugs to treat diseases e.g.

XX developmental disorders and tumors -

XX Claim 16; Page 13; 66pp; English.

XX The invention relates to genetic variants of the homeo box D3 (HOXD3)

XX gene. HOXD3 gene includes 9 polymorphic sites PS1-PS9. Haplotypes

XX (HTs) or haplotype pairs (HP) for PS1-PS9 in the HOXD3 gene are useful

XX for improving the efficiency and reliability of several steps in the

XX discovery and development of drugs for treating diseases associated

XX with HOXD3 activity, e.g., developmental disorders and tumours. HOXD3

XX isogene is useful in studying the expression and function of HOXD3 and

XX in expressing HOXD3 protein for use in screening for candidate drugs

XX to treat diseases related to HOXD3 activity and in studying the effect

XX of the variation on the biological activity of HOXD3 as well as on the

XX binding affinity of candidate drugs targeting HOXD3 for the treatment

XX of developmental disorders and tumours. An antibody against HOXD3 is

XX useful in a variety of diagnostic and prognostic formats and therapeutic

XX methods. A recombinant non-human organism is useful in studying

XX expression of the HOXD3 isogenes in vivo. Allele-specific

XX oligonucleotides (ASO) are useful as probes and primers and for

XX assaying a polymorphism in the target region. The present sequence is

XX an ASO primer used for detecting human HOXD3 gene polymorphisms.

XX Sequence 15 BP; 3 A; 7 C; 3 G; 1 T; 1 other;

Query Match 1.2%; Score 13.6; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 6.1e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 348 GCCAGCGCCCACT 361

DB 2 GCCAGCGCCCACT 15

RESULT 1104

ABK32799

ID ABK32799 standard; DNA; 15 BP.

XX AC ABK32799;

XX 23-APR-2002 (first entry)

XX Human APPBP1 gene, allele-specific oligonucleotide #29.

XX Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;

XX Alzheimer's disease; transgenic animal; platelet aggregation;

XX single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.

XX Homo sapiens.

XX WO200202820-A1.

XX 10-JAN-2002.

XX 02-JUL-2001; 2001WO-US20951.

XX 30-JUN-2000; 2000US-215511P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Sausker EA;

XX Stephens CJ;

XX WPI; 2002-164539/21.

XX Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene

XX polymorphic variants, useful e.g. in studying the expression and

XX function of APPBP1 and screening candidate drugs for treating

XX Alzheimer's disease -

XX Claim 17; Page 13; 104pp; English.

XX The invention relates to an isolated polypeptide comprising a sequence

XX which is a polymorphic variant of a reference sequence for the amyloid

XX beta precursor protein binding protein 1, 59kD (APPBP1) protein or its

XX fragment. The polymorphic variants are useful in studying the expression

XX and function of APPBP1, in expressing APPBP1 protein for use in

XX screening for candidate drugs to treat diseases related to APPBP1

XX activity, in studying the effect of the variation on the biological

XX activity of APPBP1, and the binding affinity of candidate drugs

XX targeting APPBP1 for the treatment of disorders such as Alzheimer's

XX disease. The haplotyping methods are useful in validating APPBP1 as a

XX candidate target for treating a specific condition or disease predicted

XX to be associated with APPBP1 activity, or in the design of clinical

XX trials of candidate drugs for treating a specific condition or disease

XX associated with APPBP1 activity. The transgenic animals are useful for

XX studying expression of the APPBP1 isogenes in vivo, for in vivo screening

XX and testing of drugs targeted against APPBP1 protein, and for testing the

XX efficacy of therapeutic agents and compounds for disorders related to

XX platelet aggregation in a biological system. ABK32771-ABK32327

XX represent human APPBP1 gene allele-specific oligonucleotides used in the

XX method of the invention.

XX Sequence 15 BP; 13 A; 1 C; 0 G; 0 U; 1 other;

Query Match 1.2%; Score 13.6; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 6.1e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097

DB 2 AAAAAAAAAAAAAA 15

RESULT 1105

AAT52142/c

ID AAT52142 standard; RNA; 15 BP.

XX AC AAT52142;

XX 25-MAR-2003 (updated)

XX 25-MAR-1997 (first entry)

XX Human ICAM hammerhead ribozyme target sequence (nt. position 2913).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;

XX intercellular adhesion molecule; rel A; tumour necrosis factor;

XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09523225-A2.
 PN
 XX 31-AUG-1995.
 PD
 XX
 XX 23-FEB-1995; 95WO-IB00156.
 XX
 XX 30-JAN-1995; 95US-0380734.
 PR
 XX 23-FEB-1994; 94US-0201109.
 PR
 XX 29-MAR-1994; 94US-0218934.
 PR
 XX 04-APR-1994; 94US-0222795.
 PR
 XX 07-APR-1994; 94US-0224483.
 PR
 XX 15-APR-1994; 94US-0227958.
 PR
 XX 15-APR-1994; 94US-0228041.
 PR
 XX 18-MAY-1994; 94US-0245736.
 PR
 XX 06-JUL-1994; 94US-0271280.
 PR
 XX 15-AUG-1994; 94US-0291932.
 PR
 XX 16-AUG-1994; 94US-0291433.
 PR
 XX 17-AUG-1994; 94US-0292620.
 PR
 XX 19-AUG-1994; 94US-0293520.
 PR
 XX 02-SEP-1994; 94US-0300000.
 PR
 XX 08-SEP-1994; 94US-0303039.
 PR
 XX 23-SEP-1994; 94US-0311486.
 PR
 XX 23-SEP-1994; 94US-0311749.
 PR
 XX 28-SEP-1994; 94US-0314397.
 PR
 XX 03-OCT-1994; 94US-0316771.
 PR
 XX 07-OCT-1994; 94US-0319492.
 PR
 XX 11-OCT-1994; 94US-0321993.
 PR
 XX 04-NOV-1994; 94US-0334847.
 PR
 XX 10-NOV-1994; 94US-0337608.
 PR
 XX 28-NOV-1994; 94US-0345516.
 PR
 XX 16-DEC-1994; 94US-0357577.
 PR
 XX 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowirza B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Meswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR
 XX
 PT Ribozymes having modified bases and methods for producing them
 PT for use in inhibiting disease related genes
 XX
 PS Claim 2; Page 175; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and
 CC thereby inhibit ICAM-1 expression, making them useful for reducing
 CC transplant rejection and alleviating symptoms in patients with
 CC rheumatoid arthritis, asthma and other inflammatory disorders.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 15 BP; 1 A; 1 C; 0 G; 13 U; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 6.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTTAAAAA 1096
 DB 15 TGA 1
 RESULT 1106
 AAV31906/c
 ID AAV31906 standard; DNA; 15 BP.
 XX
 XX AAV31906;
 XX
 XX 21-AUG-1998 (first entry)
 XX
 XX Peptide nucleic acid probe 49.
 DE
 XX Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;
 KW ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.
 KW
 XX Synthetic.
 OS
 OS Mycobacterium sp.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1.15
 FT /*tag= a
 FT /note= "This sequence contains a polyamide backbone
 FT instead of a deoxyribose backbone"
 FT
 XX W09815648-A1.
 PN
 XX 16-APR-1998.
 PD
 XX
 XX 03-OCT-1997; 97WO-DK00425.
 PF
 XX 05-MAY-1997; 97DX-0000512.
 PR
 XX 04-OCT-1996; 96DK-0001096.
 PR
 XX 18-OCT-1996; 96DK-0001156.
 PR
 XX (DAKO-) DAKO AS.
 PA
 XX
 XX Lund K, Mollerup TA, Stender H;
 PI
 XX WPI; 1998-240831/21.
 DR
 XX
 PT Peptide nucleic acid probes for detection of ribosomal nucleic acid
 PT of mycobacteria - allow differentiation between species of
 PT tuberculosis complex and others and can penetrate cell membranes
 PT without pretreatment
 PT
 XX Claim 22; Page 66; 106pp; English.
 PS
 XX This is the nucleotide sequence of the peptide nucleic acid (PNA)
 CC probe used in the method of the invention, to detect ribosomal
 CC nucleic acid of mycobacteria. The probes are used, in situ or in
 CC vitro, for detection of the Mycobacterium tuberculosis complex (MTC),
 CC specifically M. tuberculosis, and especially in sputum samples, but
 CC also in other body fluids, biopsy specimens, foods, soil, air and water.
 CC Particularly, they are used to diagnose, stage or monitor infection,
 CC or for identification of drug-resistant strains (which generally have
 CC mutations in rRNA).
 XX
 SQ Sequence 15 BP; 5 A; 2 C; 5 G; 3 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 6.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 540 CTTCTCGACTCTCTA 554
 DB 15 CATCTCGACTCTCTA 1

```

RESULT 1107
AAT86603
ID AAT86603 standard; DNA; 15 BP.
XX
AC AAT86603;
XX
DT 04-JUN-1998 (first entry)
XX
DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX
OS Synthetic.
XX
PN WO9745721-A1.
XX
PD 04-DEC-1997.
XX
PF 23-MAY-1997; 97WO-EP02647.
XX
PR 24-MAY-1996; 96CH-0001320.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Muscate A, Natt F, Paulus A;
XX
DR WPI; 1998-041763/04.
XX
PT Separation of electrically charged target molecules - by capillary
PT affinity gel electrophoresis using polymer-gel to which receptors
PT for target molecules are bound
XX
PS Example D2; Page 25; 41pp; English.
XX
CC A mixture of oligonucleotides (AAT86601-3) were separated by a new
CC process using capillary affinity gel electrophoresis. The invention
CC relates to selective separation of electrically charged target molecules
CC in an analytical mixture. It comprises capillary affinity gel
CC electrophoresis using a capillary tube which is at least partly filled
CC with a polymer gel. Receptors for target molecules are covalently bound
CC to the polymer. An electric field of at least 50 volts/cm is applied.
CC The capillary tube is charged with the analytical mixture. In a first
CC separation stage, the target molecules in the mixture are bound to the
CC receptors and the remaining components are eluted, optionally whilst
CC optionally in stages, so that the affinity of the target molecules for
CC the receptor is eliminated and the target molecules are eluted and
CC detected, optionally whilst splitting open. The process is useful for
CC selective separation and/or determination of charged organic compounds,
CC such as oligonucleotides, peptides or carbohydrates. It may be used,
CC e.g. for isolation of specific proteins and DNA molecules, purification
CC of antibodies, analysis of antisense compounds or screening for enzyme
CC inhibitors. The process achieves higher resolution and selectivity
CC than prior art processes, especially in the case of complex biological
CC analytical mixtures. It has high sensitivity, even with small amounts of
CC samples. The derivatised polymers may be synthesised specifically using
CC standard methods.
XX
SQ Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 other;

Query Match      1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15

RESULT 1108
AAT864409/c
ID AAT864409 standard; RNA; 15 BP.
XX
AC AAT864409;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8885.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.

```

XX OS Hepatitis C virus.
 XX PN WO9955847-A2.
 XX PD 04-NOV-1999.
 XX PF 26-APR-1999; 99WO-US09027.
 XX PR 27-APR-1998; 98US-0083217.
 XX PR 18-SEP-1998; 98US-0100842.
 XX PR 25-FEB-1999; 99US-0257608.
 XX PR 23-MAR-1999; 99US-0274553.
 XX XX (RIBO-) RIBOZYME PHARM INC.
 XX PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
 XX XX WPI; 2000-062023/05.
 XX DR Novel ribozymes for the treatment of diseases and conditions related to
 XX PT hepatitis C infection -
 XX XX Claim 1; Page 91; 123pp; English.
 XX PS The present sequence represents the preferred target sequence of an
 XX CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 XX CC the Hepatitis C virus (HCV) RNA sequence at the base position given
 XX CC in the descriptor line.
 XX CC The HCV sequence was screened for optimal ribozyme target sites using
 XX CC a computer folding algorithm and regions of the mRNA which did not form
 XX CC secondary folding structures and contained potential ribozyme cleavage
 XX CC sites were identified. Ribozymes were synthesised to target these sites
 XX CC and their activities optimised by either varying the length of the
 XX CC binding arms or by modification to prevent degradation by nucleases.
 XX CC The ribozymes of the invention inhibit gene expression and/or viral
 XX CC replication, and are used to treat diseases associated with Hepatitis C
 XX CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
 XX CC carcinoma. The ribozymes may be used in combination with interferon to
 XX CC treat HCV infection, other infectious diseases, autoimmune diseases, and
 XX CC cancer.
 XX CC Sequence 15 BP; 2 A; 7 C; 0 G; 6 U; 0 other;
 XX
 XX Query Match 1.2%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 6.6e+02;
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 772 TGGAGAGAGAGTG 786
 XX Db |||||
 XX 15 TGGAGAGAGAGTGAG 1
 XX
 XX RESULT 1110
 XX AAF80919/c
 XX ID AAF80919 standard; DNA; 15 BP.
 XX XX AC AAF80919;
 XX XX DT 02-MAY-2001 (first entry)
 XX XX DE PTGS2 allele specific oligonucleotide probe SEQ ID 25.
 XX KW Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
 XX KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
 XX KW inflammation; probe; ss.
 XX XX Homo sapiens.
 XX OS WO200107662-A1.
 XX PN 01-FEB-2001.
 XX XX

PF 24-JUL-2000; 2000WO-US20114.
 XX 22-JUL-1999; 99US-0145170.
 XX PR (GENA-) GENAISSANCE PHARM INC.
 XX PA Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
 XX PI WPI; 2001-182805/18.
 XX DR New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
 XX XX for gene therapy of inflammation and for establishing a genotype or
 XX PT haplotype -
 XX PS Disclosure; Page 21; 118pp; English.
 XX XX This invention relates to a polynucleotide sequence that is a polymorphic
 XX CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
 XX CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
 XX CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
 XX CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
 XX CC protein is represented by AAF80898. The invention includes PCR and
 XX CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
 XX CC are used to isolate and characterise the PTGS2 gene sequence, and to
 XX CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
 XX CC sequences are used to express variant PTGS2 proteins, for structural
 XX CC analysis or drug-binding studies and also in gene therapy (either
 XX CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
 XX CC useful for diagnosis, prognosis and therapy and analysis of the new, and
 XX CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
 XX CC especially for determining association between a particular trait, e.g. a
 XX CC clinical response to drugs that target PTGS2 but also disease
 XX CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
 XX CC used for developing diagnostic tests and treatments for immune-related
 XX CC disorders such as arthritis and inflammation. The polymorphisms may also
 XX CC be used to study expression and biological function of PTGS2. Transgenic
 XX CC animals that express PTGS2 are used to study expression of PTGS2
 XX CC isogenes, for in vivo drug screening and testing, and for assessing
 XX CC effects of therapeutic agents.
 XX CC Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 other;
 XX
 XX Query Match 1.2%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 6.6e+02;
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1084 AAAAAAAAAAAAAA 1098
 XX Db |||||
 XX 15 AAAAAAAAAAAAAA 1
 XX
 XX RESULT 1111
 XX AAF46503
 XX ID AAF46503 standard; DNA; 15 BP.
 XX XX AC AAF46503;
 XX XX DT 30-MAR-2001 (first entry)
 XX XX DE IGFBP2 oligonucleotide #1342.
 XX XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
 XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 XX KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
 XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 XX KW hyperneovascular condition; hyperplasia; kidney disease;
 XX KW neovascular condition of the retina; ss.
 XX XX Homo sapiens.
 XX OS WO200078341-A1.
 XX XX

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XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU00693.
XX XX
XX PR 21-JUN-1999; 99US-0140345.
XX XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX XX
XX DR WPI; 2001-041421/05.
XX PT
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by
XX PT administering UV (ultra-violet) treatment (optional) and an antiseise
XX PT nucleic acid that inhibits or reduces growth factor mediated cell
XX PT proliferation and/or inflammation -
XX PS
XX PS Example 6; Page 42; 201pp; English.
XX CC
XX CC The present invention relates to a method for ameliorating the effects
XX CC of skin disorders. The method comprises contacting the skin with an
XX CC antiseise oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antiseise
XX CC oligonucleotides of the present invention (see AAF45151 and
XX CC AAF45153-F45161). The method is useful for ameliorating the effects of
XX CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
XX CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX CC skin, a hyperneovascular condition such as a neovascular condition of the
XX CC retina, brain or skin, growth factor-mediated malignancies, other
XX CC sclerotic disease, kidney disease, hyperproliferation of the inside of
XX CC blood vessels or any other hyperplasia.
XX SQ Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 725 GGAGCTCGGTACAG 739
DB 1 GGAGCTCGGTACAG 15
RESULT 1112
AAF49042/C
ID AAF49042 standard; DNA; 15 BP.
AC AAF49042;
XX XX
XX DT 30-MAR-2001 (first entry)
XX DE
XX DE IGF-I oligonucleotide #2.
XX KW
XX KW Antiseise therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS
XX OS Homo sapiens.
XX PF
XX PF WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU00693.

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XX PR 21-JUN-1999; 99US-0140345.
XX XX
XX XX (MURD-) MURDOCH CHILDRENS RES INST.
XX PI
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX XX
XX DR WPI; 2001-041421/05.
XX XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by
XX PT administering UV (ultra-violet) treatment (optional) and an antiseise
XX PT nucleic acid that inhibits or reduces growth factor mediated cell
XX PT proliferation and/or inflammation -
XX PS
XX PS Example 8; Page 60; 201pp; English.
XX CC
XX CC The present invention relates to a method for ameliorating the effects
XX CC of skin disorders. The method comprises contacting the skin with an
XX CC antiseise oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antiseise
XX CC oligonucleotides of the present invention (see AAF45151 and
XX CC AAF45153-F45161). The method is useful for ameliorating the effects of
XX CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
XX CC skin, a hyperneovascular condition such as a neovascular condition of the
XX CC retina, brain or skin, growth factor-mediated malignancies, other
XX CC sclerotic disease, kidney disease, hyperproliferation of the inside of
XX CC blood vessels or any other hyperplasia.
XX SQ Sequence 15 BP; 1 A; 0 C; 1 G; 13 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAAA 1096
DB 15 TCAAAAAAATAAAAAA 1
RESULT 1113
ABX01462/C
ID ABX01462 standard; RNA; 15 BP.
XX AC ABX01462;
XX XX
XX DT 23-DEC-2002 (first entry)
XX XX
XX DE Hepatitis C virus substrate #1244 for HCV hammerhead ribozyme #1244.
XX KW
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX KW type I interferon; interferon alpha; interferon beta; cytostatic;
XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX OS
XX OS Hepatitis C virus.
XX PN
XX PN US2002082225-A1.
XX PD
XX PD 27-JUN-2002.
XX PF
XX PF 23-MAR-1999; 99US-0274553.
XX PR
XX PR 23-MAR-1999; 99US-0274553.
XX XX
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.

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PA (PAVC/) PAVCO P A.
 XX (MACE/) MACEJACK D.
 FI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;
 XX WPI; 2002-617759/66.
 DR
 XX
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit
 PT viral replication and are useful to treat hepatitis C virus infections
 PT and cirrhosis, liver failure or hepatocellular carcinoma -
 XX
 PS Claim 1; Page 56; 80pp; English.
 XX
 CC The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or
 CC hairpin (HP) motif where the binding arms comprise sequences
 CC complementary to one of the substrate sequences defined in the
 CC specification. The HCV ribozymes are useful for modulating the
 CC expression and/or replication of HCV. They can be used to treat
 CC cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV
 CC ribozymes are also useful for treating a condition associated with
 CC HCV infection in conjunction with one or more other drug therapies,
 CC particularly type I interferon, especially interferon alpha, beta or
 CC gamma or consensus interferon. The present sequence represents a
 CC substrate for a HCV hammerhead (HH) ribozyme.
 CC Note: Some of the sequence data for this patent did not form part of
 CC the printed specification. The complete sequence data for this patent
 CC was obtained in electronic format directly from the USPTO web site
 CC at seqdata.uspto.gov/paipedIDentry.html.
 XX
 SQ Sequence 15 BP; 2 A; 7 C; 0 G; 6 U; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 6.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 772 TGGAGAGAGAGTGTG 786
 DB 15 TGGAGAGAGAGTGTG 1
 RESULT 1114
 ABK98166/c
 ID ABK98166 standard; DNA; 15 BP.
 XX
 AC ABK98166;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Triple helix forming associated oligonucleotide #36.
 XX
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 OS Synthetic.
 XX
 XX US6403302-B1.
 XX
 PD 11-JUN-2002.
 XX
 PF 16-DEC-1993; 93US-0168920.
 XX
 PR 17-SEP-1992; 92US-0946976.
 XX
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX
 PI Dervan PB, Beal PA;
 XX
 DR WPI; 2002-536030/57.
 XX

PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 XX control gene expression -
 PS Example 6; Fig 20A; 108pp; English.
 XX
 CC The present invention relates to methods and oligonucleotides for
 CC forming a triple-helix comprising a double helical nucleic acid
 CC comprising first and second substantially complementary strands, and
 CC an oligonucleotide bound to a purine-rich target sequence within the
 CC double helical nucleic acid, where the oligonucleotide binds in a
 CC parallel and antiparallel orientation, respectively, to target
 CC sequences on alternate strands of the double helical nucleic acid.
 CC The method has therapeutic applications, where gene expression is
 CC controlled by selective triple-helix formation within expression
 CC regulatory sequences of a target gene. The oligonucleotides can be
 CC used to form triple-helices, and are useful to detect the presence or
 CC absence of specific sequences within genomic DNA for diagnostic and
 CC therapeutic purposes. The oligonucleotides can be selected to
 CC specifically bind to pathogenic double-stranded DNA including specific
 CC sequences required by pathogenic bacteria or viruses for replication or
 CC virulence, reducing their pathogenicity. Alternatively, the
 CC oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or
 CC viral origin. Such therapeutic oligonucleotides are capable of forming
 CC triple-helices with such sequences in cancerous cells containing the
 CC activated oncogene, so preferentially killing or repressing the cancer
 CC causing cell. The present sequence represents an oligonucleotide
 CC used in the methods of the present invention.
 XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 6.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 1115
 ABK98185/c
 ID ABK98185 standard; DNA; 15 BP.
 XX
 AC ABK98185;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Triple helix forming associated oligonucleotide #49.
 XX
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 OS Synthetic.
 XX
 XX US6403302-B1.
 XX
 PD 11-JUN-2002.
 XX
 PF 16-DEC-1993; 93US-0168920.
 XX
 PR 17-SEP-1992; 92US-0946976.
 XX
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX
 PI Dervan PB, Beal PA;
 XX

DR WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an

PT oligonucleotide which binds in parallel and antiparallel orientation,

PT respectively, for targeting sequences on alternate strands of DHNA to

PT control gene expression -

XX

PS Example 7; Fig 24A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for

CC forming a triple-helix comprising a double helical nucleic acid

CC comprising first and second substantially complementary strands, and

CC an oligonucleotide bound to a purine-rich target sequence within the

CC double helical nucleic acid, where the oligonucleotide binds in a

CC parallel and antiparallel orientation, respectively, to target

CC sequences on alternate strands of the double helical nucleic acid.

CC The method has therapeutic applications, where gene expression is

CC controlled by selective triple-helix formation within expression

CC regulatory sequences of a target gene. The oligonucleotides can be

CC used to form triple-helices, and are useful to detect the presence or

CC absence of specific sequences within genomic DNA for diagnostic and

CC therapeutic purposes. The oligonucleotides can be selected to

CC specifically bind to pathogenic double-stranded DNA including specific

CC sequences required by pathogenic bacteria or viruses for replication or

CC virulence, reducing their pathogenicity. Alternatively, the

CC oligonucleotide can be chosen to target a unique sequence of the

CC pathogen which is not found in the genome of pathogen's host. The

CC oligonucleotides can be used in cancer treatment by way of triple-helix

CC suppression of specific oncogenes including those of endogenous or

CC viral origin. Such therapeutic oligonucleotides are capable of forming

CC triple-helices with such sequences in cancerous cells containing the

CC activated oncogene, so preferentially killing or repressing the cancer

CC causing cell. The present sequence represents an oligonucleotide

CC used in the methods of the present invention.

XX

SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 6.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 15 AAAAAAAAAAAAAA 1

RESULT 1116

ABA97405/c

ID ABA97405 standard; DNA; 15 BP.

XX ABA97405;

AC

XX 18-JUN-2002 (first entry)

DT

DE Nucleotide sequence of oligomer # 12 used to compare mismatches.

DE

XX Protein nucleic acid molecule; PNA; ds.

KW

XX Synthetic.

OS

XX WO200168673-A1.

PN

XX 20-SEP-2001.

PD

XX 13-MAR-2001; 2001WO-US08111.

PF

XX 14-MAR-2000; 2000US-189190P.

PR

XX 30-NOV-2000; 2000US-250334P.

XX

XX (ACTI-) ACTIVE MOTIF.

PA

XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;

PI Chakhmakheau O, Buryakova A, Choob M, Hondorp K;

XX WPI; 2002-041177/05.

XX Oligonucleotides analogues useful in detection, separation and

PT purification of nucleic acid molecules, comprise monomers, dimers and

PT oligomers -

XX

PS Example 20; Page 123; 197pp; English.

XX This invention relates to oligonucleotide analogues comprising a protein

CC nucleic acid molecule (PNA) monomer. They are used in the detection and

CC separation of nucleic acid molecules and as probes, primers, linkers,

CC adapters and antisense agents on solid supports. Modifications enhance

CC their use as capture and detection probes e.g. by the incorporation of

CC biotin, digoxigenin, radioisotopes, fluorescent labels such as

CC fluorescein and reporter molecules such as alkaline phosphatase.

CC They are also used for enhancing or inhibiting the activity of an enzyme

CC or cellular activity. The compounds are stable to nucleases and

CC proteases, have high affinity, binding specificity and solubility. The

CC polyamide backbone of PNAs is resistant to both nucleases and proteases.

CC PNAs bind nucleic acid molecules with greater affinity than DNA or RNA

CC concentration. The compounds are relatively simple to synthesize and

CC are used in a wide variety of applications. This sequence

CC represents a DNA oligomer which is used to represent the effect of

XX single base mismatches on oligonucleotides.

SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 6.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 15 AAAAAAAAAAAAAA 1

RESULT 1117

ABX79839/c

ID ABX79839 standard; cDNA; 15 BP.

XX

AC ABX79839;

XX

DT 17-APR-2003 (first entry)

XX

DE EST polymorphic DNA repeat polymucleotide #164.

XX

KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;

KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;

KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

KW Haw River syndrome; Huntington's disease; fragile-X syndrome;

KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;

KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX

OS Homo sapiens.

XX

PN US6472154-B1.

XX

XX 29-OCT-2002.

PD

XX 31-DEC-1999; 99US-0475947.

PF

XX 31-DEC-1999; 99US-0475947.

PR

XX (TEXA) UNIV TEXAS SYSTEM.

PA

XX Garner HR, Wren JD, Minna JD, Fondon JW;

PI

XX WPI; 2003-208818/20.

DR

XX

PT Identifying a candidate polymorphic repeat within a coding sequence,

PT for understanding or treating genetic disease, comprises detecting

PT tandem repeats in a target coding sequence and scoring the repeats for


```

PT polymorphic probability -
XX
PS Examples; Column 779; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs.
XX
SQ Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 1118
AAQ21896/c
ID AAQ21896 standard; DNA; 16 BP.
XX
AC AAQ21896;
XX
DT 11-JUN-1992 (first entry)
XX
DE TEG-terminated exonuclease stable oligonucleotide #10.
XX
KW tetraethylene glycol; cancer; antisense; gene expression; inhibition;
KW diol; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "see comments"
FT modified_base 15 /*tag= b
FT /*mod_base= OTHER
FT /*note= "see comments"
XX
PN WO9202534-A.
XX
PD 20-FEB-1992.
XX
PF 02-AUG-1991; 91WO-US05531.
XX
PR 09-APR-1991; 91US-0682784.
PR 03-AUG-1990; 90US-0562180.
PR 13-SEP-1990; 90US-0582287.
PR 13-SEP-1990; 90US-0582457.
PR 13-SEP-1990; 90US-0582456.
XX
PA (STER ) STERLING DRUG INC.
XX
PI Weis AL, Hausheer FH, Chaturvedula PVC, Delecki DJ, Cavanaugh PF;
PI Moskwa PS, Oakes FT;
XX

```

```

DR WPI; 1992-080016/10.
XX
PT New oligo nucleoside(s) and nucleotide(s) with up to 200 bases - are
PT nuclease resistant anti sense cpds. useful for treating
PT hereditary disorders of altered genetic expression mechanisms
XX
PS Example 42; Page 70; 90pp; English.
XX
CC Two TEG molecules joined via a phosphate group are attached to the
CC 5' terminus. The cytidine residue at position 15 is attached to the
CC 3' adenosine residue by two TEG molecules which are joined via a
CC phosphate group. The diol-contg. linking group forms phosphodiester
CC bonds with C and A. The resulting oligonucleotide is resistant to
CC exonuclease degradation.
CC See also AAQ21884-Q21895 and AAQ21897-Q21918.
XX
SQ Sequence 16 BP; 3 A; 3 C; 8 G; 2 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 406 TGCTCAGCAGGCTC 420
DB 16 TGCTCAGCAGGCTC 2

RESULT 1119
AAT44591/c
ID AAT44591 standard; DNA; 16 BP.
XX
AC AAT44591;
XX
DT 03-JUL-1997 (first entry)
XX
DE Cryptosporidium parvum 18S rRNA gene primer/probe.
XX
KW Cryptosporidium parvum; 18S rRNA; ribosomal RNA; detection;
KW diagnosis; polymerase chain reaction; hybridisation probe; ss.
XX
OS Synthetic.
XX
PN WO9634978-A1.
XX
PD 07-NOV-1996.
XX
PF 06-MAY-1996; 96WO-AU00274.
XX
PR 05-MAY-1995; 95AU-0002831.
XX
PA (MACQ-) MACQUARIE RES LTD.
XX
PI (SYDN-) SYDNEY WATER CORP LTD.
XX
PI Ashbolt NJ, Dorsch M, Veal D, Vesey G, Williams KL;
XX
PD WPI; 1996-506178/50.
XX
PT Oligonucleotide for detection of viable Cryptosporidium parvum cells
PT - hybridises with unique sequences in 18S rRNA, useful as probe or
PT primer for PCR amplification
XX
PS Claim 4; Page 15; 22pp; English.
XX
CC The present sequence is for detecting viable Cryptosporidium parvum
CC cells by hybridising specifically to unique 18S rRNA sequences of
CC C. parvum. It can be used when labelled as a probe or as a primer for
CC PCR amplification of 18S rRNA. It can detect live C. parvum oocysts, or
CC other cells, particularly in water but also in other environmental or
CC clinical samples such as animal or human body fluids or excretions.
CC It does not detect dead cells, because RNA degrades too quickly in such
CC cells, or cells of other Cryptosporidium species that are not pathogenic
CC to humans.
XX

```

SQ Sequence 16 BP; 2 A; 0 C; 1 G; 13 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA 1094
 DB 15 TACTAAAAA 1
 RESULT 1120
 ABL57076
 ID ABL57076 standard; DNA; 16 BP.
 AC ABL57076;
 XX
 XX 22-JUL-2002 (first entry)
 DT
 DE Molecular beacon target sequence (single mismatch).
 XX Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;
 KW ss.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT misc_feature 9 /*tag= a
 FT /*note= "mismatch site"
 XX
 FN WO200218951-A2.
 PD 07-MAR-2002.
 PF 29-AUG-2001; 2001WO-US41941.
 PR 29-AUG-2000; 2000US-228728P.
 PR 30-MAR-2001; 2001US-280350P.
 XX (UVRQ) UNIV ROCKEFELLER.
 PA
 XX Dubertret B, Calame M, Libchaber A;
 PI
 XX WPI; 2002-401727/43.
 DR
 XX Sensitive detecting proximity changes in a system that utilizes an
 PT interacting fluorophore and quencher, for high sensitivity
 PT applications, involves utilizing a metal surface as quencher -
 XX
 PS Example 3; Page 30; 62pp; English.
 CC The present sequence is that of a single mismatch target sequence
 CC for a molecular beacon comprising an oligonucleotide probe (see
 CC ABL57069) covalently attached at the 3' end to fluorescent dye and
 CC at the 5' end to a nanoparticle. In the native state, the probe
 CC forms a hairpin conformation with hybridised termini. The
 CC proximity of the fluorophore and quencher (gold nanoparticle) in
 CC the molecular beacon results in little or no detectable
 CC fluorescence. Upon hybridisation of the central complementary
 CC stretch of the probe to a target sequence, such as the present
 CC sequence, the hairpin undergoes a conformational change resulting
 CC in an increase in fluorescence, the extent of which is proportional
 CC to the amount of target sequence present. Experiments with the
 CC present sequence and a perfectly-matched target (see ABL57071)
 CC showed that hybridisation was very specific to the matched target.
 CC The invention relates generally to the use of metal surface
 CC quenchers such as particles or films for high sensitivity
 CC applications in, for example, detection and diagnostic systems.
 XX
 SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 U; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 16;

Best Local Similarity 93.3%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAA 1098
 DB 2 AAAAAA 16
 RESULT 1121
 AAX5857
 ID AAX5857 standard; DNA; 17 BP.
 XX
 AC AAX5857;
 XX
 XX 09-JUL-1999 (first entry)
 DT
 DE Nael private proximity PCR primer #378 from WO9918240 Example 8.
 XX Labelling; tag; molecular species; identification; property;
 KW characteristic; hybridisation; amplification; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO9918240-A2.
 FN
 XX 15-APR-1999.
 PD
 PF 05-OCT-1998; 98WO-US20874.
 XX
 PR 06-OCT-1997; 97US-0944410.
 XX
 PA (STRA-) STRATAGENE.
 XX
 XX Sorge JA;
 PI
 XX WPI; 1999-264040/22.
 DR
 XX Uniquely tagged molecules identifiable by a unique property or
 PT characteristic
 PT
 XX Example 8; Page 104; 138pp; English.
 PS
 XX The present invention describes a composition comprising a mixture of
 CC different species of molecules where each species is linked to a tag
 CC that is unique to that species and that encodes at least two variable
 CC positions on that species, where the tags can be identified without the
 CC need for first isolating each of the tags prior to identification. Liquid
 CC phase hybridisation system may be used for simultaneous identification
 CC of a large subset of targets out of a very large collection of similar
 CC molecules that identify any collection of molecular species, e.g.
 CC peptides, antibodies, nucleic acids. Method bar codes collections or
 CC probes or analytes for use in a liquid phase hybridisation method. Tagged
 CC probes able to detect small changes or mutations in the target specimen.
 CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
 CC the concentration of the probe would not be limited by the solid support,
 CC both the target nucleic acids and the probes can diffuse toward each
 CC other, and signal amplification through cycling reactions could occur.
 CC Sequencing DNA with tags in combination with DNA amplification techniques
 CC means that there is no need for traditional sequencing methods or
 CC attaching to a solid phase, either the materials to be analysed or the
 CC tags. The present sequence represents a PCR primer which is used in an
 CC example from the present invention.
 XX
 SQ Sequence 17 BP; 1 A; 2 C; 12 G; 2 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 40 CGTCGAGGCGGT 54
 DB 1 GGTGCGAGGCGGT 15

```

XX 19-OCT-2000.
XX
XX
XX 11-APR-2000; 2000WO-US09721.
XX
XX 12-APR-1999; 99US-0129390.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX Claim 37; Page 90; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX
XX Sequence 17 BP; 3 A; 0 C; 2 G; 12 T; 0 other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 7.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1081 ATTAAAAA 1095
Db 16 ATTCAAAAA 2

RESULT 1124
AAC73225/C
ID AAC73225 standard; DNA; 17 BP.
XX
XX AAC73225;
XX AC
XX
XX 02-FEB-2001 (first entry)
XX
XX Forward primer #39 used in multiplexing PCR/SBE assay.
XX
XX Oligonucleotide array; genotyping; single base extension reaction; SBE;
XX PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
XX Unidentified.
XX
XX WO200058516-A2.
XX
XX 05-OCT-2000.
XX
XX 27-MAR-2000; 2000WO-US08069.
XX
XX 26-MAR-1999; 99US-0126473.
XX
XX 23-JUN-1999; 99US-0140359.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (AFY-) AFFYMETRIX INC.
XX
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
XX Ryder T, Sklar P;
XX
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
XX along with locus-specific tagged oligonucleotides useful in genotyping
XX

```

```

XX 19-OCT-2000.
XX
XX
XX 11-APR-2000; 2000WO-US09721.
XX
XX 12-APR-1999; 99US-0129390.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX Claim 37; Page 90; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX
XX Sequence 17 BP; 4 A; 0 C; 1 G; 12 T; 0 other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 7.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1081 ATTAAAAA 1095
Db 17 ATTCAAAAA 3

RESULT 1123
AAF03225/C
ID AAF03225 standard; DNA; 17 BP.
XX
XX AAF03225;
XX AC
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #1520.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US09721.
XX
XX 12-APR-1999; 99US-0129390.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX
XX Claim 37; Page 90; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRF-2 and/or the CAAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX
XX Sequence 17 BP; 4 A; 0 C; 1 G; 12 T; 0 other;
XX
XX Query Match 1.2%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 7.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1081 ATTAAAAA 1095
Db 17 ATTCAAAAA 3

RESULT 1123
AAF03225/C
ID AAF03225 standard; DNA; 17 BP.
XX
XX AAF03225;
XX AC
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #1520.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX

```

PT using single base extension reactions -
 XX Example 7; Page 51; 83pp; English.

XX The present invention relates to an oligonucleotide array comprising
 CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
 CC array is useful for genotyping a nucleic acid sample at one or more loci
 CC via single base extension (SBE) reactions. A pair of primers is used to
 CC amplify a polymorphic locus in a sample e.g. a single nucleotide
 CC polymorphism (SNP). The present sequence is one of the primers used in
 CC the method of the present invention to amplify a polymorphic sample. The
 CC amplified nucleic acid product is then used as a template in a SBE
 CC reaction with an extension primer. The SBE reaction products are used to
 CC form the oligonucleotide array.

XX Sequence 17 BP; 1 A; 9 C; 2 G; 5 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 39 AGGTCAGAGGCGG 53

DB 16 AGGTCAGAGGCGG 2

RESULT 1125

AAA36293
 ID AAA36293 standard; DNA; 17 BP.

XX AAA36293;

DT 26-JUL-2000 (first entry)

DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:359.

XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.

XX Homo sapiens.

XX WO200018960-A2.

XX 06-APR-2000.

XX 24-SEP-1999; 99WO-US22283.

XX 25-SEP-1998; 98US-0101757.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Landers JE, Jordan B, Housman DE, Charest A;

XX WPI; 2000-293181/25.

XX Detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs -

XX Disclosure; Page 63; 111pp; English.

XX A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a
 CC SNP allele. The method can be used to characterise a tumour, to generate
 CC a genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be
 CC used to perform linkage analysis. AAA35944 to AAA35947 represent

CC sequences used in the exemplification of the present invention. AAA35948
 CC to AAA36632 represent nucleotide sequences containing SNPs.

XX Sequence 17 BP; 5 A; 3 C; 3 G; 6 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 743 AGCCTTGCTCTTAA 757

DB 1 AGCCTTGCTCTTAA 15

RESULT 1126

ABA80864/C

ID ABA80864 standard; DNA; 17 BP.

XX ABA80864;

DT 24-JAN-2002 (first entry)

XX LDLR mutation correcting oligonucleotide SEQ ID NO: 3710.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 KW antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US09761.

XX 27-MAR-2000; 2000US-192176P.

XX 01-JUN-2000; 2000US-208538P.

XX 30-OCT-2000; 2000US-244989P.

XX (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -

XX Claim 7; Page 246; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin, 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolemia, thalassaemia, sickle cell anaemia,

CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX
 SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 291 CTTGTAGTCGGGCC 305
 Db 17 CTTGCAGTCGGGCC 3

RESULT 1127
 ABA80865
 ID ABA80865 standard; DNA; 17 BP.
 XX
 AC ABA80865;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3711.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 KW antilipemic; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192179P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec EB, Gamper HB, Rice MC;
 PI
 XX WPI; 2001-639230/73.
 DR
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 PS Claim 7; Page 246; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,

CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX
 SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 291 CTTGTAGTCGGGCC 305
 Db 1 CTTGCAGTCGGGCC 15

RESULT 1128
 ABA80868/c
 ID ABA80868 standard; DNA; 17 BP.
 XX
 AC ABA80868;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3714.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 KW antilipemic; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192179P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec EB, Gamper HB, Rice MC;
 PI
 XX WPI; 2001-639230/73.
 DR
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 PS Claim 7; Page 246; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX
 SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 291 CTTGTAGTCGGGCC 305
 DB 16 CTTGCAGTCGGGCC 2

RESULT 1129
 ABA80869
 ID ABA80869 standard; DNA; 17 BP.
 XX
 AC ABA80869;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3715.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192179P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec EB, Gamper HB, Rice MC;
 PI
 XX WPI; 2001-639230/73.
 DR
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 XX Claim 7; Page 246; 294pp; English.

The present invention provides single-stranded oligonucleotides which can
 be used for the targeted alteration of genomic sequences, where the
 oligonucleotide has at least one mismatch compared with the genomic
 sequence to be altered. In particular, these sequences are directed at
 the following genes: adenosine deaminase, p53, beta-globin,
 retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and

CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX
 SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 291 CTTGTAGTCGGGCC 305
 DB 2 CTTGCAGTCGGGCC 16

RESULT 1130
 ABA80872/c
 ID ABA80872 standard; DNA; 17 BP.
 XX
 AC ABA80872;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3718.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192179P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec EB, Gamper HB, Rice MC;
 PI
 XX WPI; 2001-639230/73.
 DR
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 XX Claim 7; Page 246; 294pp; English.

The present invention provides single-stranded oligonucleotides which can
 be used for the targeted alteration of genomic sequences, where the
 oligonucleotide has at least one mismatch compared with the genomic
 sequence to be altered. In particular, these sequences are directed at
 the following genes: adenosine deaminase, p53, beta-globin,
 retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 291 CTTGTAGTCGGGGCC 305
 ||||| ||||| ||||| |||||
 Db 17 CTTGCAGTCGGGGCC 3

RESULT 1131
 ABA80873
 ID ABA80873 standard; DNA; 17 BP.
 AC ABA80873;
 XX
 XX
 DT 24-JAN-2002 (first entry)
 XX
 XX
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3719.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antislacking; antianaemic; haemostatic;
 KW antileptic; ss.

XX Homo sapiens.
 OS
 XX
 XX
 PN WO200173002-A2.
 XX
 XX
 PD 04-OCT-2001.
 XX
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 XX
 PR 27-MAR-2000; 2000US-192176P.
 XX
 PR 27-MAR-2000; 2000US-192179P.
 XX
 PR 01-JUN-2000; 2000US-208538P.
 XX
 PR 30-OCT-2000; 2000US-244989P.
 XX
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX
 XX Kmtec EB, Gamper HB, Rice MC;
 PI
 XX
 XX WPI; 2001-639230/73.
 DR
 XX
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 PT
 XX
 XX
 PS Claim 7; Page 246; 294pp; English.
 XX
 XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 291 CTTGTAGTCGGGGCC 305
 ||||| ||||| ||||| |||||
 Db 1 CTTGCAGTCGGGGCC 15

RESULT 1132
 AAH80145
 ID AAH80145 standard; cDNA; 17 BP.
 XX
 AC AAH80145;
 XX
 XX
 DT 19-SEP-2001 (first entry)
 XX
 XX
 DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 109.
 XX
 KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN US6251588-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 10-FEB-1998; 98US-0021701.
 XX
 PR 10-FEB-1998; 98US-0021701.
 XX
 XX (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 XX
 XX WPI; 2001-424456/45.
 DR
 XX
 PT Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters -
 XX
 XX Example 1; Column 49; 342pp; English.

XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridise to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable
 CC to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.

SQ Sequence 17 BP; 0 A; 2 C; 7 G; 8 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 TGTCTGCTTTGGGG 147

Db 3 TGTCTGTTTGGGG 17
 RESULT 1133
 AAH80146
 ID AAH80146 standard; cDNA; 17 BP.
 XX AC AAH80146;
 XX DT 19-SEP-2001 (first entry)
 XX DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 110.
 XX KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW KW disease diagnosis; ss.
 XX OS Oryctolagus cuniculus.
 XX PN US6251588-B1.
 XX PD 26-JUN-2001.
 XX PF 10-FEB-1998; 98US-0021701.
 XX PR 10-FEB-1998; 98US-0021701.
 XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
 XX PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 XX DR WPI; 2001-424456/45.
 XX PT Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters -
 XX PS Example 1; Column 49; 342pp; English.
 CC The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridise to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable
 CC to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.
 XX SQ Sequence 17 BP; 1 A; 2 C; 7 G; 7 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 133 TGTCTGTTTGGGG 147
 DB 2 TGTCTGTTTGGGG 16
 RESULT 1134
 ABX01296/c
 ID ABX01296 standard; RNA; 17 BP.
 XX AC ABX01296;
 XX DT 12-MAR-2002 (first entry)
 XX DE Human NIGO Inozyme #566.
 XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme;
 DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 inflammatory arthropathy; central nervous system injury;
 cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 Parkinson's disease; ataxia; Huntington's disease;
 Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200159103-A2.
 XX PD 16-AUG-2001.
 XX PF 09-FEB-2001; 2001WO-US04273.
 XX PR 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, McSwiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 constructs, which down regulate expression of a CD20 gene or neurite
 growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 and central nervous system injury -
 XX Claim 88; Page 87; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NIGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NIN
 CC motif) or an amberyne (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NIGO-targeting
 CC nucleic acid is used to cleave RNA of the NIGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NIGO activity of the cell and
 CC treat a patient having a condition associated with the level of NIGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NIGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NIGO expression. The
 CC present sequence is an inozyme of the invention.

SQ Sequence 17 BP; 4 A; 4 C; 3 G; 6 U; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 792 AAATGCGAGTGA 806
Db 16 AAATGCGAGTGA 2
RESULT 1135
ID ABK01700/c
XX ABK01700 standard; RNA; 17 BP.
AC ABK01700;
XX
DT 12-MAR-2002 (first entry)
DE Human NOGO Zinzyne #22.
XX
XX Human; as; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberyne; zinzyne; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04273.
XX
XX 11-FEB-2000; 2000US-181797P.
PR 28-FEB-2000; 2000US-185516P.
PR 06-MAR-2000; 2000US-187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, McSwiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
DR
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
PT and central nervous system injury -
XX
PS Claim 88; Page 94; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO).
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
CC motif) or an amberyne (cleaving RNA with an NGN triplet), a zinzyne
CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce

CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targeting
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting
CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NOGO activity of the cell and
CC treat a patient having a condition associated with the level of NOGO. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NOGO-targeting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The
CC present sequence is a zinzyne molecule of the invention.
XX
SQ Sequence 17 BP; 4 A; 3 C; 3 G; 7 U; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 792 AAATGCGAGTGA 806
Db 15 AAATGCGAGTGA 1
RESULT 1136
ABN07676
ID ABN07676 standard; DNA; 17 BP.
XX
AC ABN07676;
XX
DT 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7669.
DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
XX 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMLP-1 -
 PT
 XX Disclosure; SEQ ID 7668; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
 CC hGDMLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 7 A; 1 C; 7 G; 2 T; 0 other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 768 GAACGTGGAGAGAG 782
 DB 3 GAGCTGGAGAGAG 17
 |||||
 RESULT 1137
 ABN07677
 ID ABN07677 standard; DNA; 17 BP.
 AC ABN07677;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7669.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 XX WO200192524-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 25-MAY-2001; 2001WO-US16981.
 PF
 XX 26-MAY-2000; 2000US-207456P.
 PR
 XX 21-SEP-2000; 2000US-234687P.
 PR
 XX 27-SEP-2000; 2000US-236359P.
 PR
 XX 04-OCT-2000; 2000GB-0024263.

PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX
 PA (ABOM-) ABOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMLP-1 -
 PT
 XX Disclosure; SEQ ID 7669; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
 CC hGDMLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 768 GAACGTGGAGAGAG 782
 DB 2 GAGCTGGAGAGAG 16
 |||||
 RESULT 1138
 ABN07678
 ID ABN07678 standard; DNA; 17 BP.
 XX
 XX ABN07678;
 AC
 XX 29-MAY-2002 (first entry)
 DT
 XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7670.
 DE
 XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 05-FEB-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.
XX PA (AEOM-) ABOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX
XX Disclosure; SEQ ID 7670; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterize
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 768 GAACGTGGAGAGAG 782
DB 1 GAGCTGGAGAGAG 15

RESULT 1139
ABN08388/c
ID ABN08388 standard; DNA; 17 BP.
XX AC ABN08388;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8380.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 05-FEB-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.
XX PA (AEOM-) ABOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX
XX Disclosure; SEQ ID 8380; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterize
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.

CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 405 CTGCTCCAGCAGGCT 419
Db 16 CTGCTCCAGCTGGCT 2
RESULT 1140
ABN08660/c
ID ABN08660 standard; DNA; 17 BP.
XX
AC ABN08660;
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8652.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) ABOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
XX proteins, or as specific biomolecule capture probes for
XX surface-enhanced laser desorption/ionization, comprises human
XX myosin-like protein hGDMPLP-1 -
PS Disclosure; SEQ ID 8652; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise

CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 32 TTCTCCAGCTGCGAG 46
Db 17 TTCTCCAGCTGCGAG 3
RESULT 1141
ABN08661/c
ID ABN08661 standard; DNA; 17 BP.
XX
AC ABN08661;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8653.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) ABOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
XX proteins, or as specific biomolecule capture probes for
XX surface-enhanced laser desorption/ionization, comprises human

PT myosin-like protein hGDMLP-1 -

PS Disclosure; SEQ ID 8653; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.

XX Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 7.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 TTCCTCCAGTGCAG 46

DB 16 TTCCTCCAGTGCAG 2

RESULT 1142

ABK18426/c

ID ABK18426 standard; RNA; 17 BP.

XX AC ABK18426;

DT 09-APR-2002 (first entry)

DE Human ERG hammerhead ribozyme target sequence, Seq ID No 1073.

XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
KW amberzyme.

OS Homo sapiens.

FN WO200188124-A2.

XX PD 22-NOV-2001.

PF 16-MAY-2001; 2001WO-US15866.

PR 16-MAY-2000; 2000US-0572021.

XX (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;

XX WPI; 2002-082995/11.

XX Novel polynucleotide which down regulates expression of Ets-related
PT gene, useful for treating cancer, diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome

PS Claim 4; Page 78; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration, verruca
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention.

XX Sequence 17 BP; 7 A; 5 C; 2 G; 3 U; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 7.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 881 TGAGGTCTGCATGT 895

DB 17 TGAGGTCTGCATGT 3

RESULT 1143

ABK19426

ID ABK19426 standard; RNA; 17 BP.

XX AC ABK19426;

DT 09-APR-2002 (first entry)

DE Human ERG Amberzyme target sequence Seq ID No 2073.

XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
KW amberzyme.

OS Homo sapiens.

FN WO200188124-A2.

XX PD 22-NOV-2001.

PF 16-MAY-2001; 2001WO-US15866.
 XX
 XX
 PR 16-MAY-2000; 2000US-0572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 PA
 XX
 XX
 PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082995/11.
 XX
 XX Novel polynucleotide which down regulates expression of Ets-related
 XX gene, useful for treating cancer, diabetic retinopathy, macular
 XX degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 XX syndrome
 XX
 XX Claim 4; Page 128; 149pp; English.
 PS
 PS The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 XX Sequence 17 BP; 7 A; 0 C; 8 G; 2 U; 0 other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.4e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1006 TGGAGAAATGGGAAGT 1020
 :|||||
 Db 1 UCGAGAAAGGGAGU 15
 RESULT 1144
 ABK19435/c
 ID ABK19435 standard; RNA; 17 BP.
 XX
 XX ABK19435;
 AC
 AC
 XX 09-APR-2002 (first entry)
 DT
 XX Human ERG Amberzyme target sequence Seq ID No 2082.
 DE
 XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 XX ophthalmological; antarthritic; antiposrotatic; virucide; osteopathic;
 XX vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 XX tumour angiogenesis; diabetic retinopathy; macular degeneration;
 XX neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 XX angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
 XX Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 XX Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
 XX

amberzyme.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200188124-A2.
 XX
 XX 22-NOV-2001.
 PD
 XX
 XX 16-MAY-2001; 2001WO-US15866.
 PF
 XX
 XX 16-MAY-2000; 2000US-0572021.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 PA
 XX
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 XX
 XX Novel polynucleotide which down regulates expression of Ets-related
 XX gene, useful for treating cancer, diabetic retinopathy, macular
 XX degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 XX syndrome
 XX
 XX Claim 4; Page 129; 149pp; English.
 PS
 PS The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 XX Sequence 17 BP; 6 A; 5 C; 2 G; 4 U; 0 other;
 SQ
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 881 TGAGTCTTCGATGT 895
 :|||||
 Db 16 TGAGTCTTCGATGT 2
 RESULT 1145
 ABK19436/c
 ID ABK19436 standard; RNA; 17 BP.
 XX
 XX ABK19436;
 AC
 AC
 XX 09-APR-2002 (first entry)
 DT
 XX Human ERG Amberzyme target sequence Seq ID No 2083.
 DE
 XX

Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulvular; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme; amberzyme.

Homo sapiens.

WO2001188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US15866.

16-MAY-2000; 2000US-0572021.

(RIBO-) RIBOZYME PHARM INC.
(GLAX) GLAXO GROUP LTD.

Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM; WPI; 2002-082995/11.

Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome -

Claim 4; Page 129; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg²⁺. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention.

Sequence 17 BP; 5 A; 6 C; 2 G; 4 U; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 881 TGAGGTCCTGCAGT 895
Db 15 TGAGGTCCTGCAGT 1

RESULT 1146
ABK26751/c

ID XX ABK26751 standard; DNA; 17 BP.
AC XX ABK26751;
DT XX 09-APR-2002 (first entry)
DE XX Reduced palmitate production genome altering oligonucleotide #47.
XX XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; DNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX Gossypium hirsutum.
OS Synthetic.
XX WO2001192512-A2.
PN XX
XX 06-DEC-2001.
PD XX
XX 01-JUN-2001; 2001WO-US17672.
PF XX
XX 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX XX
XX (UYDE) UNIV DELAWARE.
PA XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
PI WPI; 2002-106307/14.
XX XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX Claim 7; Page 170; 220pp; English.
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an RNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 17 BP; 7 A; 4 C; 3 G; 3 T; 0 other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 938 TTGTTTATGAGTCA 952
| | | | | | | | | |
DB 16 TTGTTTACGAGTCA 2

RESULT 1147

ABK26752
ID ABK26752 standard; DNA; 17 BP.

AC ABK26752;

DT 09-APR-2002 (first entry)

DE Reduced palmitate production genome altering oligonucleotide #48.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
XX o-methyl modification; DNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine herbicide resistance;
KW porphyrin herbicide resistance; triazine herbicide resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW increased stearate production; reduced palmitate production; albino plant;
KW photosynthetic process.

XX Gossypium hirsutum.

OS Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US17672.

XX 01-JUN-2000; 2000US-208538P.

XX 30-OCT-2000; 2000US-244989P.

XX 27-MAR-2001; 2001US-0818875.

XX (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful

XX for creating plants with desired phenotypes, e.g. stress tolerance,

XX improved nutritional value, herbicide or disease resistance, or

XX modified oil production -

XX Claim 7; Page 170; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a

XX genetic sequence, which comprises a single-stranded oligonucleotide

XX having a DNA domain. The DNA domain has at least one mismatch with

XX respect to the genetic sequence to be altered and further comprises

XX chemical modifications of the oligonucleotide. The chemical modifications

XX consist of o-methyl modification, an RNA modification, two or more

XX phosphorothioate linkages on a terminus, or a combination of any two or

XX more of these modifications. The oligonucleotides are useful for

XX directing repair or alteration of plant genetic information. The

XX oligonucleotides are particularly useful for creating plants with desired

XX phenotypes, e.g. environmental or abiotic stress tolerance, improved

XX nutritional value (e.g. altering amino acid content of plants or

XX conferring amino acid over production), herbicide resistance (e.g.

XX glyphosate resistance, imidazolinone and sulphonylurea herbicide

XX resistance, porphyrin herbicide resistance or triazine resistance),

XX disease resistance, modified oil production, modified starch production

XX

XX

XX

XX

XX

XX

XX

XX

XX

CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.

SQ Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 other;

Query Match

Best Local Similarity 1.2%; Score 13.4; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 938 TTGTTTATGAGTCA 952

DB 2 TTGTTTACGAGTCA 16

RESULT 1148

ABT34751/c

ID ABT34751 standard; DNA; 17 BP.

AC ABT34751;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 388.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;

XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizophrenia; protein chip; gene therapy; tumour suppression;

XX human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB04208.

XX 17-SEP-2001; 2001FR-0011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases

XX associated with tumors and cell degeneration, also related

XX polypeptides, antibodies and transfected cells -

XX Disclosure; Page 79; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX given in the specification, a sequence containing at least 15

XX consecutive nucleotides from the 17 mer sequence, a sequence with, after

XX optimal alignment, at least 80 % identity to the 17 mer sequence, a

XX sequence that hybridizes to them under highly stringent conditions, or

XX the complement of any of them, or the corresponding RNA. The novel

XX isolated nucleic acids of the invention are useful as probes and primers

XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,

XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,

XX and for production of recombinant polypeptides. Any of the nucleic acids,

XX polypeptides, vectors containing the nucleic acids, cells containing the

XX vector or antibodies directed against the polypeptides are useful for

XX preparation of pharmaceuticals for prevention and/or treatment of viral

XX diseases that are characterised by development of tumours or cell

XX degeneration, specifically cancer but also Alzheimer's disease and

XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

XX patient samples is useful for diagnosis and/or prognosis of these

XX diseases. The polypeptides can also be used to generate antibodies, and

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CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 900 ACGTATTATTAAAGTGA 914
 DB 17 ACGTATTATTAAAGTGA 3
 RESULT 1149
 ABT38926/C
 ID ABT38926 standard; DNA; 17 BP.
 XX
 AC ABT38926;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 4563.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB04208.
 XX
 PR 17-SEP-2001; 2001FR-0011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PS New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 XX
 PS Disclosure; Page 567; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene

CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 557 CCAACAGCAGGAGATC 571
 DB 15 CCAACAGAGGGATC 1
 RESULT 1150
 ABZ65372/C
 ID ABZ65372 standard; RNA; 17 BP.
 XX
 AC ABZ65372;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human HER2 DNazyme substrate #829.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US16840.
 XX
 PR 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PS Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 XX
 PS Claim 4; Page 149; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531.
 CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 CC sequences for the human ribozymes of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 9 C; 4 G; 1 U; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 142 TGGGGGCTGCAGCTC 156
 |||||

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Db      15 TGGGGCTGCAGGTC 1
RESULT 1151
AAQ38707/C
ID      AAQ38707 standard; RNA; 18 BP.
XX
XX
XX      AC      AAQ38707;
XX
XX      25-MAR-2003 (updated)
XX      15-JUL-1993 (first entry)
XX
XX      First chimeric primer for adding poly A tails.
XX
XX      oligonucleotide binding; nucleotide binding; DNA detection;
KW      binding DNA; treatment; diagnosis; testing; assay; Candida;
KW      papillomavirus; cytomegalovirus; Epstein-Barr virus; rhinovirus;
KW      hepatitis virus; liver disease; human immunodeficiency virus;
KW      herpes simplex virus; HSV; human immunodeficiency virus; HIV; AIDS;
KW      influenza virus; genetic disease; genetic abnormalities.
XX
XX      Synthetic.
XX
XX      WO9305182-A1.
XX
XX      18-MAR-1993.
XX
XX      04-SEP-1992; 92WO-US07489.
XX
XX      05-SEP-1991; 91US-0755485.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bruice TW;
XX
XX      WPI; 1993-101001/12.
XX
XX      Determ. of oligo:nucleotide(s) with specific activity for a
XX      bio:molecule - for use in therapeutics, diagnostics and research
XX      reagents
XX
XX      Disclosure; Page 27; 61pp; English.
XX
XX      This sequence was used as a PCR primer in order to add a polyA tail
XX      to the 3' end of the highest specific activity selected
XX      oligonucleotide in order to form a first strand. The primer is
XX      comprised of a 5' known sequence and a 3' polynucleotide portion corresp.
XX      to the polynucleotide tail of the first strand.
XX      (Updated on 25-MAR-2003 to correct FN field.)
XX
XX      SQ      Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 other;
XX
XX      Query Match      1.2%; Score 13.4; DB 1; Length 18;
XX      Best Local Similarity 93.3%; Pred. No. 7.8e+02;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      PS      Disclosure; Page 27; 61pp; English.
XX
XX      This sequence was used as a PCR primer in order to add a polyA tail
XX      to the 3' end of the highest specific activity selected
XX      oligonucleotide in order to form a first strand. The primer is
XX      comprised of a 5' known sequence and a 3' polynucleotide portion corresp.
XX      to the polynucleotide tail of the first strand.
XX      (Updated on 25-MAR-2003 to correct FN field.)
XX
XX      SQ      Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 other;
XX
XX      Query Match      1.2%; Score 13.4; DB 1; Length 18;
XX      Best Local Similarity 93.3%; Pred. No. 7.8e+02;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      1084 AAAAAAAAAAAAAA 1098
XX      DB      18 AAAAAAAAAAAAAACA 4
XX
XX      RESULT 1153
XX      AAT96107/C
XX      ID      AAT96107 standard; DNA; 18 BP.
XX      AC      AAT96107;
XX      XX      31-MAR-1998 (first entry)
XX      DE      First chimeric primer.
XX      KW      Determination; oligonucleotide; specific activity; therapy;
XX      target biomolecule; randomised oligonucleotide; diagnosis;
XX
XX      research; PCR; chimeric; primer; ss.
XX
XX      Synthetic.
XX      US5686242-A.
XX      11-NOV-1997.
XX      27-OCT-1994; 94US-0330000.
XX      27-OCT-1994; 94US-0330000.
XX      05-SEP-1991; 91US-0755485.
XX      04-SEP-1992; 92WO-US07489.
XX      (ISIS-) ISIS PHARM INC.
XX      Bruice TW, Lima WF;
XX      WPI; 1997-558135/51.
XX      Determination of oligo-nucleotide with specific activity for target
XX      bio-molecule - using set of randomised oligo-nucleotide(s)
XX      Disclosure; Columns 27-28; 22pp; English.
XX      The present sequence was used in the development of a method of
XX      determining an oligonucleotide having specific activity for a
XX      target biomolecule. The method comprises assaying a set of
XX      randomised oligonucleotides for activity against a target
XX      biomolecule, separating active from inactive oligonucleotides and
XX      recovering, amplifying and determining the nucleic acid sequence of
XX      the active oligonucleotides. The oligonucleotides can be used for
XX      therapeutic, diagnostic and research purposes.
XX      SQ      Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 other;
XX
XX      Query Match      1.2%; Score 13.4; DB 1; Length 18;
XX      Best Local Similarity 93.3%; Pred. No. 7.8e+02;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      1084 AAAAAAAAAAAAAA 1098
XX      DB      18 AAAAAAAAAAAAAACA 4
XX
XX      RESULT 1153
XX      AAT48840/C
XX      ID      AAT48840 standard; cDNA; 18 BP.
XX      AC      AAT48840;
XX      XX      16-SEP-1997 (first entry)
XX      DE      Rat PLA2s primer, ZW-1.
XX      KW      Polymerase chain reaction; PCR; amplify; primer; PLA2s; mutation; APC;
XX      KW      type II non-pancreatic phospholipase A2; microsatellite; colon cancer;
XX      KW      adenomatous polyposis coli; ss.
XX      XX      Synthetic.
XX      WO9641003-A1.
XX      19-DEC-1996.
XX      06-JUN-1996; 96WO-US09009.
XX      07-JUN-1995; 95US-0484359.
XX      (UYJE-) UNIV JEFFERSON THOMAS.
XX      Buchberg AM, Chepenik KP, Siracusa LD;
XX

```

DR WPI; 1997-052369/05.
XX Identifying an individual at an elevated risk of colon cancer - by
PT detecting mutation(s) in PLA2s gene
XX
PS Example 2; Page 39; 78pp; English.
XX
CC The sequences given in AAT48840-41 are primers which were used in the
CC amplification of the rat type II non-pancreatic phospholipase A2 (PLA2s)
CC gene. Mutations within this sequence may lead to an individual having
CC an increased risk of colon cancer. The method of the invention
CC comprises: (a) isolating genetic material from a tissue or body fluid
CC sample from the individual; and (b) detecting a PLA2s gene mutation
CC which is indicative of the individual is at an elevated risk of colon
CC cancer; or (b') detecting the absence of PLA2s protein or PLA2s enzyme
CC activity in an isolated protein sample which is indicative of the
CC individual having an elevated risk of colon cancer. The method allows
CC individuals with the APC (adenomatous polyposis coli) mutation to be
CC identified. In the treatment of colon cancer, the patient is
CC administered a recombinant vector incorporated within a non-toxic
CC enteric microorganism which expresses and secretes PLA2s.
XX
SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 7.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 262 ACAGGAGCACCCTCA 276
DB 16 ACAGGAGGACCTCA 2
|||||
|||||

RESULT 1154
AAZ41080
ID AAZ41080 standard; DNA; 18 BP.
XX
AC AAZ41080;
XX
DT 26-JAN-2000 (first entry)
XX
DE Human ELK-1 phosphorothioate antisense oligonucleotide SEQ ID NO:232.
XX
XX Identification; genetic target; gene modulation; human; probe;
KW antisense oligonucleotide; phosphorothioate; PCR primer;
KW nucleotide sequence-based technology; antisense drug discovery;
KW target validation; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN WO9953101-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08268.
XX
PR 18-APR-1998; 98US-0081483.
XX
PR 28-APR-1998; 98US-0067638.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsett LM, Baker BF, McNeill J, Freier SM, Sasmor HM, Brooks DG;
PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
XX
DR WPI; 1999-620446/53.
XX
XX Identifying compounds which modulate expression of nucleic acids, used
PT to provide compounds having defined physical, chemical or bioactive
PT properties, e.g. antisense activity -
XX
PS Example 24; Page 105; 264pp; English.
XX

CC A method has been developed of defining a set of compounds that modulate
CC the expression of a target nucleic acid (tNA) sequence via binding of
CC the compounds with the tNA sequence. The method comprises generating a
CC library of virtual compounds in silico according to defined criteria,
CC and evaluating in silico the binding of the virtual compounds with the
CC tNA according to defined criteria. Also described are: (1) a method of
CC defining a set of oligonucleotides (ONs) that modulate the expression of
CC a tNA sequence via binding of the ONs with the tNA sequence comprising
CC generating a library of virtual compounds in silico according to defined
CC criteria, and evaluating in silico the binding of the virtual ONs with
CC the tNA according to defined criteria; and (2) a method of defining a
CC set of compounds that modulate the expression of a tNA sequence via
CC binding of the compounds with the tNA. The methods can be used for the
CC generation and identification of synthetic compounds having defined
CC physical, chemical or bioactive properties. Information gathered from
CC assays of such compounds is used to identify nucleic acid sequences that
CC are tractable to a variety of nucleotide sequence-based technologies,
CC e.g. antisense drug discovery and target validation. AAZ40852 to
CC AAZ41220, and AAY52701 to AAY52706, represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 18 BP; 8 A; 1 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 7.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 323 CAGAGAGCTGTGGA 337
DB 4 CAGAGAGGTTGTGGA 18
|||||
|||||

RESULT 1155
AAZ06596
ID AAZ06596 standard; DNA; 18 BP.
XX
AC AAZ06596;
XX
DT 23-NOV-1999 (first entry)
XX
DE ELK-1 expression modulator #35.
XX
XX Human ELK-1; p62TCF; Ets domain transcription factor protein; apoptosis;
KW expression inhibition; infection; inflammation; tumour formation;
KW diagnosis; phosphorothioate; antisense compound; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /tag= a
FT /note= "Internucleoside phosphorothioate linkages"
FT modified_base 1..4
FT /tag= b
FT /note= "Optionally 2-methoxyethyl (2'-MOE) nucleosides
FT except cytosine residues which are
FT 5-methylcytosine"
FT modified_base 15..18
FT /tag= c
FT /note= "Optionally 2-methoxyethyl (2'-MOE) nucleosides
FT except cytosine residues which are
FT 5-methylcytosine"
XX
PN US5948680-A.
XX
PD 07-SEP-1999.
XX
XX 17-DEC-1998; 98US-0213767.
XX
XX 17-DEC-1998; 98US-0213767.
XX
PA (ISIS-) ISIS PHARM INC.
XX

PI Baker BF, Cowser LM;
 XX WPI; 1999-517959/43.
 XX Antisense compound useful for diagnosis, treatment and prevention of
 PT disease associated with ELK-1 expression
 PT Claim 3; Column 39; 31pp; English.
 PS
 PS Sequences AA206571-206607 are antisense polynucleotides targeted to a
 CC nucleic acid molecule encoding human ELK-1 (also known as p62TCF). ELK-1
 CC is a member of the ternary complex factor subfamily of Ets-domain
 CC transcription factor proteins. The polynucleotides inhibit the
 CC expression of human ELK-1, and this sequence targets the 3' untranslated
 CC region of the ELK-1 RNA. Sequences AA206571-206607 all cause at least 30%
 CC inhibition of ELK-1 expression. The antisense sequences can be used to
 CC inhibit the expression of human ELK-1 in human cells or tissues in vitro.
 CC ELK-1 uses a bipartite recognition mechanism mediated by both protein-DNA
 CC and protein-protein interactions to regulate genes by direct and indirect
 CC DNA binding and has been shown to control various signal transduction
 CC pathways and other cell functions including apoptosis. This means that
 CC antisense compounds inhibiting expression of ELK-1 can be used to treat
 CC diseases associated with its expression in animals, particularly humans
 CC and to prevent or delay infection, inflammation or tumour formation. The
 CC compounds can also be used for diagnosis, as research reagents and in
 CC kits.
 XX
 XX Sequence 18 BP; 8 A; 1 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 323 CAGAGAGCTGTGGA 337
 Db 4 CAGAGAGCTGTGGA 18

RESULT 1156
 AA211011/c
 ID AA211011 standard; DNA; 18 BP.
 AC AA211011;
 XX
 XX 29-OCT-1999 (first entry)
 DT
 XX
 XX HLA-A allele PCR primer A3-240G.
 DE
 XX
 XX HLA-A allele; PCR primer; human leukocyte antigen-A; diagnosis;
 KW allele type determination; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 PN JP11216000-A.
 XX
 XX 10-AUG-1999.
 PD
 XX
 XX 27-OCT-1998; 98JP-0305892.
 XX
 XX 29-OCT-1997; 97JP-0297145.
 PR
 XX (SHIO) SHIONOGI & CO LTD.
 PA
 XX WPI; 1999-541119/43.
 DR
 XX Distinction of HLA-A allele type - using PCR and electrophoresis
 PT
 XX Claim 5; Page 7; 21pp; Japanese.
 PS
 XX This sequence represents a PCR primer for a human leukocyte antigen-A
 CC (HLA-A) allele, and can be used in the methods of the invention. The
 CC method are for the distinction of HLA-A allele type. In the first method

CC a set of primers corresponding to each group specific to the base
 CC sequence common to each gene in at least one specific group consisting of
 CC specific HLA-A allele group is used to carry out a PCR to amplify
 CC selectively the HLA-A allele group in each specific group as a group. In
 CC the second method the amplified product obtained by the PCR is developed
 CC by electrophoresis and the presence of an amplified DNA band of a
 CC specific size is confirmed to distinct a specific type of the HLA-A
 CC allele group in each specific group as a group. Further, in the second
 CC method, if a specific type of HLA-A allele group is distinguished the
 CC following methods are further carried out: RFLP method, PCR-RFLP method,
 CC SSOP method, PCR-SSOP method, PCR-SSP method or PCR-SSCP method. The
 CC methods can be used for the diagnosis of HLA-A type in humans.
 XX
 XX Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1005 CTGGAGAGCTGGGAG 1019
 Db 15 CTGGAGAGCTGGGAG 1

RESULT 1157
 AAA64844/c
 ID AAA64844 standard; DNA; 18 BP.
 AC AAA64844;
 XX
 XX 10-NOV-2000 (first entry)
 DT
 XX
 XX S. typhimurium 23S rRNA gene probe # 4.
 DE
 XX 23S rRNA; food; personal care product; toothpaste; cosmetic; shampoo;
 KW pharmaceutical; probe; hybridisation; PCR; ss.
 XX
 XX Salmonella typhimurium.
 OS
 XX WO200036146-A1.
 PN
 XX 22-JUN-2000.
 PD
 XX
 XX 15-DEC-1999; 99WO-GB04271.
 PF
 XX
 XX 15-DEC-1998; 98GB-0027585.
 PR
 XX (CELS-) CELSIS INT PLC.
 PA
 XX Wicks B, Percy N, Owen RHG;
 XX
 XX WPI; 2000-442395/38.
 DR
 XX

Specific detection of Salmonella in a sample e.g. food or water,
 comprising using a polynucleotide which hybridizes to a region of the
 23S rRNA gene sequence from Salmonella typhimurium -
 XX Disclosure; Page 14; 17pp; English.
 XX
 XX The present invention relates to a method for detecting and identifying
 CC Salmonella in food, personal care products e.g. toothpaste, cosmetics
 CC and shampoos, pharmaceutical products and/or water. The present sequence
 CC is a nucleic acid probe specific for S. typhimurium 23S rRNA gene. The
 CC probe may be used to identify and detect Salmonella with high
 CC specificity, using probe hybridisation and PCR.
 XX
 XX Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 660 CTCATGCAGCTGAAG 674

Db 17 CACATGGAGCTGAAG 3
 RESULT 1158
 AAZ88678/C
 ID AAZ88678 standard; DNA; 18 BP.
 XX
 AC AAZ88678;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Chimeric primer #1.
 XX
 KW Primer; detection; diagnosis; ss.
 XX
 OS Unidentified.
 XX
 PN US6022691-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 07-NOV-1997; 97US-0965908.
 XX
 PR 27-OCT-1994; 94US-0330000.
 PR 05-SEP-1991; 91US-0755485.
 PR 04-SEP-1992; 92MO-US07489.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Lima WF, Bruice TW;
 XX
 DR WPI; 2000-170669/15.
 XX
 PT Assay for a chemical or drug in a sample comprises detecting binding of
 an oligonucleotide selected from a set of randomized oligonucleotides
 PT
 PS Disclosure; Column 27-28; 20pp; English.
 XX
 CC This invention describes a novel method (I) for specifically detecting
 a chemical or drug in a sample comprises contacting the sample with an
 oligonucleotide having specific activity for a target biomolecule and
 detecting the presence or absence of binding where the presence of
 binding indicates the presence of the chemical or drug in the sample.
 CC The oligonucleotide is identified by: (a) assaying a prepared set of
 randomized oligonucleotides for activity against a target biomolecule;
 CC (b) separating active from inactive oligonucleotides; (c) recovering the
 active oligonucleotides; and (d) characterizing the recovered
 oligonucleotides by microanalytical structure determination. The method
 can be used for diagnostic or research purposes.
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db 18 AAAAAAAAAAAAAACA 4
 RESULT 1159
 AAZ89746/C
 ID AAZ89746 standard; DNA; 18 BP.
 XX
 AC AAZ89746;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Human RIP-1 antisense oligonucleotide ISIS# 23929.
 XX

KW RIP-1; RalBP; RLIP; antisense inhibitor; anti-inflammatory; cytostatic;
 anti-infective; diagnose; prevent; treatment; tumour formation; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6020198-A.
 XX
 PD 01-FEB-2000.
 XX
 PF 25-SEP-1998; 98US-0161443.
 XX
 PR 25-SEP-1998; 98US-0161443.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowser LM;
 XX
 DR WPI; 2000-146889/13.
 XX
 PT Antisense inhibition of human RIP-1 expression, useful for diagnosing,
 preventing and treating conditions such as inflammation -
 PT
 PS Claim 3; Column 27; 26pp; English.
 XX
 CC This sequence represents an antisense oligonucleotide which binds to the
 3' untranslated region of RIP-1. RIP-1 (also known as RalBP1 and RLIP) is
 a GTPase activating protein (GAP) thought to be a downstream target of
 Ral. The invention relates to antisense phosphorothioate oligonucleotides
 with anti-infective, anti-inflammatory and cytostatic activity. The
 oligonucleotides are RIP-1 antisense inhibitors and are used in the
 diagnosis, prevention and treatment of conditions associated with RIP-1
 expression. Conditions associated with RIP-1 expression include various
 infections, inflammation and tumour formation.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 1 G; 7 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1004 GCTGGAGATGGGAA 1018
 Db 17 GCTGGAGATGGGGA 3
 RESULT 1160
 ABS98373
 ID ABS98373 standard; DNA; 18 BP.
 XX
 AC ABS98373;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human multidrug resistance associated protein 3 sequencing primer #13.
 XX
 KW Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
 cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
 adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 cycloxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 glutathione-S-transferase 2; GSTP2; GSTP2; histamine-N-methyl transferase;
 HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 NADPH quinone oxidoreductase 2; NQO2; sulfortransferase thermolabile;
 STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uronidase receptor; uPA;
 multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 multidrug resistance associated protein 3; cancer; prostate;
 acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 altered drug metabolism; cardiovascular function; colorectal tumour;
 central nervous system; pulmonary; immunological; sequencing.
 XX
 OS Homo sapiens.

```
XX PN WO200257410-A2.
XX AC 25-JUL-2002.
XX PF 28-NOV-2001; 2001WO-US44838.
XX PR 28-NOV-2000; 2000US-0724389.
XX PA (DNAS-) DNA SCI LAB INC.
XX PI Guida M, Hall J;
XX PF WPI; 2002-698522/75.
XX DR
XX PT Isolated nucleic acid molecules having polymorphisms in known human
XX PT genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage
XX PT markers for locating, identifying and characterizing the genes
XX PT responsible for disorder-related traits -
XX PF Example 24; Page 151; 714pp; English.
XX CC
XX CC This invention relates to the sequence of an isolated nucleic acid
XX CC molecule comprising at least one base variation from that of a known
XX CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
XX CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
XX CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase
XX CC activating protein (FLAP), glutathione-S-transferase 12 (GST12),
XX CC histamine-N-methyl transferase (HNMT), [kallikrein 2] KLK2, nicotinamide
XX CC -N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
XX CC sulfoxyltransferase thermolabile (STW), UDP-glucuronosyl transferase 2B4
XX CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance
XX CC protein 3 (MRP3), orphan nuclear receptor (NRL12), or acetylcholine
XX CC muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or
XX CC CHMR5) sequence. The polymorphisms in the human genes cited in the
XX CC invention are useful as genetic linkage markers for locating and
XX CC characterizing the genes that are responsible for specific traits within
XX CC the genome and eventually identifying the genes responsible for a
XX CC variety of disorder-related traits as a result of their e.g.,
XX CC overexpression, constitutive expression, mutation or underexpression,
XX CC which may be used in diagnosing and/or treating the disorders. The
XX CC nucleic acid molecules comprising the polymorphic sequences contained
XX CC in CYP450A1, CYP450A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2,
XX CC NRL12, STW, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful
XX CC for screening individuals for altered drug metabolism. The polymorphic
XX CC sequences contained in CYP450A1, CYP450A2, AHR, MDR1 and/or MDR3 may
XX CC also be used to screen individuals for susceptibility to cancer.
XX CC Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered
XX CC cardiovascular function, in COX2 for altered susceptibility to
XX CC colorectal tumours, in DBI or CHMR1 for altered central nervous system
XX CC function, in FLAP and HNMT for altered pulmonary, immunological or
XX CC haematological function, in KLK2 for altered serine protease activity in
XX CC the prostate, in LTF for altered immunological or haematological
XX CC function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral
XX CC nervous system function. The present sequence represents a sequencing
XX CC primer used to sequence the polymorphic genes of the invention.
XX SQ Sequence 18 BP; 2 A; 7 C; 4 G; 5 T; 0 other;
    Query Match 1.2%; Score 13.4; DB 1; Length 18;
    Best Local Similarity 93.3%; Pred. No. 7.8e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 410 CCAGCAGGCTCTCCG 424
    |||||
Db 4 CCAGCAGGCTCTCTG 18
RESULT 1161
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 7.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 410 CCAGCAGGCTCTCCG 424
    |||||
Db 4 CCAGCAGGCTCTCTG 18
RESULT 1161
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 7.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 765 GCAGAACTGGGGAAG 779
    |||||
Db 3 GCAGAACTGGGGAAG 17
RESULT 1162
AAT51286/c
ID AAT51286 standard; DNA; 19 BP.
XX AC AAT51286;
XX PF 11-NOV-1997 (first entry)
XX DE Human AD4 gene PCR primer INT1R.
XX
```

```
ABL88833
XX ID ABL88833 standard; DNA; 18 BP.
XX AC ABL88833;
XX DT 22-MAY-2002 (first entry)
XX DE HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:55.
XX KW Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX KW reverse transcriptase; binding group; ss.
XX OS Human immunodeficiency virus type 1.
XX OS Synthetic.
XX PN EP1174518-A1.
XX PF 23-JAN-2002.
XX PR 20-JUL-2000; 2000EP-0202611.
XX PR 20-JUL-2000; 2000EP-0202611.
XX PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX PI Loukachov VV, Van Gemen B, Goudsmit J;
XX PF WPI; 2002-156696/21.
XX CC Collection of binding groups for determining or typing samples,
XX CC especially clinical samples, has groups capable to identify essentially
XX CC all members of the family of nucleic acids of relatively high
XX CC significance -
XX CC Disclosure; Page 20; 166pp; English.
XX CC The present invention describes a collection of binding groups for a
XX CC family of nucleic acids comprising members of relative high and relative
XX CC low significance, where the binding groups are selected to be capable to
XX CC identify, alone or in combination, essentially all members of the family
XX CC of nucleic acids of relatively high significance. The collection of
XX CC binding groups is useful for typing of nucleic acid in a clinical sample,
XX CC by contacting the nucleic acid with the collection and determining
XX CC whether one or more binding groups bound to the nucleic acid of the
XX CC sample. This method is useful for determining whether the sample
XX CC comprises at least a part of a member of relatively high significance of
XX CC a family of nucleic acids. The collection of binding groups is useful for
XX CC diagnosing the severity of a disease caused by a pathogen containing a
XX CC member of a family of nucleic acids. ABL88779 to ABL89321 represent
XX CC oligonucleotide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 18 BP; 7 A; 2 C; 7 G; 2 T; 0 other;
    Query Match 1.2%; Score 13.4; DB 1; Length 18;
    Best Local Similarity 93.3%; Pred. No. 7.8e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 765 GCAGAACTGGGGAAG 779
    |||||
Db 3 GCAGAACTGGGGAAG 17
RESULT 1162
AAT51286/c
ID AAT51286 standard; DNA; 19 BP.
XX AC AAT51286;
XX PF 11-NOV-1997 (first entry)
XX DE Human AD4 gene PCR primer INT1R.
XX
```

KW Autosomal dominant early-onset Alzheimer's Disease; AD4; STM2;
 KW neurodegeneration; senile dementia; human chromosome 1;
 KW Volga German kindred; VG; yeast artificial chromosome library;
 KW expressed sequence tag database; polymerase chain reaction;
 KW PCR primer; Homo sapiens; ss.
 XX
 XX Synthetic.
 OS
 PN WO9703192-A2.
 XX
 XX
 PD 30-JAN-1997.
 XX
 XX
 PF 05-JUL-1996; 96WO-US11386.
 XX
 XX 14-AUG-1995; 95US-0002328.
 PR 07-JUL-1995; 95US-0000956.
 PR 28-JUL-1995; 95US-0001675.
 PR 11-AUG-1995; 95US-0002174.
 XX
 XX (DARW-) DARWIN MOLECULAR CORP.
 PA (GEHO-) GEN HOSPITAL CORP.
 PA (VAME-) VA MEDICAL CENT.
 XX
 PI Bird TD, Galas DJ, Levy-Lahad E, Mulligan J, Schellenberg GD;
 PI Tanzi RE, Wasco W;
 XX
 XX WPI; 1997-119048/11.
 DR
 XX
 XX New Alzheimer's disease related gene, AD4 - used to develop prods.
 PT for detecting pre-disposition to or for diagnosis, prevention or
 PT treatment of Alzheimer's disease
 XX
 XX Disclosure; Fig 11; 83pp; English.
 PS
 XX
 XX A genetically isolated group of families with autosomal dominant
 CC early-onset Alzheimer's Disease (AD) has been studied and initial
 CC mapping analyses have predicted the AD4 locus (also known as STM2)
 CC resides on chromosome 1. The present sequence corresponds to a PCR
 CC primer which was used during the cloning procedure to isolate and
 CC sequence the AD4 gene. The group of families has been designated
 CC the Volga German (VG) kindreds. The entire gene has been amplified
 CC from VG individuals and unaffected individuals (from VG and
 CC unrelated lineages). Sequence analysis has shown that affected
 CC individuals have a nucleotide change at codon 141 resulting in an
 CC amino acid alteration from Asn to Ile. Portions of a mutant AD4,
 CC especially one in which Asn at position 141 has been replaced by
 CC Ile, can be used in a peptide vaccine. Detection of mutant AD4, for
 CC example using antibodies specific for the protein or using nucleic
 CC acid probes specific for the mutant gene, provides a means of
 CC diagnosing Alzheimer's disease.
 XX
 XX Sequence 19 BP; 6 A; 2 C; 10 G; 1 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 8.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 418 CTCCTCGGCTGCCCC 432
 DB 17 CTCCTCGGCTGCCCC 3
 RESULT 1163
 AAV29497
 ID AAV29497 standard; DNA; 19 BP.
 XX
 XX AAV29497;
 AC
 XX
 XX 05-AUG-1998 (first entry)
 DT
 XX Serotonin 5HT7 receptor allelic variant amplifying ASA upper primer.
 DE
 XX Allelic variant; serotonin 5HT7 receptor; alcoholic offender; 5HT7leu;

KW neuropsychiatric drug; screening; allele specific amplification; ASA;
 KW PCR primer; ss.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX US5763183-A.
 XX
 XX 09-JUN-1998.
 PD
 XX
 XX 08-NOV-1996; 96US-0745269.
 PF
 XX 09-NOV-1995; 95US-0006394.
 PR 08-NOV-1996; 96US-0745269.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 PI Goldman D, Koulu M, Linnoila M, Pesonen U, Virkkunen M;
 XX
 XX WPI; 1998-347310/30.
 DR
 XX Allelic variant of serotonin 5HT7 receptor gene - is associated with
 PT alcoholic offenders and is useful for screening neuropsychiatric
 PT drugs
 XX
 XX Example 2; Column 7; 11pp; English.
 PS
 XX This PCR primer is used for allele specific amplification (ASA) of the
 CC allelic variant of the serotonin 5HT7 receptor (5HT7leu). This is
 CC used for screening large numbers of samples for 5HT7leu variant. The
 CC invention provides a method for detecting DNA that codes for a 5HT7leu
 CC allelic variant which comprises amplifying human DNA with primers capable
 CC of amplifying a sequence encoding the third intracellular loop of the
 CC human 5HT7 gene and determining if the amplified DNA comprises a sequence
 CC in which a C-to-T alteration converts a Pro codon to a Leu codon. The
 CC 5HT7leu variant and associated DNA and assays provide important
 CC investigative tools for both behavioural research and the screening of
 CC neuropsychiatric drug candidates.
 XX
 XX Sequence 19 BP; 3 A; 6 C; 3 G; 7 T; 0 other;
 Query Match 1.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 8.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 198 AGTTTCCTGGCTTCC 212
 DB 4 AGTTTCCTGGCTTCC 18
 RESULT 1164
 AAT18607/c
 ID AAT18607 standard; DNA; 14 BP.
 XX
 XX AAT18607;
 AC
 XX
 XX 06-NOV-1996 (first entry)
 DT
 XX
 XX Degenerate 3' oligo dT DDRT-PCR primer T12VA.
 XX
 XX Differential display of mRNA; reverse transcription; DDRT-PCR;
 KW human; chondrocyte; gene specific; primer; probe; isolation;
 KW interleukin-beta; IL-1beta; diagnosis; Connective tissue disease;
 KW osteoarthritis; rheumatoid arthritis;
 KW polymerase chain reaction; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX EP705842-A2.
 PN
 XX
 XX 10-APR-1996.
 PD
 XX 02-OCT-1995; 95EP-0115510.

XX PR 06-OCT-1994; 94EP-0115751.
 XX PA (FARH) HOECHST AG.
 XX FI Bartnik E, Margerie D;
 XX DR WPI; 1996-181045/19.
 XX PT Diagnosis and treatment of IL-1 mediated connective tissue diseases
 XX PT - using osteopontin, calnexin, TSG-6 gene prod., genes encoding them
 XX PT or antibodies to them
 XX PS Example; Page 15; 31pp; English.
 XX CC The present sequence is 1 of 4 degenerate 3' oligo dT primers,
 XX CC which were used along with 25 arbitrary 5' oligodecamer primers for
 XX CC the differential display of human chondrocyte mRNA by reverse
 XX CC transcription and PCR (DDRT-PCR). Sequence analysis revealed the
 XX CC sequences of 52 cDNA clones, which were then searched against DNA
 XX CC databases for homology to known human genes. The cDNA mols. can be
 XX CC used for the prodn. of gene specific primers and probes to isolate
 XX CC genes induced by treating (esp. human) chondrocytes with
 XX CC interleukin-beta (IL-1beta), and for the diagnosis of IL-1beta
 XX CC related connective tissue diseases, in partic. osseousarthritis or
 XX CC rheumatoid arthritis.
 XX SQ Sequence 14 BP; 1 A; 0 C; 0 G; 12 T; 1 other;

Query Match 1.2%; Score 13.2; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 6.7e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
 DB 14 TTAATAAAAAAAAAA 1

RESULT 1165
 AAZ36741/c
 ID AAZ36741 standard; DNA; 14 BP.
 AC AAZ36741;

XX DT 13-MAR-2000 (first entry)
 XX DE Anchored oligo(dT) primer T13V used for modified differential display.

XX KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
 XX KW differentially expressed nucleic acid; disease state; cancer;
 XX KW autoimmune disease; infectious disease; aging; developmental disorder;
 XX KW proliferative disorder; neurological disorder; toxicity; primer;
 XX KW treatment resistance; differential expression; drug discovery;
 XX KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
 XX OS Synthetic.

XX FN WO9955913-A2.
 XX PD 04-NOV-1999.
 XX PF 27-APR-1999; 99WO-US09119.
 XX PR 27-APR-1998; 98US-0083331.
 XX PR 27-AUG-1998; 98US-0098070.
 XX PR 04-FEB-1999; 99US-0118624.

XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 XX FI McClelland M, Welsh J, Trenkle T;
 XX DR WPI; 2000-086388/07.
 XX CC

PT Measuring expression of low abundance reduced complexity target nucleic
 XX acid molecules -
 XX PS Example 3; Page 91; 187pp; English.
 XX CC AAZ36739-41 represent oligo(dT) primers used for modified differential
 XX CC display, in the method of the invention. The specification describes a
 XX CC method for measuring the level of two or more nucleic acid molecules in
 XX CC a target. The method comprises contacting a probe with an arbitrarily or
 XX CC statistically sampled target and detecting the amount of specific
 XX CC binding of the target to the probe. The methods can be used to identify
 XX CC differentially expressed nucleic acid molecules associated with disease
 XX CC states, such as cancer, autoimmune disease, infectious disease, aging,
 XX CC developmental disorder, proliferative disorder or neurological disorder.
 XX CC Alternatively the methods can be used to assess the efficacy or toxicity
 XX CC of a resistance to a treatment. Also the methods can be used to
 XX CC determine differential expression of nucleic acid molecules in response
 XX CC to a stimulus, e.g. a chemical, drug or growth factor (especially
 XX CC epidermal growth factor), radiation, stress or a pathogen. The methods
 XX CC can also be used to determine co-regulated genes that can be potential
 XX CC targets for drug discovery.

SQ Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 1 other;

Query Match 1.2%; Score 13.2; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 6.7e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAATAAAAAAAAAA 1096
 DB 14 BAAATAAAAAAAAAA 1

RESULT 1166
 AAD44142
 ID AAD44142 standard; DNA; 14 BP.
 AC AAD44142;

XX DT 13-DEC-2002 (first entry)
 XX DE Oligo-dT PCR primer #2 used to illustrate the method of the invention.

XX KW Sequential consensus region-directed amplification; gene expression;
 XX KW disease diagnosis; gene analysis; human; matrix metalloproteinase;
 XX KW PCR; primer; ss.
 XX OS Unidentified.

XX FN US6277571-B1.
 XX PD 21-AUG-2001.
 XX PF 30-SEP-1998; 98US-0163485.
 XX PR 03-OCT-1997; 97US-108152P.
 XX PA (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.

XX FI Fillmore H, Broadus W, Gillies G;
 XX DR WPI; 2002-412824/44.

XX PT Sequential consensus region-directed amplification for sorting mixture
 XX PT of DNAs into 2 or more subsets or distinguishing gene expression
 XX PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
 XX PS Example; Fig 1C; 19pp; English.

XX CC The invention relates to a method of sequential consensus region-directed
 XX CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 XX CC distinguishing gene expression patterns in 2 samples. The methods, kits
 XX CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or

XX 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)
 XX
 XX Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
 DE
 XX Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV;
 KW RSV; HPV; malignancy; hepatitis; inflammation; ss.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH modified_base 5
 FT /tag= a
 FT /mod_base= m5c
 FT modified_base 18
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 XX
 PN W09209705-A1.
 XX
 PD 11-JUN-1992.
 XX
 XX 25-NOV-1991; 91WO-US08811.
 XX
 PR 23-NOV-1990; 90US-0617907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0686544.
 PR 17-APR-1991; 91US-0686546.
 PR 17-APR-1991; 91US-0686547.
 PR 27-SEP-1991; 91US-0766733.
 XX
 XX (GILE-) GILEAD SCI INC.
 PA
 XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 PI WPI; 1992-217083/26.
 XX
 XX New oligomers contg. modified bases - which form a triplex with
 PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 PT hepatitis, herpes, malignancy and inflammation
 XX
 PS Claim 12; Page 72; 77pp; English.
 XX
 CC The synthetic oligomer is capable of forming a triplex at
 CC physiological pH with a purine rich target sequence by coupling
 CC into the major groove of the duplex. The specific target sequence
 CC of this oligomer is the human tumour necrosis factor receptor mRNA
 CC beginning at nucleotide 2354 contg. a purine rich sequence concd. on
 CC one strand of the duplex. The oligomer, and others like it are useful
 CC in diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
 CC tumours and inflammation. The triple helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions.
 CC See also A025452-25501 and A030226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PD field.)
 XX
 SQ Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 672

AAQ30448/c
 ID AAQ30448 standard; DNA; 18 BP.
 XX
 AC AAQ30448;
 XX
 DT 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)
 XX
 XX Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
 DE
 XX Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV;
 KW RSV; HPV; malignancy; hepatitis; inflammation; ss.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH modified_base 5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "N6 methyl-8-oxo-2' deoxyadenine"
 FT modified_base 18
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 XX
 PN W09209705-A1.
 XX
 PD 11-JUN-1992.
 XX
 XX 25-NOV-1991; 91WO-US08811.
 XX
 PR 23-NOV-1990; 90US-0617907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0686544.
 PR 17-APR-1991; 91US-0686546.
 PR 17-APR-1991; 91US-0686547.
 PR 27-SEP-1991; 91US-0766733.
 XX
 XX (GILE-) GILEAD SCI INC.
 PA
 XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 PI WPI; 1992-217083/26.
 XX
 XX New oligomers contg. modified bases - which form a triplex with
 PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 PT hepatitis, herpes, malignancy and inflammation
 XX
 PS Claim 12; Page 72; 77pp; English.
 XX
 CC The synthetic oligomer is capable of forming a triplex at
 CC physiological pH with a purine rich target sequence by coupling
 CC into the major groove of the duplex. The specific target sequence
 CC of this oligomer is the human tumour necrosis factor receptor mRNA
 CC beginning at nucleotide 2354 contg. a purine rich sequence concd. on
 CC one strand of the duplex. The oligomer, and others like it are useful
 CC in diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
 CC tumours and inflammation. The triple helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions.
 CC See also AAQ25452-25501 and AAQ30226-447.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PD field.)
 XX
 SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 17 AAAAAAAAAAATAAAA 1

RESULT 673
AAV54165/C
ID. AAV54165 standard; cDNA; 18 BP.

XX AAV54165;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 2.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.

XX Synthetic.

XX WO9839437-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

XX 05-MAR-1997; 97JP-0050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,
XX preventing or treating diseases associated with apoptosis

XX Example 1; Page 47; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method
XX of the invention, involving the use of novel apoptosis-related DNAs
XX and proteins. The inventions can be used as diagnostic reagents for
XX apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
XX in immunohistological staining, as apoptosis inhibitors. It can also
XX be used for treatment of apoptosis-related diseases.

XX Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1082 TTAATAAAAAAAAAAAAA 1098
Db 18 TCAAAAAAAAAAAAAAAAA 2

RESULT 674
AAV54166/C
ID. AAV54166 standard; cDNA; 18 BP.

XX AAV54166;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 3.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.

XX Synthetic.

XX WO9839437-A1.

XX

PD 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

XX 05-MAR-1997; 97JP-0050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,
XX preventing or treating diseases associated with apoptosis

XX Example 1; Page 48; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method
XX of the invention, involving the use of novel apoptosis-related DNAs
XX and proteins. The inventions can be used as diagnostic reagents for
XX apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
XX in immunohistological staining, as apoptosis inhibitors. It can also
XX be used for treatment of apoptosis-related diseases.

XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1082 TTAATAAAAAAAAAAAAA 1098
Db 18 TCAAAAAAAAAAAAAAAAA 2

RESULT 675

AAV54168/C

ID. AAV54168 standard; cDNA; 18 BP.

XX AAV54168;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 5.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.

XX Synthetic.

XX WO9839437-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

XX 05-MAR-1997; 97JP-0050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,
XX preventing or treating diseases associated with apoptosis

XX Example 1; Page 48; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method
XX of the invention, involving the use of novel apoptosis-related DNAs
XX and proteins. The inventions can be used as diagnostic reagents for
XX apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent


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PT tissue -
XX Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90640-51) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 other;
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 TTAATAAAAAAAAAAAAAA 1100
DB 18 AGTAAAAAAAAAAAAAAAAA 2
RESULT 679
AAZ90647/c
ID AAZ90647 standard; DNA; 18 BP.
XX
AC AAZ90647;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #8.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-0225228.
XX
PR 23-JUL-1998; 98JP-0225228.
XX
PA (NISH) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal
PT tissue -
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90640-51) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 other;
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAAAAAAA 1099
DB 18 TGAATAAAAAAAAAAAAAA 2
RESULT 680
AAZ90648/c
ID AAZ90648 standard; DNA; 18 BP.
XX
AC AAZ90648;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #9.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-0225228.
XX
PR 23-JUL-1998; 98JP-0225228.
XX
PA (NISH) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal
PT tissue -
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90640-51) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAAAAAAA 1098
DB 18 TGAATAAAAAAAAAAAAAA 2
RESULT 681
AAV01328/c
ID AAV01328 standard; DNA; 19 BP.
XX
AC AAV01328;
XX
DT 23-MAR-1998 (first entry)
XX
DE S-antigen PCR primer for universal mammalian STS's.
XX
KW PCR primer; polymerase chain reaction; amplification; UM-STS;
KW universal mammalian sequence tagged site; genomic map; clone; ss.
XX
OS Synthetic.
XX
PN WO9731012-A1.
XX
PD 28-AUG-1997.
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Db 18 TCATAAAAAAAAAAAAAA 2
RESULT 680
AAZ90648/c
ID AAZ90648 standard; DNA; 18 BP.
XX
AC AAZ90648;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #9.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-0225228.
XX
PR 23-JUL-1998; 98JP-0225228.
XX
PA (NISH) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal
PT tissue -
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90640-51) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAAAAAAA 1098
DB 18 TGAATAAAAAAAAAAAAAA 2
RESULT 681
AAV01328/c
ID AAV01328 standard; DNA; 19 BP.
XX
AC AAV01328;
XX
DT 23-MAR-1998 (first entry)
XX
DE S-antigen PCR primer for universal mammalian STS's.
XX
KW PCR primer; polymerase chain reaction; amplification; UM-STS;
KW universal mammalian sequence tagged site; genomic map; clone; ss.
XX
OS Synthetic.
XX
PN WO9731012-A1.
XX
PD 28-AUG-1997.
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XX 18-FEB-1997; 97WO-US02403.
XX 22-FEB-1996; 96US-0012061.
XX (UNMI ) UNIV MICHIGAN.
XX (UNMS ) UNIV MICHIGAN STATE.
XX Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
XX WPI; 1997-435083/40.
XX New oligonucleotide primers amplifying gene regions conserved among
XX mammals - useful for developing genomic maps, isolating clones and
XX making cross-species comparisons
XX Claim 2; Page 13; 26pp; English.
XX The present sequence represents a specifically claimed oligonucleotide
XX PCR primer. The oligonucleotide can be used for polymerase chain
XX reaction (PCR) amplification of DNA, specifically regions of specific
XX genes that are conserved among mammalian species, i.e. pairs of
XX oligonucleotides from the present specification represent universal
XX mammalian sequence-tagged site (UM-STS) primers. The primers are used
XX to develop genomic maps, to isolate clones from libraries, to make
XX cross-species comparisons and to develop additional genetic markers.
XX UM-STS allow genomic comparisons to be made between more species.
XX Sequence 19 BP; 1 A; 7 C; 3 G; 8 T; 0 other;
XX Query Match 1.4%; Score 15.4; DB 1; Length 19;
XX Best Local Similarity 94.1%; Pred. NO. 3.8e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 326 AGAAGCTGGGAGCAAC 342
XX 18 AGAAGCTGGGAGCAAC 2
XX Db
XX RESULT 682
XX AAV12302
XX ID AAV12302 standard; DNA; 20 BP.
XX AC AAV12302;
XX DT 17-JUN-1998 (first entry)
XX DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.
XX KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;
XX housekeeping gene; identification; modulator; metastasis; neoplastic;
XX papilloma; atherosclerosis; angiogenesis; viral infection; ss.
XX OS Homo sapiens.
XX PN WO9800532-A2.
XX PD 08-JAN-1998.
XX PF 30-JUN-1997; 97WO-CA00454.
XX PR 01-JUL-1996; 96US-0021152.
XX PS (WRIG/) WRIGHT J A.
XX PA (YOUN/) YOUNG A H.
XX PI Wright JA, Young AH;
XX WPI; 1998-086958/08.
XX New oligo-nucleotide(s) complementary to untranslated regions of
XX housekeeping genes - are useful in, e.g. identifying modulators of
XX tumour growth/metastasis and inhibiting growth of neoplastic cells
XX Claim 4; Page 29; 64pp; English.
XX The present sequence represents a 3'-untranslated region (3'UTR) fragment
XX of ribonucleotide reductase R1. The present invention describes: (1)
XX oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)
XX or their analogues of a UTR of a housekeeping gene; (2) antisense ON
XX (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous
XX to ON, and able to cleave it; (4) DNA sequence encoding ON, AON and Rb;
XX (5) an antibody (Ab) that binds to ON, AON and Rb; (6) a nt probe ntP
XX that hybridise to ON, AON and Rb. ON, AON, Rb and Ab are used to modulate
XX (especially inhibit) growth of tumour cells (especially neoplastic cells)
XX and to reduce their capacity for metastasis. The above may also be used
XX to treat benign proliferative disorders e.g. papillomas, atherosclerosis,
XX angiogenesis and viral infections, e.g. human immunodeficiency virus,
XX hepatitis or herpes. ON may further be used: (i) to identify modulators
XX of tumour growth/metastasis; (ii) to identify compounds (especially
XX potential antitumour agents) that inhibit or enhance interaction between
XX ON and its binding substances; (iii) as probes for detecting related
XX sequences, and (iv) to generate Ab, used for detection and quantification
XX of UTR especially for monitoring progress of cancer therapy. SON inhibit
XX tumorigenicity of neoplastic cells, particularly where these are
XX resistant to hydroxyurea.
XX Sequence 20 BP; 17 A; 1 C; 2 G; 0 U; 0 other;
XX Query Match 1.4%; Score 15.4; DB 1; Length 20;
XX Best Local Similarity 94.1%; Pred. NO. 4e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX 1 AAAAAAAAAAAAAAAAAA 17
XX Db
XX RESULT 683
XX AAC82912/c
XX ID AAC82912 standard; DNA; 20 BP.
XX AC AAC82912;
XX DT 21-MAR-2001 (first entry)
XX DE Human beta-actin derived oligonucleotide #5.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
XX OS Homo sapiens.
XX PN DE19923966-A1.
XX PD 30-NOV-2000.
XX PF 25-MAY-1999; 99DE-1023966.
XX PR 25-MAY-1999; 99DE-1023966.
XX PS (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PI Boekenkamp D, Hoppe H, Burgstaller P;
XX WPI; 2001-050938/07.
XX Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure -
XX Examples; Fig 1; 8pp; German.
XX This invention describes a novel recognition system comprising at least
XX 1 recognition unit bound to a support, each recognition unit comprising a

```

CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.

SQ Sequence 20 BP; 3 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1080 TATTAAAAAATAAAA 1096
 Db 17 TCTTAAAAAATAAAA 1

RESULT 684

AAD33168

ID AAD33168 standard; DNA; 20 BP.

XX AC AAD33168;

XX 01-JUL-2002 (first entry)

XX ApoE cDNA amplifying RT-PCR primer, ApE/pl.

XX Phytanic acid; non-insulin dependent diabetes mellitus; NIDDM; obesity;

XX Glucose tolerance; food supplement; feed supplement; hyperinsulinaemia;

XX hyperlipidaemia; hypertension; insulin therapy; hypercholesterolaemia;

XX hypertriglyceridaemia; primer; apolipoprotein E; RT-PCR; ApoE;

XX reverse transcription PCR; ss.

XX Unidentified.

XX EP117789-A2.

XX 06-FEB-2002.

XX 30-JUL-2001; 2001EP-0118230.

XX 04-AUG-2000; 2000EP-0116948.

XX (ROCH-) ROCHE VITAMINS AG.

XX Fluehmann B, Heim M, Hunziker W, Weber P;

XX WPI; 2002-270864/32.

XX New composition comprising phytanic acid or its derivatives, useful for

XX treating or preventing non-insulin dependent diabetes mellitus,

XX impaired glucose tolerance and related obesity -

XX Example 3; Page 8; 29pp; English.

XX The invention relates to the use of phytanic acid or its derivatives

XX for the treatment or prevention of diabetes mellitus. The invention

XX also relates to a method for treating or preventing non-insulin

XX dependent diabetes mellitus (NIDDM) or other conditions associated

XX with impaired glucose tolerance such as obesity using phytanic acid

XX or its derivatives. The phytanic acid, their derivatives or their

XX precursors are useful as pharmaceutical compounds or supplements to

XX foods or feeds for the treatment or prevention of type II or NIDDM,

XX hyperlipidaemia, hypercholesterolaemia, hyperinsulinaemia, syndrome X,

XX hypertension, hypertriglyceridaemia, impaired glucose tolerance and

XX related obesity. They are also useful in insulin therapy in combination

XX with known active compounds. The present sequence is apolipoprotein E

XX (ApoE) cDNA amplifying reverse transcription PCR (RT-PCR) primer used

XX in the exemplification of the invention.

SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 457 TCCAGGAAGAGCTCCAG 473

Db 3 TCCAGGAAGAGCTGCAG 19

RESULT 685

AAD26141

ID AAD26141 standard; DNA; 21 BP.

XX AC AAD26141;

XX 30-NOV-1999 (first entry)

XX Human polymorphic region 330.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;

XX cell viability; loss of heterozygosity; precancerous condition; OSI;

XX allele specific inhibitor; somatic cell; diagnosis; prevention;

XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;

XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;

XX graft versus host disease; malignant cell removal; bone marrow; ss.

XX Homo sapiens.

XX WO9841648-A2.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-US05419.

XX 20-MAR-1997; 97US-0041057.

XX (VARI-) VARIAGENICS INC.

XX Housman D, Ledley FD, Stanton VP;

XX WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for

XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic

XX plaque, dysplastic lesions, endometriosis or graft versus host disease

XX Disclosure; Figure 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor

XX potentially useful for treatment of cancer, where the inhibitor is

XX active on a gene vital for cell growth or viability, and where the gene

XX is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is

XX used for preventing the development of cancer in a patient having a

XX precancerous condition, by administering to the patient a first allele

XX specific inhibitor (ASI) targeted to an allele of a first essential gene

XX present in cells of the precancerous condition, where the normal somatic

XX cells of the patient are heterozygous for the first gene, the inhibitor

XX is active on at least one but less than all allelic forms of the gene

XX present in a population and targets only one allelic form present in the

XX normal somatic cells, and the first gene. The products and methods can

XX be used in the diagnosis, prevention and treatment of LOH disorders,

XX e.g. cancers, atherosclerotic plaques, premalignant metaplastic or

XX dysplastic lesions, benign tumours, endometriosis, polycystic kidney

XX disease, and graft versus host disease. The method can also be used to

XX remove malignant cells from bone marrow transplants. AAZ5812-226825

XX represent human polymorphic sites described in the method of the

XX invention.

XX Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 other;

XX Query Match 1.4%; Score 15.4; DB 1; Length 21;

Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 686

AAZ26142

ID AAZ26142 standard; DNA; 21 BP.

AC AAZ26142;

XX 30-NOV-1999 (first entry)

XX Human polymorphic region 331.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;

XX cell viability; loss of heterozygosity; precancerous condition; ASI;

XX allele specific inhibitor; somatic cell; diagnosis; prevention;

XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;

XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;

XX graft versus host disease; malignant cell removal; bone marrow; ss.

XX Homo sapiens.

XX WO9841648-A2.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-US05419.

XX 20-MAR-1997; 97US-0041057.

XX (VARI-) VARIAGENTS INC.

XX Housman D, Ledley ED, Stanton VP;

XX WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for

XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic

XX plaque, dysplastic lesions, endometriosis or graft versus host disease

XX Disclosure; Figure 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor

XX potentially useful for treatment of cancer, where the inhibitor is

XX active on a gene vital for cell growth or viability, and where the gene

XX is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is

XX used for preventing the development of cancer in a patient having a

XX precancerous condition, by administering to the patient a first allele

XX specific inhibitor (ASI) targeted to an allele of a first essential gene

XX present in cells of the precancerous condition, where the normal somatic

XX cells of the patient are heterozygous for the first gene, the inhibitor

XX is active on at least one but less than all allelic forms of the gene

XX present in a population and targets only one allelic form present in the

XX normal somatic cells, and the first gene. The products and methods can

XX be used in the diagnosis, prevention and treatment of LOH disorders,

XX e.g. cancers, atherosclerotic plaques, premalignant metaplastic or

XX dysplastic lesions, benign tumours, endometriosis, polycystic kidney

XX disease, and graft versus host disease. The method can also be used to

XX remove malignant cells from bone marrow transplants. AAZ25812-ZZ6825

XX represent human polymorphic sites described in the method of the

XX invention.

XX Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 other;

XX Query Match 1.4%; Score 15.4; DB 1; Length 21;

XX Best Local Similarity 94.1%; Pred. No. 4.2e+02;

XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 687

AAZ21594/c

ID AAZ21594 standard; DNA; 21 BP.

XX AAZ21594;

XX 02-DEC-1999 (first entry)

XX PCR primer INSPR for amplifying HIV integrase cDNA.

XX PCR primer; HIV; integrase; IN; inhibitor; DNA insertion; treatment;

XX viral replication; reverse transcriptase; protease inhibitor;

XX combination therapy; resistant strain; ss.

XX Synthetic.

XX Human immunodeficiency virus.

XX WO9948371-A1.

XX 30-SEP-1999.

XX 26-MAR-1999; 99WO-US06700.

XX 27-MAR-1998; 98US-0079764.

XX 17-JUL-1998; 98US-0093208.

XX (REGC) UNIV CALIFORNIA.

XX Robinson WE, King PJ, Reinecke MG;

XX WPI; 1999-571930/48.

XX bis-(3,4-Dihydroxycinnamoyl)tartaric acid analogues for treatment of

XX HIV infections -

XX Disclosure; Page 35; 68pp; English.

XX PCR primers AAZ21589-Z21594 are used to amplify the HIV integrase cDNA.

XX This primer corresponds to nucleotides 4016-4036 of the integrase

XX sequence. The HIV integrase (IN) cDNA was used in the generation of an

XX L-chloric acid resistant strain of HIV. The invention relates to new

XX compounds that are IN inhibitors. The inhibitors are novel compounds

XX that potentially and selectively inhibit HIV integrase. The inhibitors are

XX structural analogues of bis-(3,4-Dihydroxycinnamoyl) tartaric acid.

XX Integrase has the minimal activities needed for integration. In vitro

XX the enzyme processes the HIV DNA for insertion in to the host cell's

XX nucleus. IN also cleaves double stranded DNA and facilitates the

XX insertion of the HIV DNA in to the cleavage site. IN also covalently

XX links the HIV DNA to the cleaved ends of the host DNA. The new compounds

XX block the actions of IN, and therefore block viral replication. The

XX compounds are synergistic with reverse transcriptase and protease

XX inhibitors, acting at a different part of the HIV replication cycle. The

XX new inhibitors are used, preferably in combination therapy with reverse

XX transcriptase inhibitors and protease inhibitors in the treatment of

XX HIV.

XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 other;

XX Query Match 1.4%; Score 15.4; DB 1; Length 21;

XX Best Local Similarity 94.1%; Pred. No. 4.2e+02;

XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 471 CAGGAACCTTGGCATTC 487

DB 21 CAGGAATTTGGCATTC 5

RESULT 688

```
AAE24290/c
ID  AAF24290 standard; DNA; 21 BP.
XX
AC  AAF24290;
XX
DT  03-APR-2001 (first entry)
XX
DE  Complementary nucleic acid detection method related sequence #5.
XX
KW  Complementary nucleic acid; gene analysis; polymorphism; variation;
XX  DNA chip; primer; ss.
XX  OS  Unidentified.
XX  PN  EP1065278-A2.
XX
PD  03-JAN-2001.
XX
PF  07-JUN-2000; 2000EP-0112235.
XX
PR  07-JUN-1999; 99JP-0159339.
XX  (FUJF ) FUJI PHOTO FILM CO LTD.
XX
PI  Makino Y, Abe Y, Ogawa M, Takagi M, Takenaka S, Yamashita K;
XX  WPI; 2001-140003/15.
XX
PT  Determining complementarity of nucleotide fragment for gene analysis,
XX  by comparing flow of electric current from or to electroconductive
XX  substrate through DNA fragment, with reference obtained from its
XX  complement
XX
PS  Example 1; Page 12; 28pp; English.
XX
CC  The present invention provides a method for analysing a nucleic acid
XX  strand to determine the degree of complementarity between two sequences.
XX  This involves the measurement of an electric current along the annealed
XX  strands compared to a standard. This is useful in the analysis of genetic
XX  polymorphisms and variation between genes.
XX
SQ  Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 other;
XX
Query Match 1.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 21 AAAAAAAAAATAAAAAAAAA 5

RESULT 689
ABX99283
ID ABX99283 standard; RNA; 21 BP.
XX
AC ABX99283;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #13.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-0828034.
XX
PR 07-APR-2000; 2000US-195852P.
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XX (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a
XX 3 nucleotide-long template to which a 2 nucleotide-long primer is
XX annealed, and template and primer which do not form a stable duplex in
XX the absence of HCV NS5B
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
XX virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
XX complementary nucleic acid primer which is annealed to the 3' terminus of
XX the template, where the template is at least three nucleotides and the
XX primer is two or three nucleotides, and the template and primer do not
XX form a stable duplex in solution in the absence of the HCV NS5B protein.
XX The complex is useful for detecting HCV replicase activity and permits
XX establishment of sensitive RNA-dependent RNA polymerase assays to screen
XX and evaluate antiviral inhibitors and to improve the specificity and
XX efficacy of the inhibitors. The complex is also useful in the development
XX of a reliable system for determining kinetic and thermodynamic constants
XX of HCV NS5B-catalysed nucleotide incorporation and investigation of
XX mechanistic inhibitors for mis-incorporation or chain termination.
XX Specifically, the short RNA template and primer pairs are useful in
XX screening assays which are used for determining kinetic, thermodynamic
XX and mechanistic properties of NS5B replication and ultimately in the
XX development of inhibitors of NS5B. Newly identified inhibitors of
XX replicase activity may be used for developing anti-HCV pharmaceuticals.
XX Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
XX templates.
XX
SQ Sequence 21 BP; 16 A; 3 C; 1 G; 1 U; 0 other;
XX
Query Match 1.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAACA 17

RESULT 690
ABX79794/c
ID ABX79794 standard; cDNA; 21 BP.
XX
AC ABX79794;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #119.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX Friedrich's ataxia; myotonic dystrophy; hyperandrogenemia;
XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 23-OCT-2002.
XX
PF 31-DEC-1999; 99US-0475947.
XX
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PR 31-DEC-1999; 99US-0475947.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX
XX Identifying a candidate polymorphic repeat within a coding sequence,
XX for understanding or treating genetic disease, comprises detecting
XX tandem repeats in a target coding sequence and scoring the repeats for
XX polymorphic probability -
XX
XX Examples; Column 495; 598pp; English.
XX
XX The invention discloses a method for identifying a candidate polymorphic
XX repeat within a coding sequence (expressed sequence tag, EST), which
XX comprises detecting tandem repeats in a target coding sequence, scoring
XX the repeats for polymorphic probability and generating a dataset
XX correlating the repeats with polymorphic probability to identify a
XX candidate polymorphic repeat. The computational methods (polymorphic
XX marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX useful for identifying and detecting candidate polymorphic repeats in
XX human genes, which can be used to understand, treat or eliminate genetic
XX diseases, predispositions or adverse drug-treatment reactions. Examples
XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX the polymorphic repeats identified for a search of human ESTs.
XX
XX Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1100
DB 21 AAAAAAAAAATAAAAAA 5
RESULT 691
AAH27758/c
ID AAH27758 standard; DNA; 16 BP.
XX
XX AAH27758;
XX
XX 15-AUG-2001 (first entry)
XX
XX Primer used in human LUNX cDNA isolation.
XX
XX LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001078772-A.
XX
XX 27-MAR-2001.
XX
XX 07-SEP-1999; 99JP-0253186.
XX
XX 07-SEP-1999; 99JP-0253186.
XX
XX (SAKA ) OTSUKA PHARM CO LTD.
XX
XX WPI; 2001-313367/33.
XX
XX Polynucleotide encoding LUNX gene product useful for the detection of
XX cancer especially micrometastatic cancer -
XX
XX Example 1; Page 27; 30pp; Japanese.
XX
```

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CC This invention relates to the human LUNX protein and the polynucleotide
CC sequence encoding it. The invention includes a vector containing a LUNX
CC polynucleotide, a host cell transformed with the vector, and an antibody
CC that binds to LUNX. The gene can be used for cancer diagnosis and
CC diagnosis of micrometastatic cancer and for the production of the LUNX
CC gene product. The present sequence represents a primer used in the
CC isolation of cDNA encoding human LUNX.
XX
XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 1 other;
SQ
Query Match 1.4%; Score 15.2; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAATAAAAAAAAAA 1097
DB 16 TBAATAAAAAAAAAA 1
RESULT 692
AAF82119/c
ID AAF82119 standard; DNA; 16 BP.
XX
XX AAF82119;
XX
XX 27-JUN-2001 (first entry)
XX
XX Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
XX Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
XX diagnosis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001025389-A.
XX
XX 30-JAN-2001.
XX
XX 15-JUL-1999; 99JP-0201279.
XX
XX 15-JUL-1999; 99JP-0201279.
XX
XX (SAKA ) OTSUKA PHARM CO LTD.
XX
XX WPI; 2001-303742/32.
XX
XX TSA7005 gene, encoding a polypeptide useful for the diagnosis and
XX treatment of diseases associated with its expression -
XX
XX Example 1; Page 24; 25pp; Japanese.
XX
XX The present sequence represents a PCR primer which is used in an example
XX from the present invention for the isolation of human TSA7005 gene. The
XX human TSA7005 protein shares 32% homology with human and mouse Reg
XX proteins, and 34% homology with the rat Reg protein. TSA7005 has
XX pancreatic beta cell growth activity and hypoglycaemic activity. The
XX TSA7005 protein can be used for the diagnosis and treatment of diseases
XX associated with the gene and its expression product.
XX
XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 1 other;
SQ
Query Match 1.4%; Score 15.2; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAATAAAAAAAAAA 1097
DB 16 TBAATAAAAAAAAAA 1
RESULT 693
AAI8388/c
ID AAI8388 standard; DNA; 17 BP.
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XX AC AAX18388;
XX DT 11-MAY-1999 (first entry)
XX DE RT-PCR primer of the invention SEQ ID 29.
XX KM RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX OS Synthetic.
XX PN JP11032765-A.
XX PD 09-FEB-1999.
XX PF 18-JUL-1997; 97JP-0208312.
XX PR 18-JUL-1997; 97JP-0208312.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX DR WPI; 1999-183822/16.
XX PT Peptides having at least two new nucleotides - useful as primers in
XX RT-PCR
XX PS Example 1; Page 12; 19pp; Japanese.
XX CC This sequence represents a primer of the invention. The invention relates
XX CC to sequences of at least two nucleotides of formula:
XX CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
XX CC X = a labelled compound and/or a nucleotide with voluntary sequence;
XX CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
XX CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
XX CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
XX CC k = natural number of 3 or over indicating the repetition of gamma, in
XX CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
XX CC guanine and/or cytosine. The new nucleotides are useful as primers for
XX CC RT-PCR and determination of base sequences. The new sequences allow for
XX CC reproductivity and highly efficient analysis of gene sequences.
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;

Query Match 1.4%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 16 BAAAAAATAAAAAAAAAA 1

RESULT 694
AAS14174/C
ID AAS14174 standard; DNA; 17 BP.
XX AC AAS14174;
XX DT 18-DEC-2001 (first entry)
XX DE Modified Poly-T Primer #1 used in construction of probe sets.
XX KW WRAP-Probe; gene expression array; global amplification; RNA array; ss;
XX KW tissue microarray; drug discovery assay; reporter binding site; forensic;
XX KW diagnostic; genomic analysis; universal linker; poly-T primer.
XX OS Synthetic.
XX PN WO200166802-A1.
XX PD 13-SEP-2001.
XX PF 09-MAR-2001; 2001WO-US07508.

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XX PR 09-MAR-2000; 2000US-187982P.
XX PA (GENE-) GENETAG TECHNOLOGY INC.
XX PI Shafer DA;
XX DR WPI; 2001-596845/67.
XX PT Novel probe sets with common universal linkers at one or both ends
XX PT (WRAP probes) for gene expression arrays to provide global
XX PT amplification of probe set and to provide common equivalent signalling
XX PT regardless of length
XX PS Disclosure; Page 88; 97pp; English.
XX CC The invention relates to a probe set for gene expression arrays to
XX CC provide common equivalent signalling per probe and global amplification
XX CC of the set. The probe set has a pool of modified cDNA probes, each probe
XX CC having a central target specific segment copied from a portion of a
XX CC single mRNA transcript and a universal linker (a WRAP-Probe) located on
XX CC one or both terminal ends. The universal linker has reporter binding
XX CC sites to join common reporters to the probes and primer binding sites to
XX CC copy and amplify the probe. The probes and reporters are useful in
XX CC diagnostic or drug discovery assays for a wide range of biomedical
XX CC samples, including detection of nucleic acids and gene expression
XX CC profiles in human diagnostics, forensics and genomic analysis. The
XX CC methods are useful for amplifying and identifying any unknown DNA
XX CC fragment and also for improving sensitivity with tissue microarrays or
XX CC RNA arrays. The methods improve the quantification of gene expression and
XX CC allow highly improved detection of rare transcripts or very small
XX CC samples. This sequence represents a poly-T primer used in the
XX CC construction of probe sets.
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;

Query Match 1.4%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 16 BAAAAAATAAAAAAAAAA 1

RESULT 695
AAZ09195
ID AAZ09195 standard; DNA; 20 BP.
XX AC AAZ09195;
XX DT 19-OCT-1999 (first entry)
XX DE Oligonucleotide 7 for DNA analysis.
XX KW Primer; DNA analysis; amplification; hybridisation; ss.
XX OS Synthetic.
XX PN JP11196874-A.
XX PD 27-JUL-1999.
XX PF 14-JAN-1998; 98JP-0005399.
XX PR 14-JAN-1998; 98JP-0005399.
XX PA (HITA ) HITACHI LTD.
XX DR WPI; 1999-496652/42.
XX PT Analysis of DNA fragment - comprises addition of known common
XX PT oligonucleotide, amplification of resultant DNA fragment and

```

PT analysis and labelling of amplified DNA

XX Example 1; Page 12; 17pp; Japanese.

XX This invention describes a novel method for the analysis of a DNA
 CC fragment which comprises: (i) addition of a known common oligonucleotide
 CC sequence to at least one terminal of each DNA fragment, (ii)
 CC amplification of the resultant DNA fragment as a primer using a first
 CC common primer containing a complementary nucleotide sequence to the above
 CC mentioned known common oligonucleotide sequence, a second common primer
 CC containing a complementary nucleotide sequence to the prepared known
 CC common oligonucleotide sequence optionally having been introduced with
 CC complementary nucleotide sequence at a terminal, and a specific primer
 CC capable of hybridisation with a DNA fragment containing whole or
 CC part of the gene having known sequence, to give amplified DNA, (iii)
 CC analysis of the amplified DNA to find the information of the DNA
 CC fragment, in which the specific primer is designed to prepare fragments
 CC of the common first and second primers and to give short fragment of
 CC amplified DNA and (iv) labelling them to make their differentiation.
 CC Differentiation of informations of known and unknown genes readily
 CC provides information of unknown gene and simultaneous monitoring of
 CC signals derived from minor genes. Furthermore, labelling of DNAs
 CC according to functions of known genes can be performed. AAZ09189-Z09201
 CC represent oligonucleotide primers used to illustrate the method
 CC of the invention.

XX Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 4.4e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1080 TATTAAAAAATAAAAAA 1099

Db 1 TCTCAAAAAAATAAAAAA 20

RESULT 696

AAC58043/C

ID AAC58043 standard; DNA; 20 BP.

XX AAC58043;

XX 25-JAN-2001 (first entry)

XX Human PRO1410 forward PCR primer SEQ ID NO:65.

XX Human; tumor; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection; hybridisation;
 KW probe; PCR primer; ss.

XX Homo sapiens.

XX WO200053750-A1.

XX PD 14-SEP-2000.

XX 02-DEC-1999; 99WO-US28551.

XX 08-MAR-1999; 99WO-US05028.

XX 01-SEP-1999; 99WO-US20111.

XX 29-OCT-1999; 99US-0162506.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28634.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

XX WPI; 2000-594320/56.

XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals, and to identify inhibitors of PRO

PT polypeptide activity or expression -

XX Example 20; Page 122; 226pp; English.

XX The present invention describes an antibody that binds to a human
 CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;
 CC PRO3434; PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354;
 CC PRO4397; PRO407; PRO1555; PRO1036; PRO2038; and PRO2262. (I) has
 CC anticancer activity and can be used to diagnose tumours in mammals, by
 CC detecting complex formation when the antibody is contacted with test
 CC cells. Increased expression of genes encoding (I) can also be detected
 CC to diagnose tumours. Agents which inhibit the activity of (I),
 CC especially the antibodies, or an antisense oligonucleotide which
 CC hybridises to genes encoding (I), can be used to inhibit tumour growth,
 CC preferably by inducing cell death. Methods from the present invention
 CC can be used to identify compounds which inhibit the biological activity
 CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation
 CC probes used in examples from the present invention for human PRO
 CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

Query Match

Best Local Similarity 1.4%; Score 15.2; DB 1; Length 20;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 621 TCACACAGCGCTCAGTCCCG 640

Db 20 TAAACAGCGCTCAGTCCGT 1

RESULT 697

ABA82154

ID ABA82154 standard; DNA; 20 BP.

XX ABA82154;

XX 25-JAN-2002 (first entry)

XX Zmax1 gene region physical map preparation STS marker #113.

XX Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
 KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
 KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
 KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200177327-A1.

XX PD 18-OCT-2001.

XX 21-JUN-2000; 2000WO-US16951.

XX 05-APR-2000; 2000US-0543771.

XX 05-APR-2000; 2000US-0544398.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Carulli JP, Little RD, Recker RR, Johnson ML;

XX WPI; 2001-657171/75.

XX New high bone mass (HBM) and Zmax1 genes and proteins useful for
 PT modulating bone mass for the treatment of e.g. osteoporosis -

XX Disclosure; Page 33; 443pp; English.

XX The present invention describes the human Zmax1 gene and the high bone
 CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and

CC HBM genes have osteopathic activities. The genes can be used in gene
 CC therapy, antisense therapy and in the production of vaccines. They
 CC can be used in the diagnosis and treatment of bone disorders including
 CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous
 CC dysplasia. AB#2038 to AB#2700 and AAG68168 to AAG68193 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 617 CATCTCAACGCGCTCAGT 636
 DB 1 CATCCACACATCACTCAGT 20

RESULT 698
 AAF54523/C
 ID AAF54523 standard; DNA; 20 BP.

XX AAF54523;

XX 02-APR-2001 (first entry)

DE Primer #132 used in the identification of proteins.

KW Secreted; transmembrane; gene therapy; ss.

XX Unidentified.

OS WO200078961-A1.

XX 28-DEC-2000.

PF 18-FEB-2000; 2000WO-US04342.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 16-DEC-1999; 99WO-US30095.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

XX (GETH) GENENTECH INC.

PI Baker KP, Bolstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PV, Grimaldi CC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
 PI Watanabe CK, Williams PM, Wood W;

XX WPI; 2001-071395/08.

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT utfull as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -

PS Example 143; Page 507; 787pp; English.

XX The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 621 TCAACGAGCGCTCAGTCCG 640
 DB 20 TAAACAAGCGCTCAGTCTGTG 1

RESULT 699
 AAC82913/C
 ID AAC82913 standard; DNA; 20 BP.

XX AAC82913;

XX 21-MAR-2001 (first entry)

DE Human beta-actin derived oligonucleotide #6.

XX Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.

XX Homo sapiens.

XX DE19923966-A1.

XX 30-NOV-2000.

PF 25-MAY-1999; 99DE-1023966.

PR 25-MAY-1999; 99DE-1023966.

XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

PI Boekenkamp D, Hoppe H, Burgstaller P;

XX WPI; 2001-050938/07.

PT Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -

XX Examples; Fig 1; 8pp; German.

XX This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.

XX Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1078 ACTATTAAAAA 1097
 DB 20 ACACTTAAAAA 1

RESULT 700
 AAC82918/C
 ID AAC82918 standard; DNA; 20 BP.

XX AAC82918;

XX DT 21-MAR-2001 (first entry)
 XX DE Human S-9 derived oligonucleotide #2.
 XX KW Recognition system; screening; identification; pharmaceutical; toxin;
 XX KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 XX KW herbicide; fungicide; pesticide; beta-actin; human; ss.
 XX OS Homo sapiens.
 XX XX DE19923966-A1.
 XX PD 30-NOV-2000.
 XX PF 25-MAY-1999; 99DE-1023966.
 XX PR 25-MAY-1999; 99DE-1023966.
 XX PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
 XX PI Boekenkamp D, Hoppe H, Burgstaller P;
 XX DR WPI; 2001-050938/07.
 XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -
 XX PS Examples; Fig 1; 8pp; German.
 XX CC This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.
 XX SQ Sequence 20 BP; 3 A; 1 C; 2 G; 14 T; 0 other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1078 ACTATTAAAAA 1097
 DB 20 ACGCTTTAAAAA 1
 RESULT 701
 ABN80967/C
 ID ABN80967 standard; DNA; 20 BP.
 XX AC ABN80967;
 XX DT 15-JUL-2002 (first entry)
 XX DE Mouse caspase 7 phosphorothioate oligonucleotide SRQ ID NO:145.
 XX KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
 KW hyperproliferative disorder; cancer; bone metabolism; infection;
 KW cholesterol disorder; inflammation; tumour; phosphorothioate; ss.
 XX OS Mus musculus.
 XX XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /*tag= a

FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) wing"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) wing"
 XX PN WO200222640-A1.
 XX PD 21-MAR-2002.
 XX PF 10-SEP-2001; 2001WO-US28232.
 XX PR 11-SEP-2000; 2000US-0659860.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Zhang H, Watt AT;
 XX DR WPI; 2002-401902/43.
 XX PT Novel antisense compounds targeted to nucleic acids encoding caspase 7,
 PT for modulating gene expression and treating diseases associated with
 PT expression of caspase 7 in humans -
 XX PS Claim 3; Page 89; 138pp; English.
 XX CC The present invention describes a compound (I) 8-50 nucleobases in
 CC length targeted to a nucleic acid molecule encoding caspase 7, which
 CC specifically hybridises with and inhibits the expression of caspase 7.
 CC (I) has antiinflammatory and cytostatic activities, and can be used in
 CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
 CC useful for inhibiting the expression of caspase 7 in human cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with caspase 7 including inflammatory condition,
 CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
 CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
 CC as research reagent and kits. (I) is useful prophylactically to prevent
 CC or delay infection, inflammation or tumour formation. The present
 CC sequence represent a mouse caspase 7 inhibiting chimeric phosphorothioate
 CC oligonucleotide having 2'-MOE wings and a deoxy gap, which is used in an
 CC example from the present invention.
 XX SQ Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 other;
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 612 GTGGCCATCTCAACCCAGCGC 631
 DB 20 GTGGCCATCTCAACCCAGCGC 1
 RESULT 702
 ABK44387/C
 ID ABK44387 standard; DNA; 20 BP.
 XX AC ABK44387;
 XX DT 05-JUN-2002 (first entry)
 XX DE Human onco-gene p16, PCR primer #4.
 XX KW Nucleic acid probe; gene engineering; medicine; onco-gene;
 KW PCR; primer; ss; p16.
 XX OS Synthetic.

PN WO200202814-A1.
 XX 10-JAN-2002.
 XX 04-JUL-2001; 2001WO-JP05783.
 XX 05-JUL-2000; 2000JP-0204177.
 XX 26-APR-2001; 2001JP-0129603.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX Mineno J, Meiyyanto E, Ishida N, Takeya T, Asada K, Kato I;
 XX WPI; 2002-179635/23.
 XX Detection of nucleic acids, useful in gene engineering, biochemistry
 PT and medicine, comprising a labeled polynucleotide probe partly
 PT hybridisable with a polyadenine nucleotide moiety of a target nucleic
 PT acid,
 XX
 XX Example 1; Page 40; 51pp; Japanese.
 XX The invention describes a labeled polynucleotide probe that is partly
 CC hybridisable with a polyadenine nucleotide moiety of a target nucleic
 CC acid. The method discussed in the invention is useful for the detection
 CC of nucleic acids in gene engineering, biochemistry and medicine. This
 CC sequence represents a PCR primer used in the amplification of onco-genes
 CC and associated with the polynucleotide probes discussed in the invention.
 XX
 XX Sequence 20 BP; 4 A; 5 C; 10 G; 1 T; 0 other;
 SQ
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 372 CGTCTGCGCGTCTGCTGGC 391
 ||||| ||||| |||||
 Db 20 CGTCTGCGCGTCTGCGCCTGGC 1
 RESULT 703
 ABK22951
 ID ABK22951 standard; DNA; 20 BP.
 XX
 XX ABK22951;
 DT 09-APR-2002 (first entry)
 XX Human Zmax1 cDNA forward PCR primer #57.
 DE
 XX Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
 KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
 KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
 KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
 KW bone development disorder; antiarteriosclerotic; cardiovascular;
 KW osteopathic; cerebroprotective.
 XX
 XX Homo sapiens.
 OS
 XX WO200192891-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 25-MAY-2001; 2001WO-US16946.
 XX
 XX 26-MAY-2000; 2000US-0578900.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
 XX
 XX Carulli JP, Little RD, Recker RR, Johnson ML;
 PI
 XX WPI; 2002-097784/13.

XX Identifying molecules involved in lipid regulation, useful for
 PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
 PT identifying a molecule that binds to high bone mass gene or its
 PT corresponding wild type gene -
 XX
 XX Disclosure; Page 38; 409pp; English.
 XX
 XX The invention relates to a method for identifying a molecule involved in
 CC lipid regulation comprising identifying a molecule that binds to or
 CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
 CC gene, Zmax1. Compounds identified by the method are useful for treating,
 CC diagnosing, preventing or screening for normal and abnormal
 CC lipid-associated conditions, including arteriosclerosis, cardiovascular
 CC disease, stroke, and osteoporosis. The compounds may also be used in the
 CC treatment or prevention of diabetic atherosclerosis, neurovascular
 CC conditions caused by plaque build-up, poor circulation due to plaque
 CC build-up and associated poor wound healing. The methods may be used in
 CC gene therapy, pharmaceutical development, and diagnostic assays for bone
 CC development disorders. Molecules identified by comparison of Zmax1 and
 CC HBM systems can be used as surrogate markers in pharmaceutical
 CC development, in diagnosis of human or animal bone disease, and in the
 CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
 CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
 CC and adapters of the invention.
 XX
 XX Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 other;
 SQ
 Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 617 CATCTCAACGAGCGTCTCAGT 636
 ||||| ||||| |||||
 Db 1 CATCCCAACCATCACTCAGT 20
 RESULT 704
 ABA05915/C
 ID ABA05915 standard; DNA; 20 BP.
 XX
 XX ABA05915;
 DT 05-MAR-2002 (first entry)
 XX
 XX Hepatitis B virus diagnostic PCR primer SEQ ID NO 5.
 DE
 XX Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
 KW PCR primer; ss.
 KW
 XX Hepatitis B virus.
 OS
 XX EP1152063-A1.
 PN
 XX 07-NOV-2001.
 PD
 XX 03-MAY-2000; 2000EP-0109436.
 XX
 XX 03-MAY-2000; 2000EP-0109436.
 FR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Schroeder KH, Koike K;
 PI
 XX WPI; 2002-068256/10.
 DR
 XX Diagnosing hepatitis B virus (HBV) infection stages and determining the
 PT risk for hepatocellular carcinoma, comprises identifying full length
 PT HBV transcripts and truncated HBV transcripts in a serum sample -
 XX
 XX Example 1; Page 6; 25pp; English.
 PS
 XX The invention relates to diagnosis of hepatitis B virus (HBV) infection
 CC

CC stages comprising identification of full length HBV transcripts (I) and
 CC truncated HBV transcripts (II) in a serum sample, where the ratio of
 CC I:II is indicative of a particular infection stage. The method is useful
 CC for diagnosing HBV infection stages and determining the risk for
 CC developing hepatocellular carcinoma. The present sequence is that of a
 CC HBV diagnostic PCR primer, useful for the invention.
 XX
 SQ Sequence 20 BP; 0 A; 1 C; 3 G; 16 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1079 CTATTATAAAAAAAAAAAAAA 1098
 DB 20 CCAGCAAAAAAAAAAAAAAAAA 1

RESULT 705
 ABI97523
 ID ABI97523 standard; DNA; 20 BP.
 XX
 AC ABI97523;

DT 16-FEB-2002 (first entry)

DE Capture oligonucleotide Zip ID#4610 oligo #9.

KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

XX WO200179548-A2.

XX 25-OCT-2001.

XX 04-APR-2001; 2001WO-US10958.

XX 14-APR-2000; 2000US-197271P.

XX (CORR) CORNELL RES FOUND INC.

XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX WPI; 2002-034366/04.

XX Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch -

XX Example 5; Fig 29; 30pp; English.

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning

CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI92074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 XX

SQ Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 115 AGAAACGGGAAGGAAGGATG 134
 DB 1 AGCCACGGGAAGGAAGGATG 20

RESULT 706
 ABL45369/C
 ID ABL45369 standard; DNA; 20 BP.
 XX
 AC ABL45369;

DT 11-APR-2002 (first entry)

DE Human chromosome 21q22.1 PCR primer SEQ ID NO:2413.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
 KW genome; PCR primer; ss.

XX Homo sapiens.

XX JP2001321190-A.

XX 20-NOV-2001.

XX 12-MAR-2001; 2001JP-0068285.

XX 10-MAR-2000; 2000JP-0066716.

XX (RIKA) RIKAGAKU KENKYUSHO.

XX (GENO-) GENOTEX YG.

XX WPI; 2002-144136/19.

XX Arraying genome clones -

XX Claim 6; Page 52; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42357 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 XX specifically claimed for use in the present invention.

SQ Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 314 GAAGAAGCTGCAGAGAGCTG 333
Db 20 GCAGGAATGCAGAGAGCTG 1

RESULT 707
ACC45534
ID ACC45534 standard; DNA; 20 BP.
XX AC
XX ACAC45534;
XX DT
XX 02-JUN-2003 (first entry)
XX Human HBM STS marker forward primer #57.
XX
XX Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
XX osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
OS Homo sapiens.
PN WC200292764-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US14876.
PR 11-MAY-2001; 2001US-290071P.
PR 17-MAY-2001; 2001US-291311P.
PR 01-FEB-2002; 2002US-353058P.
PR 04-MAR-2002; 2002US-361293P.
XX
(GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
XX Babij P, Bax PJ, Yaworsky PJ, Bodine PV;
XX WPI; 2003-129278/12.
XX
XX New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density -
XX
XX Disclosure; Page 54; 603pp; English.

The invention relates to novel transgenic animals expressing the high bone mass (HBM) gene, expressing the corresponding wild type HBM gene, comprising an alteration of the gene encoding LRP5 or LRP6, or expressing an LRP5 that is modulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are for the study of bone density modulation or bone mass modulation. The polynucleotides of the invention may have a use in gene therapy. The transgenic animals and nucleic acids are for the study of bone density modulation, where the bone mass is modulated relative to non-transgenic animals of the same species in more than one parameter selected from bone density, bone strength, trabecular number, bone size, or bone tissue connectivity. The transgenic animals, nucleic acids and methods are useful for identifying molecules involved in bone development, and for developing pharmaceutical compositions, which may be employed for treating or preventing bone diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of the bone. The transgenic animals and nucleic acids are also useful in methods for diagnosing diseases involved in bone development, or characterised by reduced bone density or mass. The present sequence is used in the exemplification of the invention.

Db 1 AAAAAAAAAATTAATAAAAAAAAAA 20

RESULT 709
AAZ26499
ID AAZ26499 standard; DNA; 21 BP.
XX AC
XX AAZ26499;
XX 30-NOV-1999 (first entry)
XX Human polymorphic region 698.
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX Homo sapiens.
OS WO9841648-A2.
XX 24-SEP-1998.
XX 19-MAR-1998; 98WO-US05419.
XX 20-MAR-1997; 97US-0041057.
XX (VARI-) VARIAGENICS INC.
XX Housman D, Ledley PD, Stanton VP;
XX WPI; 1998-521232/44.
XX Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
PS Disclosure; Figure 7; 605pp; English.
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC represent human polymorphic sites described in the method of the
CC invention.
XX SQ Sequence 21 BP; 13 A; 3 C; 0 G; 5 T; 0 other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1095
DE 2 CTACTTCAAAAAA 21

RESULT 710
AAF79922/c
ID AAF79922 standard; DNA; 21 BP.
XX AC
XX AAF79922;
XX 11-JUN-2001 (first entry)
XX PCR primer used to amplify human and murine GL50 cDNA sequences.
XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine; PCR primer; ss.
XX Homo sapiens.
OS Mus musculus.
XX WO200121796-A2.
XX 29-MAR-2001.
XX 21-SEP-2000; 200WO-US25892.
XX 21-SEP-1999; 99US-0155043.
XX (GEMY) GENETICS INST INC.
XX Ling V, Dunussi-Joannopolulos K;
XX WPI; 2001-244938/25.
XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX Disclosure; Page 117; 195pp; English.
XX PCR primers AAF79922-27 were used to amplify sequences from the 3'
CC end of cDNA encoding human and murine GL50 polypeptides. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50
CC molecules can be used in vaccines. GL50 polynucleotides can be used
CC to locate gene regions associated with genetic disease, in tissue
CC typing, and in forensic identification of a biological sample.
XX SQ Sequence 21 BP; 2 A; 11 C; 5 G; 3 T; 0 other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 782 GTGTGAGCGCAACTGCGAGG 801
DB 20 GTGCGAGCGCAGACTGCGGG 1

RESULT 711
AAC91374/c
ID AAC91374 standard; DNA; 21 BP.
XX AC
XX AAC91374;
XX 16-MAR-2001 (first entry)
XX Oligo JT-296 for construction of annexin expression vector pJ117.
DE Human; annexin; chelation site; nuclear imaging; apoptosis;
KW transplant rejection; pJ117; ss.

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XX OS Homo sapiens.
XX PN WO200073332-A1.
XX PD 07-DEC-2000.
XX PF 25-MAY-2000; 2000WO-US14324.
XX PR 01-JUN-1999; 99US-0324096.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Tait JF, Brown DS;
XX DR WPI; 2001-080465/09.
XX PT Novel modified annexin useful for imaging vascular thrombi and
XX PT apoptosis, has N-terminal chelation site comprising amino acid
XX PT extension which comprises a glycine and a cysteine residue -
XX PS
XX PS Example 1; Page 12; 39pp; English.
XX CC The present sequence was used in the construction of an expression
XX CC vector encoding a modified annexin having an N-terminal
XX CC chelation site, which comprises an amino acid extension including a
XX CC glycine and a cysteine residue. The modified annexin is useful for
XX CC imaging vascular thrombi or apoptosis which is associated with response
XX CC to a chemotherapeutic agent or with rejection as a result of
XX CC transplantation. The modified annexin can effectively chelate a
XX CC radionuclide and retain annexin bioactivity. It can be readily prepared
XX CC in high radiochemical yield and with high radiochemical purity. In
XX CC contrast to conventional conjugation chemistries that provide a
XX CC distribution of conjugation products, the modified annexin has a single
XX CC chelation site remote from the site of biological activity.
XX SQ Sequence 21 BP; 5 A; 9 C; 4 G; 3 T; 0 other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 600 TGGCGGGTGCACGTGGCCAT 619
Db 21 TGGCAGGTGGCTGTGGCCAT 2
RESULT 712
ABK15655/c
ID ABK15655 standard; DNA; 21 BP.
XX AC ABK15655;
XX DT 21-MAY-2002 (first entry)
XX DE Anchored oligo-dt reverse primer.
XX KW ss; lipoxigenase; RCI-1; transgenic; plant; plant antifungal;
XX KW rice chemically induced cDNA; promoter; transit peptide; plastid;
XX KW fungal mycotoxin inhibitor; plant breeding; PCR; primer.
XX OS Synthetic.
XX PN WO200206490-A1.
XX PD 24-JAN-2002.
XX PF 12-JUL-2001; 2001WO-EF08085.
XX PR 13-JUL-2000; 2000GB-0017275.
XX PR 15-SEP-2000; 2000GB-0022739.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA (UYZU-) UNIV ZUERICH.
XX Dudler R, Schaffrath, Lawton KA;
XX WPI; 2002-188550/24.
XX PT Novel isolated nucleic acid encoding a promoter which is capable of
XX PT driving chemically inducible but not wound- or pathogen-inducible
XX PT expression of an associated nucleotide sequence -
XX PS
XX PS Example 3; Page 30; 88pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (a promoter of
XX CC rice chemically induced cDNA (RCI-1), which encodes a lipoxigenase)
XX CC capable of driving chemically-inducible but not wound- or pathogen-
XX CC inducible expression of an associated nucleotide sequence. Also
XX CC included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone
XX CC for the lipoxigenase gene, promoter fragments, the lipoxigenase transit
XX CC peptide which directs expressed proteins to the plastid, a vector
XX CC comprising the promoter or fragments and a transgenic plant comprising
XX CC the vector. The promoter or fragments are useful for expressing a
XX CC nucleotide sequence of interest. The transit peptide is useful for
XX CC targeting an associated protein of interest to plastids. A nucleic acid
XX CC which expresses polypeptide having lipoxigenase activity is useful for
XX CC inhibiting fungal mycotoxins when transformed into a plant. The
XX CC lipoxigenase is useful for inhibiting fungal mycotoxins. The promoter is
XX CC useful for regulating transcription of a chemically inducible but not
XX CC wound or pathogen inducible gene, which involves applying a chemical
XX CC regulator to a plant or seed containing a chemically regulatable
XX CC nucleotide sequence. Transgenic plants as described above are useful for
XX CC breeding improved plant lines that for example increase the effectiveness
XX CC of conventional methods such as herbicide or pesticide treatment or allow
XX CC to dispense with the methods due to their modified genetic properties.
XX CC New crops with improved stress tolerance can be obtained that, due to
XX CC their optimised genetic equipment yield harvested product of better
XX CC quality than products that were not able to tolerate comparable adverse
XX CC developmental conditions. The present sequence is an anchored oligo-dt
XX CC reverse RT-PCR primer (reverse transcriptase PCR) used to isolate the
XX CC cDNA encoding rice lipoxigenase.
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 16 T; 1 other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 4.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1083 TAAAAAATAAAAAA 1098
Db 21 BAAAAAATAAAAAA 6
RESULT 713
AAQ79184
ID AAQ79184 standard; DNA; 15 BP.
XX AC AAQ79184;
XX DT 25-MAR-2003 (updated)
XX DT 21-JUN-1995 (first entry)
XX DE Nuclease resistant oligonucleotide.
XX KW Nuclease resistant oligonucleotide; inhibition of gene expression;
XX KW 9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 14
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "9-methyl-acyclo-adenosine"
XX FT
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PR 28-SEP-1994; 94US-0314397.
PR 03-OCT-1994; 94US-0316771.
PR 07-OCT-1994; 94US-0319492.
PR 11-OCT-1994; 94US-0321993.
PR 04-NOV-1994; 94US-0334847.
PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345516.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX
FA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them
PT for use in inhibiting disease related genes
PT
PS Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for
CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and
CC thereby inhibit ICAM-1 expression, making them useful for reducing
CC transplant rejection and alleviating symptoms in patients with
CC rheumatoid arthritis, asthma and other inflammatory disorders.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
XX
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
XX
RESULT 716
AAT52138/c
ID AAT52138 standard; RNA; 15 BP.
XX
XX AAT52138;
AC
XX
DT 25-MAR-2003 (updated)
DT 25-MAR-1997 (first entry)
XX
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2911).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome;
KW AIDS; ss.
XX
OS Homo sapiens.

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XX PN W09523225-A2.
XX PD 31-AUG-1995.
XX PF 23-FEB-1995; 95WO-1B00156.
XX PR 30-JAN-1995; 95US-0380734.
XX PR 23-FEB-1994; 94US-0201109.
XX PR 29-MAR-1994; 94US-0218934.
XX PR 04-APR-1994; 94US-0222795.
XX PR 07-APR-1994; 94US-0224483.
XX PR 15-APR-1994; 94US-0227958.
XX PR 18-APR-1994; 94US-0228041.
XX PR 18-MAY-1994; 94US-0245736.
XX PR 06-JUL-1994; 94US-0271280.
XX PR 15-AUG-1994; 94US-0291932.
XX PR 16-AUG-1994; 94US-0291433.
XX PR 17-AUG-1994; 94US-0292620.
XX PR 19-AUG-1994; 94US-0293520.
XX PR 02-SEP-1994; 94US-0300000.
XX PR 08-SEP-1994; 94US-0303039.
XX PR 23-SEP-1994; 94US-0311486.
XX PR 28-SEP-1994; 94US-0311749.
XX PR 03-OCT-1994; 94US-0316771.
XX PR 07-OCT-1994; 94US-0319492.
XX PR 11-OCT-1994; 94US-0321993.
XX PR 04-NOV-1994; 94US-0334847.
XX PR 10-NOV-1994; 94US-0337608.
XX PR 28-NOV-1994; 94US-0345516.
XX PR 16-DEC-1994; 94US-0357577.
XX PR 23-DEC-1994; 94US-0363233.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them
PT for use in inhibiting disease related genes
PT
PS Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for
CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
CC mRNA at the nucleotide base position indicated in the DE line.
CC Regions of the mRNA that do not form secondary folding
CC structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and
CC thereby inhibit ICAM-1 expression, making them useful for reducing
CC transplant rejection and alleviating symptoms in patients with
CC rheumatoid arthritis, asthma and other inflammatory disorders.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
XX
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
XX

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XX PS Disclosure; Page 154; 720pp; French.
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15
XX CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
XX CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
XX CC sequence that hybridizes to them under highly stringent conditions, or
XX CC the complement of any of them, or the corresponding RNA. The novel
XX CC isolated nucleic acids of the invention are useful as probes and primers
XX CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
XX CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
XX CC and for production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention.
XX SQ Sequence 17 BP; 4 A; 8 C; 3 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 956 GCTGGGCGAGGTGG 969
DB 17 GCTGGGCGATGGG 4

RESULT 1665
ABT35974/c
ID ABT35974 standard; DNA; 17 BP.
XX AC ABT35974;
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 1611.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB04208.
XX PR 17-SEP-2001; 2001PR-0011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313353/30.
XX PT New isolated nucleic acid, useful for treating viral diseases
XX PT associated with tumors and cell degeneration, also related
XX PT polypeptides, antibodies and transfected cells -
XX PS Disclosure; Page 221; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15
XX CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
XX CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
XX CC sequence that hybridizes to them under highly stringent conditions, or
XX CC the complement of any of them, or the corresponding RNA. The novel
XX CC isolated nucleic acids of the invention are useful as probes and primers
XX CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
XX CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
XX CC and for production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention.
XX SQ Sequence 17 BP; 4 A; 8 C; 3 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 GTTTTGTGTTTATGA 948
DB 16 GTTTTGTGTTTATGA 3

RESULT 1666
ABT36096/c
ID ABT36096 standard; DNA; 17 BP.
XX AC ABT36096;
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 1733.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB04208.
XX PR 17-SEP-2001; 2001PR-0011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313353/30.
XX PT New isolated nucleic acid, useful for treating viral diseases
XX PT associated with tumors and cell degeneration, also related
XX PT polypeptides, antibodies and transfected cells -
XX PS Disclosure; Page 235; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,

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CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.

SQ Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1031 CCTGGCTTTCATAG 1044
| | | | |
Db 17 CCTGGCATTCATAG 4

RESULT 1667
ABT36562/c
ID ABT36562 standard; DNA; 17 BP.

AC ABT36562;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 2199.

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

OS Homo sapiens.

PN WC2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001PR-0011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -

PS Disclosure; Page 290; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after

CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.

SQ Sequence 17 BP; 7 A; 6 C; 3 G; 1 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 137 TCGTTTGGGGCTG 150
| | | | |
Db 17 TTCTTTGGGGCTG 4

RESULT 1668
ABT37233/c
ID ABT37233 standard; DNA; 17 BP.

AC ABT37233;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 2870.

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

OS Homo sapiens.

PN WC2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001PR-0011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -

PS Disclosure; Page 368; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or

CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 956 GCTGGCGAGGTGG 969
 |||||
 Db 17 GCTGGCGAGGTGG 4

RESULT 1669
 ABT37801
 ID ABT37801 standard; DNA; 17 BP.

AC ABT37801;

XX 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 3438.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

OS Homo sapiens.

XX WO2003025175-A2.

PN 27-MAR-2003.

PD 17-SEP-2002; 2002WO-IB04208.

PF 17-SEP-2001; 2001FR-0011978.

PR (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -

XX Disclosure; Page 435; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers

CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 1 A; 6 C; 3 G; 7 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 GATCCTCCTGCCT 581
 |||||
 Db 1 GATCCTCCTGCCT 14

RESULT 1670
 ABT39985/c
 ID ABT39985 standard; DNA; 17 BP.

AC ABT39985;

XX 13-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 5622.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

OS Homo sapiens.

XX WO2003025175-A2.

PN 27-MAR-2003.

PD 17-SEP-2002; 2002WO-IB04208.

PF 17-SEP-2001; 2001FR-0011978.

PR (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -

XX Disclosure; Page 691; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,

CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.

XX SQ Sequence 17 BP; 2 A; 10 C; 3 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 597 CGGTGGCGGTGGA 610

DB 16 CGGAGCGCGGTGGA 3

RESULT 1671

ACA06427/C

ID ACA06427 standard; RNA; 17 BP.

XX ACA06427;

XX 03-JUN-2003 (first entry)

DE NFKB sub-unit modulating inozyme substrate #246.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherap; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection;
 KW ss.

XX Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-0864785.

XX 15-AUG-1994; 94US-0291932.

PR 07-DEC-1992; 92US-0987132.

PR 18-MAY-1994; 94US-0245466.

PR 23-DEC-1996; 96US-0777916.

XX (STIN/) STINCHOMB D T.

PA (MCSW) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression
 PT of a sequence encoding a subunit of nuclear factor kappa B useful for

PT treating cancer, inflammatory disorders and autoimmune diseases -
 XX Claim 3; Page 30; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC chemotherapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel
 CC enzymatic nucleic acid molecule.

XX SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 245 GCTCTTGAAGGACT 258

DB 14 GCTCTTGAAGGCT 1

RESULT 1672

ABZ60277/C

ID ABZ60277 standard; RNA; 17 BP.

XX ABZ60277;

XX 21-MAR-2003 (first entry)

XX Human K-Ras DNazyme substrate #389.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

PR 06-JUN-2001; 2001US-296249P.

PR 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 58; Page 92; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 U; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1028 GGGCTGGCTTCA 1041
|||||
Db 17 GGGCTGGCTTCA 4
RESULT 1673
ABZ60283
ID ABZ60283 standard; RNA; 17 BP.
XX
AC ABZ60283;
XX
XX
XX 21-MAR-2003 (first entry)
XX Human K-Ras DNAzyme substrate #395.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US16840.
XX
XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 58; Page 92; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 58; Page 92; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for

CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 5 A; 2 C; 5 G; 5 U; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 1.1e+03;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1035 GCTTTCATAGTCAG 1048
|||||
Db 3 GCUUUCAGAGAGAG 16
RESULT 1674
ABZ61269/c
ID ABZ61269 standard; RNA; 17 BP.
XX
XX AC ABZ61269;
XX
XX 21-MAR-2003 (first entry)
XX Human H-Ras DNAzyme target #60.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US16840.
XX
XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 58; Page 112; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 2 A; 8 C; 5 G; 2 U; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 722 TCAGGAGCTGCGGT 735
DB 16 TCAGGAGCCGCGT 3

RESULT 1675
ABZ61967
ID ABZ61967 standard; RNA; 17 BP.
XX AC ABZ61967;
XX DT 21-MAR-2003 (first entry)
XX DE Human H-Ras DNazyme target #758.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PN WO200297114-A2.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US16840.
XX PR 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX PS Claim 58; Page 125; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and
XX CC anti-rheumatic activity. The nucleic acid molecules are useful for
XX CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX CC acids are also useful for treating breast, ovarian, colorectal, lung,
XX CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX CC The sequences shown in ABZ6524, ABZ6530 - ABZ6585 represent substrate/target
XX CC sequences for the human ribozymes of the invention.
XX SQ Sequence 17 BP; 6 A; 6 C; 4 G; 1 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGCCACAGCCAGCT 19
DB 1 AGCCACAGACAGCU 14

RESULT 1676
ABZ64762/c
ID ABZ64762 standard; RNA; 17 BP.
XX
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AC ABZ64762;
XX 21-MAR-2003 (first entry)
XX DE Human HER2 DNazyme substrate #219.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PN WO200297114-A2.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US16840.
XX PR 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX PS Claim 4; Page 137; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and
XX CC anti-rheumatic activity. The nucleic acid molecules are useful for
XX CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX CC acids are also useful for treating breast, ovarian, colorectal, lung,
XX CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
XX CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
XX CC sequences for the human ribozymes of the invention.
XX SQ Sequence 17 BP; 5 A; 6 C; 3 G; 3 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 ATGCAACTGTGGTT 90
DB 15 ATGCCACTGTGGTT 2

RESULT 1677
ABZ64765/c
ID ABZ64765 standard; RNA; 17 BP.
XX AC ABZ64765;
XX DT 21-MAR-2003 (first entry)
XX DE Human HER2 DNazyme substrate #222.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
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XX WO2002971114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US16840.
XX
XX 29-MAY-2001; 2001US-294140P.
XX
XX 06-JUN-2001; 2001US-296249P.
XX
XX 10-SEP-2001; 2001US-318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 4; Page 137; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and
XX anti-rheumatic activity. The nucleic acid molecules are useful for
XX reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX acids are also useful for treating breast, ovarian, colorectal, lung,
XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
XX sequences for the human ribozymes of the invention.
XX
XX Sequence 17 BP; 2 A; 4 C; 6 G; 5 U; 0 other;
XX
XX Query Match 1.1%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 92.9%; Pred. No. 1.1e+03;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 671 GAAGCTCACAGTG 684
XX | | | | | | | |
XX 17 GCAGCTCACAGTG 4
XX
XX RESULT 1678
XX ABZ64766/c
XX ID ABZ64766 standard; RNA; 17 BP.
XX
XX AC ABZ64766;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human HER2 DNzyme substrate #223.
XX
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2002971114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US16840.
XX
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2002971114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US16840.
XX
XX KW Human; ribozyme; short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 4; Page 138; 185pp; English.
XX
XX PS
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PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 4; Page 137; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and
XX anti-rheumatic activity. The nucleic acid molecules are useful for
XX reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX acids are also useful for treating breast, ovarian, colorectal, lung,
XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
XX sequences for the human ribozymes of the invention.
XX
XX Sequence 17 BP; 3 A; 4 C; 5 G; 5 U; 0 other;
XX
XX Query Match 1.1%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 92.9%; Pred. No. 1.1e+03;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 670 TGAAGCTCACAGAT 683
XX | | | | | | | |
XX 14 TGCAGCTCACAGAT 1
XX
XX RESULT 1679
XX ABZ64806
XX ID ABZ64806 standard; RNA; 17 BP.
XX
XX AC ABZ64806;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human HER2 DNzyme substrate #263.
XX
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2002971114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US16840.
XX
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2002971114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US16840.
XX
XX KW Human; ribozyme; short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
XX Claim 4; Page 138; 185pp; English.
XX
XX PS
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XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

XX SQ Sequence 17 BP; 0 A; 10 C; 3 G; 4 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 1.1e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 423 CGGCTGCCCTGCGC 436
||| :|||:|
Db 4 CGUCUGCCCCCGC 17

RESULT 1680
ABZ64876/c
ID ABZ64876 standard; RNA; 17 BP.
XX AC ABZ64876;
XX DT 21-MAR-2003 (first entry)
XX DE Human HER2 DNzyme substrate #333.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PA WO200297114-A2.
XX PI Mcswiggen J;
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US16840.
XX PR 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX PS Claim 4; Page 139; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

XX SQ Sequence 17 BP; 2 A; 7 C; 6 G; 2 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 GCAGGCTCTCCGCGC 426
||||| :|
Db 17 GCAGGCTCTCCGCGC 4

RESULT 1681
ABZ64877/c
ID ABZ64877 standard; RNA; 17 BP.
XX AC ABZ64877;
XX DT 21-MAR-2003 (first entry)
XX DE Human HER2 DNzyme substrate #334.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PA WO200297114-A2.
XX PI Mcswiggen J;
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US16840.
XX PR 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX PS Claim 4; Page 139; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

XX SQ Sequence 17 BP; 2 A; 7 C; 6 G; 2 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 GCAGGCTCTCCGCGC 426
||||| :|
Db 17 GCAGGCTCTCCGCGC 4

```
Db      14 GCAGGCTGTCCGGC 1
RESULT 1682
ABZ64901/c
ID      ABZ64901 standard; RNA; 17 BP.
XX
AC      ABZ64901;
XX
DT      21-MAR-2003 (first entry)
XX
DE      Human HER2 DNazyme substrate #358.
XX
KW      Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW      enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW      anti-rheumatic; cancer; AIDS; ss.
XX
OS      Homo sapiens.
XX
PN      WO200297114-A2.
XX
PD      05-DEC-2002.
XX
PF      29-MAY-2002; 2002WO-US16840.
XX
PR      29-MAY-2001; 2001US-294140P.
PR      06-JUN-2001; 2001US-296249P.
PR      10-SEP-2001; 2001US-318471P.
XX
PA      (RIBO-) RIBOZYME PHARM INC.
XX
PI      Mcswiggen J;
XX
DR      WPI; 2003-140484/13.
XX
PT      Novel short interfering RNA and enzymatic nucleic acid useful for
PT      treating cancer, modulates the expression of a nucleic acid encoding
PT      HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS      Claim 4; Page 139; 185pp; English.
XX
CC      The invention relates to a novel short interfering RNA (siRNA) nucleic
CC      acid molecule or an enzymatic nucleic acid molecule, that modulates
CC      expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC      human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC      acid molecule of the invention has cytostatic, anti-HIV, and
CC      anti-rheumatic activity. The nucleic acid molecules are useful for
CC      reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC      acids are also useful for treating breast, ovarian, colorectal, lung,
CC      prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC      The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531.
CC      ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC      sequences for the human ribozymes of the invention.
XX
SQ      Sequence 17 BP; 2 A; 4 C; 7 G; 4 U; 0 other;
Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      6 AGCCACAGCAGCT 19
      ||||| ||||| |||||
Db      17 AGCCCCAGCAGCT 4
RESULT 1683
ABZ64966/c
ID      ABZ64966 standard; RNA; 17 BP.
XX
AC      ABZ64966;
XX
DT      21-MAR-2003 (first entry)
XX
DE      Human HER2 DNazyme substrate #828.
XX
KW      Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW      enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW      anti-rheumatic; cancer; AIDS; ss.
XX
OS      Homo sapiens.
XX
PN      WO200297114-A2.
XX
PD      05-DEC-2002.
XX
DE      Human HER2 DNazyme substrate #423.
XX
KW      Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW      enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW      anti-rheumatic; cancer; AIDS; ss.
XX
OS      Homo sapiens.
XX
PN      WO200297114-A2.
XX
PD      05-DEC-2002.
XX
PF      29-MAY-2002; 2002WO-US16840.
XX
PR      29-MAY-2001; 2001US-294140P.
PR      06-JUN-2001; 2001US-296249P.
PR      10-SEP-2001; 2001US-318471P.
XX
PA      (RIBO-) RIBOZYME PHARM INC.
XX
PI      Mcswiggen J;
XX
DR      WPI; 2003-140484/13.
XX
PT      Novel short interfering RNA and enzymatic nucleic acid useful for
PT      treating cancer, modulates the expression of a nucleic acid encoding
PT      HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS      Claim 4; Page 141; 185pp; English.
XX
CC      The invention relates to a novel short interfering RNA (siRNA) nucleic
CC      acid molecule or an enzymatic nucleic acid molecule, that modulates
CC      expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC      human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC      acid molecule of the invention has cytostatic, anti-HIV, and
CC      anti-rheumatic activity. The nucleic acid molecules are useful for
CC      reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC      acids are also useful for treating breast, ovarian, colorectal, lung,
CC      prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC      The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531.
CC      ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC      sequences for the human ribozymes of the invention.
XX
SQ      Sequence 17 BP; 4 A; 2 C; 8 G; 3 U; 0 other;
Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      476 ACTTGGCATTCTCTC 489
      ||||| ||||| |||||
Db      17 ACTCGGCATTCTCTC 4
RESULT 1684
ABZ65371/c
ID      ABZ65371 standard; RNA; 17 BP.
XX
AC      ABZ65371;
XX
DT      21-MAR-2003 (first entry)
XX
DE      Human HER2 DNazyme substrate #828.
XX
KW      Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW      enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW      anti-rheumatic; cancer; AIDS; ss.
XX
OS      Homo sapiens.
XX
PN      WO200297114-A2.
XX
PD      05-DEC-2002.
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XX PF 29-MAY-2002; 2002WO-US16840.
XX PR 29-MAY-2001; 2001US-294140P.
XX PR 06-JUN-2001; 2001US-296249P.
XX PR 10-SEP-2001; 2001US-318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J;
XX XX
XX DR WPI; 2003-140484/13.
XX XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX PS
XX PS Claim 4; Page 149; 185pp; English.
XX XX
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytostatic, anti-HIV, and
XX CC anti-rheumatic activity. The nucleic acid molecules are useful for
XX CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
XX CC acids are also useful for treating breast, ovarian, colorectal, lung,
XX CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
XX CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
XX CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
XX CC sequences for the human ribozymes of the invention.
XX SQ Sequence 17 BP; 2 A; 10 C; 3 G; 2 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 143 GGGGGCTGCAGCTC 156
Db 17 GGGGGCTGCAGGTC 4

RESULT 1685
AAV16025
ID AAV16025 standard; DNA; 18 BP.
XX AC AAV16025;
XX XX
XX DT 21-MAY-1998 (first entry)
XX XX
XX DE PCR primer used to identify Sox-2 gene mutations in mice.
XX KW Mutation; Sox-2; mutational screening; recessive; phenotypic alteration;
XX KW mouse model; FGF-4; PCR primer; amplify; ss.
XX OS Synthetic.
XX OS Mus sp.
XX XX
XX FN WO9744485-A1.
XX XX
XX PD 27-NOV-1997.
XX XX
XX PF 16-MAY-1997; 97WO-GB01354.
XX PR 17-MAY-1996; 96GB-0010355.
XX XX
XX PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX XX
XX PI Goodfellow PN;
XX XX
XX DR WPI; 1998-018536/02.
XX XX

PT Identification of mutation(s) in genes of interest - without prior
PT observation of phenotypic alteration in the mutated organism or cell
XX
XX Example 6; Page 43; 66pp; English.
XX
XX CC PCR primers AAV16019-36 were used to identify mutations in Sox-2 using
XX CC the method of the invention. The method comprises testing a nucleic acid
XX CC sample from a mutated organism for a mutation in a gene of interest
XX CC without the prior observation of a phenotypic alteration in the mutated
XX CC organism resulting from the mutation. Sox-2 is a member of the Sox gene
XX CC family, and is involved in transcriptional regulation of the FGF-4
XX CC gene. FGF-4 codes for a signalling protein whose expression is essential
XX CC for postimplantation mouse development, and, at later embryonic stages,
XX CC for limb patterning and growth. Mutagenised mice in which a Sox-2
XX CC mutation is identified can be studied and provide a mouse model for a
XX CC mutant human sox-2 gene. The method provides mutational screening
XX CC based on genomic and genetic techniques rather than on phenotypic
XX CC observation. The method identifies and characterises genes via
XX CC mutagenesis to identify genes encoding products which may have
XX CC therapeutic benefit. The method also identifies the presence of
XX CC mutations in a gene which do not rely solely upon prior matching of a
XX CC gene with a disease. Heterozygotic organisms can also be screened to
XX CC identify those carrying a mutation in a copy of a gene of interest even
XX CC though the gene may be recessive and therefore causes no phenotypic
XX CC alteration.
XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 1.1%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 240 GCTCAGCTCTTGAAGGA 256
Db 2 GCTCTGCATCAGGGA 18

RESULT 1686
AAV84480/c
ID AAV84480 standard; DNA; 18 BP.
XX AC AAV84480;
XX XX
XX DT 10-SEP-1999 (first entry)
XX XX
XX DE PCR primer for Human EDIRF II coding sequence.
XX KW Embryo derived interleukin related factor; diagnosis; detection; therapy;
XX KW EDIRF-related disease; immune disorder; haematopoietic disorder;
XX KW developmental disorder; inflammatory disease; arthritis; psoriasis;
XX KW EDIRF II; PCR primer; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9932632-A1.
XX XX
XX PD 01-JUL-1999.
XX XX
XX PF 18-DEC-1998; 98WO-US27068.
XX XX
XX PR 19-DEC-1997; 97US-0994890.
XX XX
XX PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX XX
XX PI Holtzman DA;
XX XX
XX DR WPI; 1999-418929/35.
XX XX
XX PT Nucleic acid encoding embryo-derived interleukin-related factors
XX PS Example 2; Page 75; 116pp; English.
XX XX

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CC This sequence is a PCR primer for DNA encoding the embryo-derived
 CC interleukin-related factor (EDIRF) of the invention, designated human
 CC EDIRF II. The EDIRF DNA and protein sequences (and their homologues),
 CC antibodies (Ab) specific for EDIRF, and other modulators are used:
 CC (i) in screening and detection assays, e.g. for chromosome mapping,
 CC tissue typing or forensic studies; (ii) in diagnosis, prognosis or
 CC monitoring clinical trials; and (iii) for treating or preventing
 CC EDIRF-related diseases (especially immune, haematopoietic,
 CC differentiative, developmental or inflammatory disease, including
 CC arthritis and psoriasis. The EDIRF coding sequence, or its fragments, are
 CC also useful as probes and primers (for detecting related sequences and
 CC disease-associated mutations, also for mutagenesis), for expressing
 CC recombinant EDIRF and as source of antisense, ribozyme and peptide
 CC nucleic acids for inhibiting translation of EDIRF-derived mRNA. EDIRF is
 CC used to raise Ab (useful for detecting EDIRF, including forms with
 CC aberrant post-translational modification, for affinity purification and
 CC therapeutically) and to screen for specific modulators (e.g. peptides or
 CC peptidomimetics).

XX Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 other;
 SQ Query Match 1.1%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 142 TGGGGCTGCAGCTCA 158
 Db 17 TGTGGCTGCACCTGCA 1

RESULT 1687
 AAA05269
 ID AAA05269 standard; DNA; 18 BP.
 AC AAA05269;
 XX 19-MAY-2000 (first entry)
 XX PCR primer D-F used in Sox-2 amplicon generation.

XX PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; C-kit; Tryp-1;
 KW Pax-6; mutation detection; therapeutic target identification; mouse;
 KW mast cell growth factor; ss.

XX Mus sp.
 OS US6015670-A.
 PN 18-JAN-2000.

XX 14-NOV-1997; 97US-0970740.

XX 17-MAY-1996; 96US-0017824.

PR 16-MAY-1997; 97US-0857946.

XX (HEXA-) HEXAGEN TECHNOLOGY LTD.

XX Goodfellow PN;

XX WPI; 2000-181139/16.

XX Detecting mutations in selected genes, useful e.g. for identifying
 PT therapeutic targets or products, by analysing DNA in mutated embryonic
 PT stem cells without phenotypic characterization -

XX Example 6; Column 32; 66pp; English.

XX PCR primers AAA05245-A05406 are used to generate amplicons from the
 CC mouse Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Trp-1 gene, Sry
 CC gene, MGF (mast cell growth factor) gene, c-kit gene, and the Pax-6 gene.
 CC The primers are used in a method for the identification of a mutation in
 CC a selected gene in a tissue without the prior observation of a
 CC phenotypic alteration in the mutated organism or cell. The method is used

CC to identify mutations in a selected gene that encode products of
 CC potential therapeutic activity or that are potential targets,
 CC particularly where the gene of interest has been identified as a
 CC candidate gene by positional cloning. Other applications are determining
 CC functions of genes; detecting the range of phenotypes associated with
 CC different mutations in a particular gene and identification of
 CC particular mutations. Animals containing an identified mutation are used
 CC as models for studying diseases or their treatment, and cells from them
 CC for in vitro assessment of drug action. Interbreeding of mutant mice is
 CC used to investigate genetic interaction in the overall phenotype.

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

SQ Query Match 1.1%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 240 GCTCAGCTCTTGAGGA 256

Db 2 GCTCTGCATGAGGA 18

RESULT 1688

AAZ43284

ID AAZ43284 standard; DNA; 18 BP.

XX AAZ43284;

XX 11-FEB-2000 (first entry)

XX Murine Sox2 gene PCR primer 7.

XX Screening; mutation; treatment; disease; drug discovery;
 KW PCR primer; ss.

XX Mus musculus.

XX US5994075-A.

XX 30-NOV-1999.

XX 16-MAY-1997; 97US-0857946.

XX 17-MAY-1996; 96US-0017824.

XX (HEXA-) HEXAGEN TECHNOLOGY LTD.

XX Goodfellow PN;

XX WPI; 2000-038255/03.

XX Identifying a mutation in a gene of interest in an organism useful for
 PT identifying genes encoding products which may have therapeutic benefits

XX Example 7; Column 69-70; 70pp; English.

XX This invention describes a novel mutational screening method based on
 CC genomic and genetic techniques to identify and characterize a mutation
 CC in a gene of interest without first selecting a phenotypic
 CC characteristic. The screening methods are useful for identifying genes
 CC encoding products which may have therapeutic benefit for treating human
 CC or animal diseases. The method can be used for the DNA mutation
 CC screening of a class or a family of genes providing a rapid assay for
 CC identifying mutant genes. The methods produce organisms which can be used
 CC for drug discovery e.g. providing a model for the study and treatment of
 CC a disease state, allow in vitro assessment of drug activity and
 CC interbreeding of mutants which allow investigation of gene interactions
 CC in the overall phenotype. A range of phenotypes associated with different
 CC mutations, and specified mutations in a gene of interest can be
 CC determined. The method can be adapted to screen for a mutation in two or
 CC more genes of interest in an organism. The methods allow mutations in a
 CC gene of interest to be identified without having to rely on matching a

CC Gene with a disease. AAZ43260-Z43421 represent PCR primers used in the
CC method of the invention.

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 1.1%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 240 GCTCAGCTCTTGAGGA 256

DB 2 GCTCTGCACATGAGGA 18

RESULT 1689

AAQ75672

ID AAQ75672 standard; DNA; 21 BP.

AC AAQ75672;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes

XX Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of
CC and a plural type of labelled reverse transcription primers
CC (GENSEQ files AAQ75547-Q75798) and using the aggregate of
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.1%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 929 TTTTCAGCTTTGTTTATGA 948

DB 2 TTTT TTTT TTTT TTTTATGA 21

RESULT 1690

AAS63416/C

ID AAS63416 standard; DNA; 22 BP.

XX AAS63416;

AC

XX

DT

XX

DE

XX

KW

KW

XX

OS

XX

PN

XX

PD

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PF

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PR

PR

PR

PR

PR

PR

PR

PR

PR

XX

PA

XX

PI

PI

XX

DR

XX

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

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CC

CC

CC

CC

CC

CC

CC

CC

CC

CC


```

RESULT 1230
AAF29889
ID AAF29889 standard; DNA; 13 BP.
XX
AC AAF29889;
XX
DT 03-APR-2001 (first entry)
XX
DE Fragment 1 #2.
XX
KW Cloning; exon shuffling; store; adapter; ss.
XX
OS Unidentified.
XX
PN WO200100816-A1.
XX
PD 04-JAN-2001.
XX
PF 27-JUN-2000; 2000WO-GB02512.
XX
PR 28-JUN-1999; 99NO-0001325.
XX
PR 20-JUN-2000; 2000NO-0003190.
XX
PR 20-JUN-2000; 2000NO-0003191.
XX
PA (COMP-) COMPLETE GENOMICS AS.
XX
PA (JONE/) JONES E L.
XX
PI Lexow P;
XX
DR WPI; 2001-123006/13.
XX
PT Attaching fragments of first nucleic acids to second nucleic acids by
PT use of adapters complementary to first single stranded regions on the
PT first molecules but which have a different single stranded region at
PT the other terminus -
XX
PS Disclosure; Fig 3; 100pp; English.
XX
CC The present invention relates to attaching a fragment of first and
CC second nucleic acid molecules involves use of an adapter molecule
CC which is complementary to a single stranded region generated on the
CC target but which has a different single stranded region at its
CC other terminus and therefore modifies single stranded regions
CC presented for binding by the target. Attaching first and second
CC nucleic acid molecules may be used in cloning. The method can
CC also be used for exon shuffling other recombinations that are
CC relevant in connection with artificial evolutionary systems.
XX
SQ Sequence 13 BP; 13 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
Db 1 AAAAAAAAAAAAAA 13

RESULT 1231
AAF31563/c
ID AAF31563 standard; DNA; 13 BP.
XX
AC AAF31563;
XX
DT 09-APR-2001 (first entry)
XX
DE Model sequence.
XX
KW DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate;

```

```

KW AIDS; atherosclerosis; ss.
XX
OS Synthetic.
XX
PN WO200102419-A1.
XX
PD 11-JAN-2001.
XX
PF 05-JUL-2000; 2000WO-US40304.
XX
PR 07-JUL-1999; 99US-0349033.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Manoharan M, Maier M, An H;
XX
DR WPI; 2001-138117/14.
XX
PT New oligomers for use as research reagent, for treating disease caused
PT by undesired production of proteins, and for diagnosing and treating
PT AIDS, atherosclerosis -
XX
PS Example 44; Page 72; 110pp; English.
XX
CC The present invention relates to C3' methylene hydrogen phosphate
CC oligomers. The oligomers may be used as research reagents, for
CC treating disease caused by undesired production of proteins
CC and for diagnosing and treating AIDS and atherosclerosis.
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 12 T; 1 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
Db 13 AAAAAAAAAAAAAA 1

RESULT 1232
AAF31569/c
ID AAF31569 standard; DNA; 13 BP.
XX
AC AAF31569;
XX
DT 09-APR-2001 (first entry)
XX
DE Sequence with 2'-O-methyl-3'-methylphosphonate monomer.
XX
KW DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate;
XX
OS AIDS; atherosclerosis; ss.
XX
PN WO200102419-A1.
XX
PD 11-JAN-2001.
XX
PF 05-JUL-2000; 2000WO-US40304.
XX
PR 07-JUL-1999; 99US-0349033.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Manoharan M, Maier M, An H;
XX
DR WPI; 2001-138117/14.
XX
PT New oligomers for use as research reagent, for treating disease caused
PT by undesired production of proteins, and for diagnosing and treating
PT AIDS, atherosclerosis -
XX

```

CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC oligo dT PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 14 BP; 13 A; 0 C; 0 G; 0 U; 1 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 6.7e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 1 AAAAAAAAAAAAAA 14
 RESULT 1167
 AAD44148
 ID AAD44148 standard; DNA; 14 BP.
 XX
 AC AAD44148;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Oligo-dT PCR primer #8 used to illustrate the method of the invention.
 XX
 KW Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase;
 KW PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 XX US6277571-B1.
 PN 21-AUG-2001.
 XX
 XX 30-SRP-1998; 98US-0163485.
 PF
 XX 03-OCT-1997; 97US-108152P.
 PR
 XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 PA
 PI Fillmore H, Broadus W, Gillies G;
 XX
 XX WPI; 2002-412824/44.
 DR
 XX
 XX Sequential consensus region-directed amplification for sorting mixture
 PT of DNAs into 2 or more subsets or distinguishing gene expression
 PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
 PS Example; Fig 1C; 19pp; English.
 XX
 CC The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC oligo dT PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 14 BP; 12 A; 0 C; 0 G; 1 T; 1 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 6.7e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAAAAAAAAA 1096
 Db 1 TAAAAAAAAAAAAA 14
 RESULT 1168
 AAX18386/C
 ID AAX18386 standard; DNA; 15 BP.

XX
 AC AAX18386;
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE RT-PCR primer of the invention SEQ ID 27.
 XX
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 PN JP11032765-A.
 XX
 PD 09-FEB-1999.
 XX
 XX 18-JUL-1997; 97JP-0208312.
 PF
 XX 18-JUL-1997; 97JP-0208312.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX WPI; 1999-183822/16.
 DR
 XX
 XX Peptides having at least two new nucleotides - useful as primers in
 PT RT-PCR
 XX
 PS Example 1; Page 12; 19pp; Japanese.
 XX
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
 CC guanine and/or cytosine. The new nucleotides are useful as primers for
 CC RT-PCR and determination of base sequences. The new sequences allow for
 CC reproductive and highly efficient analysis of gene sequences.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 7.1e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAAAAAAAAA 1096
 Db 14 BAAAAAAAAAAAAA 1
 RESULT 1169
 AAN90456
 ID AAN90456 standard; DNA; 18 BP.
 XX
 AC AAN90456;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-NOV-1989 (first entry)
 XX
 XX Oligonucleotide probe specific for Bacteroides gingivalis.
 DE
 XX Bacteroides gingivalis; oligonucleotide probe; periodontal
 KW disease; mouth diseases; rRNA; species-specific.
 XX
 OS Bacteroides gingivalis.
 XX
 XX WO8906704-A.
 PN
 XX 27-JUL-1989.
 PD
 XX 09-JAN-1989; 89WO-US000072.
 PF

XX 11-JAN-1988; 88US-0142106.
 XX (MICR-) MICROPROBE CORP.
 XX Schwartz DE, Kanemoto RH, Watanabe SM, Dix K;
 XX WPI; 1989-233857/32.
 XX
 XX Oligonucleotide probes for detection of periodontal pathogens
 PT - comprising a segment of nucleic acid capable of hybridising to
 PT bacterial ribosomal RNA.
 XX Claim 7; page 43; 53pp; English.
 XX
 XX Oligonucleotide probe (Bg-1B) below, specific for Bacteroides
 CC gingivalis, was derived by primer UP4B/1B. It is a species-
 CC specific probe that hybridises to the rRNA of B. gingivalis.
 CC It is highly sensitive and highly specific for detecting
 CC oral pathogens. AAN90419-87 can also distinguish
 CC between bacterial species, types and subtypes.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;
 SQ
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 216 CCTCTCCAGAGTGCACG 233
 Db 1 CCTCTCCGAGTTACG 18
 RESULT 1170
 AAQ10847
 ID AAQ10847 standard; DNA; 18 BP.
 XX
 XX AAQ10847;
 DT 08-MAY-1991 (first entry)
 DE Probe to N-terminal region of MAB T84.66 gamma heavy chain.
 XX
 XX MAB T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
 KW human adenocarcinoma; mouse-human chimaeric antibody; ss.
 XX
 XX Mus musculus.
 XX
 XX W09101990-A.
 XX
 XX 21-FEB-1991.
 XX
 XX 19-JUL-1990; 90WO-US04049.
 XX
 XX 26-JUL-1989; 89US-0385102.
 XX
 XX (CITY) CITY OF HOPE.
 XX
 XX Shively JE, Riggs AD, Neumaier M;
 XX
 XX WPI; 1991-073486/10.
 XX
 XX Novel anti-CEA antibody - comparable to ATCC Accession No. BH
 PT 8747, produced by recombinant DNA, used in diagnosis of tumours
 XX
 XX Disclosure; Page 6; 24pp; English.
 XX
 XX The heavy chain variable region of murine MAB 84.66 was cloned as
 CC follows: Hybridoma DNA was extracted, completely restricted with
 CC EcoRI and run on a gel. Fragments were extracted and ligated in the
 CC EcoRI site of Lambda-ZAP-Phage were packaged and plated. Plaque
 CC screening was with a 991bp XbaI fragment from the mouse

CC enhancer region, a 1.5kb cDNA fragment from the heavy chain
 CC constant region gene of hybridoma CEA.66-E3 and a 5.4kb EcoRI
 CC fragment containing an aberrantly rearranged heavy chain from
 CC Sp2/0. Positive clones were further characterised by hybridisation
 CC to J-region oligonucleotides and a probe specific to the N-terminal
 CC region. This probe was used to allow upstream characterisation of
 CC the promoter region.
 CC See also AAQ10834-Q10846, AAQ10848 and AAQ11098.
 XX
 XX Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 other;
 SQ
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 660 CTCATGCGAGCTGAAGCTC 677
 Db 1 CTGCTGCGAGCTGAACCTC 18
 RESULT 1171
 AAQ29050
 ID AAQ29050 standard; DNA; 18 BP.
 XX
 XX AAQ29050;
 DT 25-MAR-2003 (updated)
 DT 26-FEB-1993 (first entry)
 XX
 XX Unique 5' PCR primer #7 for kappa light chain variable region.
 XX
 XX Dicitronic expression vector; fusion PCR; antibody; cDNA library;
 KW ss.
 XX
 XX Synthetic.
 XX
 XX W09215678-A1.
 XX
 XX 17-SEP-1992.
 XX
 XX 27-FEB-1992; 92WO-US01475.
 XX
 XX 01-MAR-1991; 91US-0663442.
 XX
 XX (STRA-) STRATAGENE.
 XX
 XX Sorge JA;
 XX
 XX WPI; 1992-331724/40.
 XX
 XX Prodn. of dicitronic DNA library used to make antibodies, etc. -
 PT includes forming 1st and 2nd PCR admixtures, subjecting them to
 PT PCR thermo-cycles, sepg. double stranded DNA, hybridising, etc.
 XX
 XX Claim 14; Page 38; 143pp; English.
 XX
 XX This inside PCR primer is used in fusion PCR, working in combination
 CC with an outside PCR primer to amplify a target nucleic acid sequence,
 CC in this case the kappa light chain variable region. The fusion PCR
 CC reaction is used to produce two fragments with cohesive termini,
 CC which when mixed hybridise to form an overlapping DNA duplex that is
 CC internally primed. Subsequent PCR extends the non-overlapping region
 CC to form a hybrid DNA mol. that is dicitronic contg. a first
 CC polypeptide coding sequence and a second polypeptide coding region
 CC linked by a dicitronic bridge. This method thus allows fusion of
 CC heavy and light chains prior to vector ligation, avoiding
 CC the cumbersome separate cloning of fragments.
 CC (Updated on 25-MAR-2003 to correct FN field.)
 XX
 XX Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 other;
 SQ
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;

```

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 862 GTGATGAGCCCAACTCCA 879
Db 1 GTGATGAGCCCAACTCCA 18

RESULT 1172
AAQ31225
ID AAQ31225 standard; DNA; 18 BP.
XX
AC AAQ31225;
XX
DT 25-MAR-2003 (updated)
DT 24-MAR-1993 (first entry)
XX
DE G-CSF targetting vector construction PCR primer 24.
XX
KW Polymerase chain reaction; high yield protein production; ss.
XX
OS Synthetic.
XX
FN WO9219255-A1.
XX
PD 12-NOV-1992.
XX
PF 05-MAY-1992; 92WO-US03686.
XX
PR 06-MAY-1991; 91US-0696216.
XX
PA (CELL-) CELL GENESYS INC.
XX
PI Klapholz S, Sherwin S, Skoultschi A;
XX
DR WPI; 1992-398523/48.
XX
PT Expression of wild-type or altered mammalian proteins - using
PT amplifiable gene to provide multiple copies of the target gene
PT which may be modified by in-vivo mutagenesis
XX
PS Example; Page 35; 53pp; English.
XX
CC The sequence is that of a PCR primer which was used in the construction
CC of G-CSF targetting vectors. It was used in the generation by PCR
CC of an XbaI to blunt-ended fragment contg. nucleotides +180 to
CC +1480 of the G-CSF gene., as part of the construction of a YAC
CC targetting vector, pYGT2. This was part of a method of producing
CC high yields of wild type or modified mammalian protein without the
CC necessity of isolating the message or doing the various manipulations
CC associated with genetic engineering, e.g. isolation of large genomic
CC genes.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 957 CTGGCAGGCTGGCAG 974
Db 1 CTGGCAGGCTGGCAG 18

RESULT 1173
AAQ79940/c
ID AAQ79940 standard; cDNA; 18 BP.
XX
AC AAQ79940;
XX
DT 25-MAR-2003 (updated)
DT 06-SEP-1995 (first entry)
XX

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DE Murine Kin17 oligo E.
XX
KW chromosomal rearrangement; kin17 protein; SOS DNA repair system;
KW RecA; genotoxic agent; zinc finger; DNA binding protein;
KW PCR primer; hybridisation probe; ss.
XX
OS Synthetic.
XX
FN FR2706487-A1.
XX
PD 23-DEC-1994.
XX
PF 15-JUN-1993; 93FR-0007171.
XX
PR 15-JUN-1993; 93FR-0007171.
XX
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Angulo-Mora JF, Frelat G, Guilly M, Mauffrey P;
PI Tissler A;
XX
DR WPI; 1995-039031/06.
XX
PT Purified murine kin17 protein prepn. for detecting chromosomal
PT rearrangements - also related antibodies, human and murine DNA,
PT primers, probes and vectors, used to assess damage caused by
PT genotoxic agents
XX
PS Claim 14; Page 34; 54pp; French.
XX
CC The murine Kin17 protein includes a zinc finger domain (see AAR66766),
CC recognises single- and double-stranded DNA (partic. regions of
CC secondary structure), has apparent mol. wt. 43 kD and is recognised
CC by both anti-kin17 antibodies and antibodies against the RecA
CC protein of E.coli. The Kin17 protein is involved in DNA repair; it
CC can be used to monitor chromosomal rearrangements following exposure
CC to genotoxic agents. Specific oligonucleotides (AAQ79937-Q79947)
CC derived from the kin17 genomic DNA sequence, are claimed and can be
CC used as hybridisation probes or as amplification primers.
CC Oligos E and F are pref. used together in a primer pair.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 5 A; 4 C; 4 G; 5 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 468 CTCGAGGAAGCTTGGCATT 485
Db 18 CTCAGTAAGACTTGGCAGT 1

RESULT 1174
AAQ50703
ID AAT50703 standard; RNA; 18 BP.
XX
AC AAT50703;
XX
DT 07-MAR-1997 (first entry)
XX
DE Rabbit CETP hairpin ribozyme target sequence #160.
XX
KW Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
KW LDL; ss.
XX
OS Oryctolagus cuniculus.
XX

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PN WO9620279-A1.
 XX 04-JUL-1996.
 XX 11-DEC-1995; 95WO-US16000.
 XX 23-DEC-1994; 94US-0363240.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (WARN) WARNER LAMBERT CO.
 XX Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
 XX WPI; 1996-321852/32.
 XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
 XX - useful for preventing or treating initial development, progression
 XX or regression of vascular diseases, esp. familial
 XX hypercholesterolaemia
 XX Claim 4; Page 54; 72pp; English.
 XX AAT50699-T50754 represent target sequences for the rabbit cholesterol
 XX ester transfer protein (CETP) hairpin ribozymes (see AAT50643-T50698).
 XX CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
 XX between plasma lipoproteins. The numbering of the targets refers to the
 XX position of the cleavage site in full length CETP. The ribozyme then
 XX binds to 4-6 nucleotides 5', and a variable number 3', of this site. The
 XX ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
 XX blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
 XX the reverse cholesterol transport (RCT) pathway can be inhibited (or
 XX eliminated) thereby preventing the reduction in size density of the high
 XX density lipoproteins (HDL), prolonging HDL half life, and therefore
 XX increasing HDL levels. The ribozymes can be used to treat conditions
 XX associated with abnormal levels of CETP, specifically atherosclerosis,
 XX peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
 XX familial hypercholesterolaemia, hypobetalipoproteinaemia, vascular
 XX complications of diabetes, transplant, attherosclerosis and angioplasty
 XX restenosis. By inhibiting CETP, the levels of HDL and low density
 XX lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 XX decrease in LDL levels, and a corresponding increase in HDL levels). The
 XX ribozymes can also be used diagnostically to study genetic drift and
 XX mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
 XX target specific regions of the CETP gene, they have low non-specific
 XX activity.
 XX Sequence 18 BP; 2 A; 7 C; 6 G; 3 U; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. NO. 8.4e+02;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 99 CTCCTCGGACTGGTCAAG 116
 Db 1 CUCCUCGCGCGGUCUAG 18
 RESULT 1175
 AAX75617/c
 ID AAX75617 standard; RNA; 18 BP.
 XX
 XX AAX75617;
 XX 28-JUL-1999 (first entry)
 XX Mouse flt-1 VEGF receptor hairpin ribozyme substrate #76.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 XX foetal liver kinase 1; ss.
 XX Homo sapiens.
 XX WO9715662-A2.
 XX 01-MAY-1997.
 XX 25-OCT-1996; 96WO-US17480.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 XX foetal liver kinase 1; ss.

OS Mus sp.
 XX WO9715662-A2.
 XX 01-MAY-1997.
 XX 25-OCT-1996; 96WO-US17480.
 XX 11-JAN-1996; 96US-0584040.
 XX 26-OCT-1995; 95US-0005974.
 XX (CHIR) CHIRON CORP.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 XX mRNA stability - useful for treating e.g. tumour angiogenesis,
 XX psoriasis, rheumatoid arthritis, etc., in a human patient
 XX Claim 4; Page 188; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate
 XX the synthesis, expression and/or stability of a mRNA encoding 1 or more
 XX receptors of vascular endothelial growth factor (VEGF). A patient
 XX (preferably human) having a condition associated with the level of the
 XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 XX be treated by administering the nucleic acid molecule or the expression
 XX vector to the patient. AAX75725 to AAX75752 represent specific examples
 XX of nucleic acid molecules from the present invention.
 XX Sequence 18 BP; 2 A; 7 C; 4 G; 5 U; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. NO. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1016 GAAGTGTAAAGCTGGGCGCT 1033
 Db 18 GAAGCAGAAAGCTGGGCGCT 1
 RESULT 1176
 AAX71707/c
 ID AAX71707 standard; RNA; 18 BP.
 XX
 XX AAX71707;
 XX 28-JUL-1999 (first entry)
 XX Human KDR VEGF receptor hairpin ribozyme substrate #5.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 XX foetal liver kinase 1; ss.
 XX Homo sapiens.
 XX WO9715662-A2.
 XX 01-MAY-1997.
 XX 25-OCT-1996; 96WO-US17480.
 XX 11-JAN-1996; 96US-0584040.
 XX 26-OCT-1995; 95US-0005974.

PA (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX WPI; 1997-259017/23.
 XX
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 XX Claim 4; Page 118; 218pp; English.
 XX
 XX The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flt-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 XX Sequence 18 BP; 4 A; 5 C; 5 G; 4 U; 0 other;
 SQ
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 187 GTGGCGGTCAGTTC 204
 DB | | | | | | | | | | | | | | | | | |
 18 GAGGCCAAGTCAGTTC 1
 RESULT 1177
 AAT88311
 ID AAT88311 standard; DNA; 18 BP.
 XX
 XX AAT88311;
 XX
 XX 23-JAN-1998 (first entry)
 DT
 DE Oligonucleotide primer O_K3L5.
 XX
 XX Oligonucleotide primer; preparation; library; CDR3;
 KW complementarity determining region; ss.
 XX
 XX Synthetic.
 XX
 XX WO9708320-A1.
 XX
 XX 06-MAR-1997.
 XX
 XX 19-AUG-1996; 96WO-EP03647.
 XX
 XX 18-AUG-1995; 95EP-0113021.
 XX
 XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 XX
 XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
 XX WPI; 1997-179277/16.
 XX
 XX Preparation of human derived antibody gene library - using synthetic
 PT consensus sequences, and signal consensus antibody gene as universal
 PT framework for highly diverse antibody libraries
 XX
 XX Example 5; Fig 37; 436pp; English.
 XX
 XX The present sequence is an oligonucleotide primer used in the
 CC preparation of complementarity determining region 3 (CDR3)
 CC libraries.

XX
 SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 303 GCCCTGTCATGGGAAGAC 320
 DB | | | | | | | | | | | | | | | | | |
 1 GCCCTGCAAGCGGAAGAC 18
 RESULT 1178
 AAT58613
 ID AAT58613 standard; DNA; 18 BP.
 XX
 XX AAT58613;
 XX
 XX 25-MAR-2003 (updated)
 DT 22-APR-1997 (first entry)
 XX
 XX Human G-CSF gene (nucleotides +1180 to +1480) PCR primer.
 DE
 XX Human; granulocyte colony stimulating factor; G-CSF; targetting vector;
 KW mammalian gene activation; yeast artificial chromosome; YAC;
 KW polymerase chain reaction; PCR primer; ss.
 XX
 XX Synthetic.
 XX
 XX US5578461-A.
 XX
 XX 26-NOV-1996.
 XX
 XX 05-AUG-1993; 93US-0102567.
 XX
 XX 07-JAN-1993; 93US-0001898.
 PR 06-NOV-1989; 89US-0432069.
 PR 05-AUG-1993; 93US-0102567.
 XX
 XX (CELL-) CELL GENESYS INC.
 XX
 XX Klapholz S, Sherwin S, Skultchi A;
 PI WPI; 1997-020405/02.
 XX
 XX Prodn. of mammalian gene prods. in cell culture - using continuous
 PT cell line contg. heterologous regulatory sequence integrated by
 PT homologous recombination
 XX
 XX Disclosure; Column 15; 20pp; English.
 XX
 XX Expression of mammalian target genes is achieved by using chromosomal
 CC target DNA, either native primary cells or yeast artificial chromosomes
 CC (YACs) in a yeast host, where the YACs include a fragment comprising
 CC the target gene. An amplifiable gene is integrated (using homologous
 CC recombination) into the mammalian fragment at a site to allow for
 CC amplification. The resulting construct (optionally modified by in
 CC vivo mutagenesis) can be transformed into a mammalian expression
 CC host and integrated into the host genome, either randomly or by
 CC homologous recombination. The amplifiable gene can then be
 CC expressed and host cells which produce high yields of the desired
 CC protein are selected. In a specific example of this new method,
 CC YAC targetting vector pYGT2 was constructed to create sequences
 CC capable of directing the modification of the human G-CSF polypeptide;
 CC vector pYGT2 contains: a 5'-targetting region (i.e. nucleotides +1180
 CC to +1480 of the G-CSF gene), an IGS2 heavy chain cDNA encoding the
 CC hinge, CH2 and CH3 domains, an SV40 early polyadenylation site, the
 CC yeast HIS2 selectable marker, and a 3'-targetting region (i.e.
 CC nucleotides +1496 to +2599 of the G-CSF gene). The present sequence
 CC is that of a PCR primer which was used in the construction of pYGT2.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 957 CTGGGCAAGGTGGCACAG 974
| | | | | | | | | | | | | | | | | |
Db 1 CTGGGCAAGGTGGCGTAG 18

RESULT 1179
AAV16025/c
ID AAV16025 standard; DNA; 18 BP.
XX AC AAV16025;
XX 21-MAY-1998 (first entry)
XX PCR primer used to identify Sox-2 gene mutations in mice.
XX Mutation; Sox-2; mutational screening; recessive; phenotypic alteration;
XX mouse model; FGF-4; PCR primer; amplify; ss.
XX Synthetic.
XX OS Mus sp.
XX PN WQ9744485-A1.
XX 27-NOV-1997.
XX 16-MAY-1997; 97WO-GB01354.
XX 17-MAY-1996; 96GB-0010355.
XX (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX Goodfellow PN;
XX WPI; 1998-018536/02.
XX Identification of mutation(s) in genes of interest - without prior
XX observation of phenotypic alteration in the mutated organism or cell
XX Example 6; Page 43; 66pp; English.

CC PCR primers AAV16019-36 were used to identify mutations in Sox-2 using
CC the method of the invention. The method comprises testing a nucleic acid
CC sample from a mutated organism for a mutation in a gene of interest
CC without the prior observation of a phenotypic alteration in the mutated
CC organism resulting from the mutation. Sox-2 is a member of the Sox gene
CC family, and is involved in transcriptional regulation of the FGF-4
CC gene. FGF-4 codes for a signalling protein whose expression is essential
CC for postimplantation mouse development, and, at later embryonic stages,
CC for limb patterning and growth. Mutagenised mice in which a Sox-2
CC mutation is identified can be studied and provide a mouse model for a
CC mutant human sox-2 gene. The method provides mutational screening
CC based on genomic and genetic techniques rather than on phenotypic
CC observation. The method identifies and characterises genes via
CC mutagenesis to identify genes encoding products which may have
CC therapeutic benefit. The method also identifies the presence of
CC mutations in a gene which do not rely solely upon prior matching of a
CC gene with a disease. Heterozygotic organisms can also be screened to
CC identify those carrying a mutation in a copy of a gene of interest even
CC though the gene may be recessive and therefore causes no phenotypic
CC alteration.

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 TCCTCCAGGTGCAGAGG 50

KW Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.

XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9953101-AL.
 PN
 XX 21-OCT-1999.

XX 13-APR-1999; 99WO-US08268.
 XX 13-APR-1998; 98US-0081483.
 XX 28-APR-1998; 98US-0067638.
 XX (ISIS-) ISIS PHARM INC.

XX Cowsert LM, Baker BF, McNeil J, Freier SM, Sasmor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 PI WPI; 1999-620446/53.
 DR
 XX Identifying compounds which modulate expression of nucleic acids, used
 PT to provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity -
 XX

PS Example 18; Page 97; 264pp; English.
 XX
 XX A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of
 CC the compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria,
 CC and evaluating in silico the binding of the virtual compounds with the
 CC tNA according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONS) that modulate the expression of
 CC a tNA sequence via binding of the ONS with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONS with
 CC the tNA according to defined criteria; and (2) a method of defining a
 CC set of compounds that modulate the expression of a tNA sequence via
 CC binding of the compounds with the tNA. The methods can be used for the
 CC generation and identification of synthetic compounds having defined
 CC physical, chemical or bioactive properties. Information gathered from
 CC assays of such compounds is used to identify nucleic acid sequences that
 CC are tractable to a variety of nucleotide sequence-based technologies,
 CC e.g. antisense drug discovery and target validation. AAZ40852 to
 CC AAZ41220, and AAY52701 to AAY52706, represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 18 BP; 5 A; 8 C; 2 G; 3 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 614 GGCAATCTCAACGAGCGC 631
 |||||
 DB 1 GGCAATCTCAACACCTC 18

RESULT 1182
 AAZ41175/c
 ID AAZ41175 standard; DNA; 18 BP.
 XX
 AC AAZ41175;
 XX

DT 26-JAN-2000 (first entry)
 XX
 XX Human G-alpha-11 phosphorothioate antisense oligonucleotide #79.

DE Identification; genetic target; gene modulation; human; probe;
 XX
 KW antisense oligonucleotide; phosphorothioate; PCR primer;

KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.

XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9953101-AL.
 PN
 XX 21-OCT-1999.

XX 13-APR-1999; 99WO-US08268.
 XX 13-APR-1998; 98US-0081483.
 XX 28-APR-1998; 98US-0067638.
 XX (ISIS-) ISIS PHARM INC.

XX Cowsert LM, Baker BF, McNeil J, Freier SM, Sasmor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 PI WPI; 1999-620446/53.
 DR
 XX Identifying compounds which modulate expression of nucleic acids, used
 PT to provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity -
 XX

PS Example 27; Page 109; 264pp; English.
 XX
 XX A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of
 CC the compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria,
 CC and evaluating in silico the binding of the virtual compounds with the
 CC tNA according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONS) that modulate the expression of
 CC a tNA sequence via binding of the ONS with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONS with
 CC the tNA according to defined criteria; and (2) a method of defining a
 CC set of compounds that modulate the expression of a tNA sequence via
 CC binding of the compounds with the tNA. The methods can be used for the
 CC generation and identification of synthetic compounds having defined
 CC physical, chemical or bioactive properties. Information gathered from
 CC assays of such compounds is used to identify nucleic acid sequences that
 CC are tractable to a variety of nucleotide sequence-based technologies,
 CC e.g. antisense drug discovery and target validation. AAZ40852 to
 CC AAZ41220, and AAY52701 to AAY52706, represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 661 TCATGACGTGAAGCTCA 678
 |||||
 DB 18 TCCTGACGTGAACCTGA 1

RESULT 1183
 AAZ41210
 ID AAZ41210 standard; DNA; 18 BP.
 XX
 AC AAZ41210;
 XX

DT 26-JAN-2000 (first entry)
 XX
 XX Human AKT-1 phosphorothioate antisense oligonucleotide SEQ ID NO:362.

DE Identification; genetic target; gene modulation; human; probe;
 XX
 KW antisense oligonucleotide; phosphorothioate; PCR primer;

PT associated with G-alpha-11
 PS Example 15; Column 41; 38pp; English.
 CC
 CC The present invention describes inhibitory antisense compounds of 8-30
 CC nucleotides, targeted to a nucleic acid molecule encoding human
 CC G-alpha-11. AA219468 to AA219547 represent human G-alpha-11
 CC phosphorothioate antisense oligonucleotides given in the present
 CC invention. The oligonucleotides may be useful for the treatment of
 CC diseases associated with G-alpha-11.
 XX
 SQ Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 661 TCATGCAGCTGAAGCTCA 678
 Db 18 TCCTGCAGCTGAACCTGA 1
 RESULT 1186
 AAX87332/C
 ID AAX87332 standard; DNA; 18 BP.
 XX
 AC AAX87332;
 XX
 XX 27-SEP-1999 (first entry)
 DT Reverse transcription primer P1.
 DE
 XX SAG gene; sensitive to apoptosis; mouse; cancer; tumour;
 KW neurodegenerative disease; muscular dystrophy; wound healing;
 KW vulvar; therapy; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9932514-A2.
 PN
 XX 01-JUL-1999.
 PD
 XX 15-DEC-1998; 98WO-US26705.
 PF
 XX 11-SEP-1998; 98US-0099840.
 PR 19-DEC-1997; 97US-0068179.
 XX
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX Sun Y;
 PI
 XX WPI; 1999-430152/36.
 DR
 XX SAG: Sensitive to Apoptosis Gene and related proteins, useful for
 PT promoting cell growth and protecting cells against apoptosis
 PS Example 1; Page 14; 84pp; English.
 XX
 CC This primer was used for reverse transcription of RNA isolated
 CC from mouse tumour lines L-R101 (epidermal tumour cell line) and
 CC H-Tx (spontaneously transformed liver line). It was also used as
 CC the reverse primer in PCR amplification of the resulting cDNA.
 CC Primers P1 and P2 (see AAX87333) reproducibly detected differential
 CC expression of a gene between 1,10-phenanthroline (Op)-treated and
 CC OP-nontreated L-R101 and H-Tx cells. An OP-inducible clone was
 CC used as a probe to isolate a full-length clone (see AAX87313)
 CC corresponding to the mouse sensitive to apoptosis gene (SAG). SAG
 CC is a redox-sensitive, haem-binding protein domain that promotes
 CC cell growth, protects cells from apoptosis, scavenges oxygen
 CC radicals and can be used for the reversion of a tumour phenotype.
 XX
 SQ Sequence 18 BP; 2 A; 1 C; 1 G; 13 T; 1 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 8.4e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1096
 Db 18 BAAAAAATAAAAAA 5
 RESULT 1187
 AAX84480
 ID AAX84480 standard; DNA; 18 BP.
 XX
 AC AAX84480;
 XX
 DT 10-SEP-1999 (first entry)
 XX
 XX PCR primer for Human EDIRF II coding sequence.
 DE
 XX Embryo derived interleukin related factor; diagnosis; detection; therapy;
 KW EDIRF-related disease; immune disorder; haematopoietic disorder;
 KW developmental disorder; inflammatory disease; arthritis; psoriasis;
 KW EDIRF II; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9932632-A1.
 PN
 XX 01-JUL-1999.
 PD
 XX 18-DEC-1998; 98WO-US27068.
 PF
 XX 19-DEC-1997; 97US-0994890.
 PR
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PA
 XX Holtzman DA;
 PI
 XX WPI; 1999-418929/35.
 DR
 XX Nucleic acid encoding embryo-derived interleukin-related factors
 PS Example 2; Page 75; 116pp; English.
 XX
 CC This sequence is a PCR primer for DNA encoding the embryo-derived
 CC interleukin-related factor (EDIRF) of the invention, designated human
 CC EDIRF II. The EDIRF DNA and protein sequences (and their homologues),
 CC antibodies (Ab) specific for EDIRF, and other modulators are used:
 CC (i) in screening and detection assays, e.g. for chromosome mapping,
 CC tissue typing or forensic studies; (ii) in diagnosis, prognosis or
 CC monitoring clinical trials; and (iii) for treating or preventing
 CC EDIRF-related diseases (especially immune, haematopoietic,
 CC differentiative, developmental or inflammatory disease, including
 CC arthritis and psoriasis). The EDIRF coding sequence, or its fragments, are
 CC also useful as probes and primers (for detecting related sequences and
 CC disease-associated mutations, also for mutagenesis), for expressing
 CC recombinant EDIRF and as source of antisense, ribozyme and peptide
 CC nucleic acids for inhibiting translation of EDIRF-derived mRNA. EDIRF is
 CC used to raise Ab (useful for detecting EDIRF, including forms with
 CC aberrant post-translational modification, for affinity purification and
 CC therapeutically) and to screen for specific modulators (e.g. peptides or
 CC peptidomimetics).
 XX
 SQ Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 664 TGCAGCTGAAGCTCACAG 681
 Db 1 TGCAGCTGAAGCTCACAG 18

```

RESULT 1188
AAZ70705/c
ID AAZ70705 standard; DNA; 18 BP.
AC AAZ70705;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5061.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 8; Page 1310; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX
XX N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 other;
XX
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 446 GCCAGATGCCCTTCCAGGA 463
DB 18 GTCAGATCCCTCCAGGA 1
XX
RESULT 1189
AAZ63616
ID AAZ63616 standard; DNA; 18 BP.
XX
XX AAZ63616;
AC

```

```

XX
XX 04-DEC-2000 (first entry)
XX
XX Fragment of the 16S ribosomal RNA gene of Legionella species.
XX
XX Nucleic acid reference material; polymerase chain reaction; PCR;
XX nucleic acid amplification; 16S ribosomal RNA gene; ss.
XX
XX Legionella hackeliae.
XX
XX WO2000046401-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-GB00305.
XX
XX 03-FEB-1999; 99GB-0002422.
XX
XX (LGCT-) LGC TEDDINGTON LTD.
XX
XX McDowell DG;
XX
XX WPI; 2000-514968/46.
XX
XX New nucleic acid reference material comprising two reference sequences
XX for use in the polymerase chain reaction and for verifying nucleic acid
XX amplification reactions by acting as a control -
XX
XX Example 1; Fig 1B; 54pp; English.
XX
XX The specification describes a nucleic acid reference material, which
XX comprises two reference sequences, each with a pair of primer binding
XX sites which are the same except for the substitution of one or a few
XX nucleotide bases. The reference material is used in the polymerase chain
XX reaction (PCR). The reference material is used as a control for
XX verifying nucleic acid amplification reactions. The reference material is
XX designed to be used in isolation in PCR systems or simultaneously within
XX PCR assays, to control for and allow the measurement of PCR specificity
XX and sensitivity. Amplification reactions that can be verified include
XX ligase chain reaction, gapped ligase chain reaction, strand displacement
XX amplification, nucleic acid sequence based amplification and
XX self-sustained sequence replication. The reference material is
XX particularly useful where detection of target sequences in medical or
XX environmental samples is desired. AAZ63609-21 represent internal
XX fragments of the 16S ribosomal RNA gene. A fragment of the 16S
XX ribosomal RNA gene of L. pneumophila was used to produce a reference
XX material of the invention.
XX
XX Sequence 18 BP; 5 A; 3 C; 9 G; 1 T; 0 other;
XX
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 322 GCAGAGAGAGCTCTGGAGC 339
DB 1 GCAGAGAGAGCTGGGACC 18
XX
RESULT 1190
AAZ63619
ID AAZ63619 standard; DNA; 18 BP.
XX
XX AAZ63619;
AC
XX
XX 04-DEC-2000 (first entry)
XX
XX Fragment of the 16S ribosomal RNA gene of Legionella species.
XX
XX Nucleic acid reference material; polymerase chain reaction; PCR;
XX nucleic acid amplification; 16S ribosomal RNA gene; ss.
XX
XX Legionella spiritensis.

```

XX PN WO200046401-A1.
 XX PD 10-AUG-2000.
 XX PF 02-FEB-2000; 2000WO-GB00305.
 XX PR 03-FEB-1999; 99GB-0002422.
 XX PA (LGCT-) LGC TEDDINGTON LTD.
 XX PI McDowell DG;
 XX PI WPI; 2000-514968/46.
 XX DR
 XX PS New nucleic acid reference material comprising two reference sequences
 XX PT for use in the polymerase chain reaction and for verifying nucleic acid
 XX PT amplification reactions by acting as a control -
 XX PS Example 1; Fig 1B; 54pp; English.
 XX CC The specification describes a nucleic acid reference material, which
 XX CC comprises two reference sequences, each with a pair of primer binding
 XX CC sites which are the same except for the substitution of one or a few
 XX CC nucleotide bases. The reference material is used in the polymerase chain
 XX CC reaction (PCR). The reference material is used as a control for
 XX CC verifying nucleic acid amplification reactions. The reference material is
 XX CC designed to be used in isolation in PCR systems or simultaneously within
 XX CC PCR assays, to control for and allow the measurement of PCR specificity
 XX CC and sensitivity. Amplification reactions that can be verified include
 XX CC ligase chain reaction, gapped ligase chain reaction, strand displacement
 XX CC amplification, nucleic acid sequence based amplification and
 XX CC self-sustained sequence replication. The reference material is
 XX CC particularly useful where detection of target sequences in medical or
 XX CC environmental samples is desired. AAA63609-21 represent internal
 XX CC fragments of the 16S ribosomal RNA gene. A fragment of the 16S
 XX CC ribosomal RNA gene of L. pneumophila was used to produce a reference
 XX CC material of the invention.
 XX SQ Sequence 18 BP; 5 A; 3 C; 9 G; 1 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 322 GCAGAGAGCTGTGGAGC 339
 Db 1 GGAGAGAGCTGGGACC 18
 RESULT 1191
 AAA52856
 ID AAA52856 standard; DNA; 18 BP.
 XX AC AAA52856;
 XX DT 15-SEP-2000 (first entry)
 XX DE Human CD44 antisense oligonucleotide ISIS# 18745.
 XX KW Human; CD44; cell surface adhesion receptor; cytostatic; antirheumatic;
 XX KW antiinflammatory; antiarthritic; CD44 antisense inhibition;
 XX KW hyperproliferative disorder; cancer; inflammatory disorder;
 XX KW rheumatoid arthritis; ss.
 XX OS Homo sapiens.
 XX PN WO200035935-A1.
 XX PD 22-JUN-2000.
 XX PF 14-DEC-1999; 99WO-US29576.
 XX PT

PR 17-DEC-1998; 98US-0213719.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Bennett CF, Cowsett LM;
 XX PI WPI; 2000-431564/37.
 XX DR
 XX PT New antisense compound, that inhibits the expression of human cell
 XX PT surface adhesion receptor CD44, for treating hyperproliferative
 XX PT disorders and inflammatory conditions, such as cancer and rheumatoid
 XX PT arthritis -
 XX PS Example 15; Page 77; 105pp; English.
 XX CC The present sequence is one of a large number of antisense
 XX CC oligonucleotides designed to target different regions of the human CD44
 XX CC mRNA. CD44 is a multifunctional human cell surface adhesion receptor.
 XX CC The oligonucleotides were analysed for effect on CD44 mRNA levels by
 XX CC quantitative real-time PCR analysis. Antisense oligonucleotides that
 XX CC inhibit CD44 expression can be used to treat CD44-associated conditions
 XX CC including hyperproliferative disorders, such as cancer, and inflammatory
 XX CC conditions, such as rheumatoid arthritis. The antisense compounds
 XX CC hybridise to CD44 nucleic acids, thus allowing sandwich and other assays
 XX CC to be easily constructed.
 XX CC Note: The sequence has a phosphorothioate backbone and may be either an
 XX CC oligodeoxynucleotide or a chimeric oligonucleotide containing
 XX CC 2'-methoxyethyl (2'-MOE) wings and a deoxy gap. The ISIS number given
 XX CC above corresponds to the oligodeoxynucleotide sequence.
 XX SQ Sequence 18 BP; 3 A; 3 C; 6 G; 6 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 510 GCCAGTTTGGCATTTGGG 527
 Db 1 GCCATTCTGGAATTGGG 18
 RESULT 1192
 AAZ95030
 ID AAZ95030 standard; DNA; 18 BP.
 XX AC AAZ95030;
 XX DT 15-AUG-2000 (first entry)
 XX DE Prostate cancer diagnostic marker Prol14 forward PCR primer.
 XX KW Prostate cancer; cancer specific gene; CSG; expressed sequence tag;
 XX KW EST; diagnosis; monitoring; staging; imaging; therapy; metastasis;
 XX KW marker; human; Prol14; PCR primer; ss.
 XX OS Homo sapiens.
 XX PN WO200023111-A1.
 XX PD 27-APR-2000.
 XX PF 19-OCT-1999; 99WO-US24331.
 XX PR 19-OCT-1998; 98US-0104737.
 XX PA (DIAD-) DIADEXUS LLC.
 XX PI Salceda S, Recipon H, Cafferkey R;
 XX PI WPI; 2000-339531/29.
 XX DR
 XX PT Diagnosing, staging and monitoring the presence and metastases of
 XX PT prostate cancer especially useful for treating prostate cancer

PT comprises measuring changes in cancer specific gene levels -
 PS Example 2; Page 40; 74pp; English.
 XX
 CC The present sequence is that of the forward primer used in the
 CC real-time quantitative PCR amplification of cancer specific
 CC gene Prol14 (see AAZ95010 and AAZ95011). Prol14 mRNA expression is
 CC higher in prostate than any other healthy tissues examined
 CC indicative of it being a diagnostic marker for diseases of the
 CC prostate, especially cancer. The invention provides ESTs and
 CC full-length contigs for CSGs (see AAZ9498-295017). The CSGs,
 CC polypeptides encoded by them, and antibodies that specifically
 CC bind CSG are used in claimed methods for detecting, diagnosing,
 CC monitoring, staging, imaging and treating prostate cancer.
 XX
 SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 516 TTGGCATTCTGGAGTCAA 533
 Db 1 TGGGCATCTGGGTGTCAA 18
 RESULT 1193
 ID AAZ93459/c
 XX AAZ93459 standard; DNA; 18 BP.
 AC AAZ93459;
 XX
 DT 24-JUL-2000 (first entry)
 XX
 DE TRADD antisense oligonucleotide.
 XX
 KW TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;
 KW programmed cell death; antisense; inhibition; treatment; therapy;
 KW septic shock; inflammation; cancer; antiinflammatory; human; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_binding complement (1..18)
 FT /*tag= a
 FT /note= "Complementary to bases 389-372 of the human
 FT TRADD sequence described in GENESEQ record
 FT AAZ93431"
 XX
 PN WO200012527-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US19614.
 XX
 PR 28-AUG-1998; 98US-0143212.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowser LM;
 XX
 DR WPI; 2000-237846/20.
 XX
 PT New antisense compounds that limit the expression of human TRADD
 PT protein, useful in the treatment and diagnosis of cancer, inflammation
 PT and septic shock
 XX
 PS Claim 3; Page 51; 85pp; English.
 XX
 CC The intracellular protein TRADD has been identified as a critical
 CC link between tumour necrosis factor (TNF) receptor binding and
 CC downstream activation of NF-kappa-B. Overexpression of native TRADD
 CC activates NF-kappa-B in the absence of TNF and dominant negative

CC mutants of TRADD block TNF-induced NF-kappa-B activation. A second
 CC effect of TNF in many cell types is the induction of apoptosis
 CC (programmed cell death). TRADD overexpression has been shown to
 CC mimic TNF induction of apoptosis as well. Data indicates that TRADD
 CC and other downstream effector proteins are the rate limiting step
 CC of TNF action and would therefore serve as the most efficient
 CC targets for inhibition of TNF-induced events. Antisense
 CC oligonucleotides capable of inhibiting TRADD function may therefore
 CC be useful in a number of therapeutic, diagnostic and research
 CC applications. Inhibiting expression of TRADD by contacting human
 CC cells or tissues with the antisense compound may be used to treat a
 CC disease or condition associated with TRADD expression, for example,
 CC septic shock, inflammation, or cancer. TRADD antisense
 CC oligonucleotides of varying inhibitory capabilities are listed in
 CC GENESEQ records AAZ93438-293517. The antisense oligonucleotides
 CC exhibit enhanced inhibitory capabilities when they have 2'-MOE
 CC wings and a deoxy gap.
 XX
 SQ Sequence 18 BP; 3 A; 5 C; 8 G; 2 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 625 CCAGCGCTCAGTCCCGCT 642
 Db 18 CCAGCACTCGGTCCCGCT 1
 RESULT 1194
 ID AAA10825/c
 XX AAA10825 standard; DNA; 18 BP.
 AC AAA10825;
 XX
 DT 14-JUL-2000 (first entry)
 XX
 DE G-alpha-il antisense oligonucleotide ISIS# 25743.
 XX
 KW G-alpha-il; G protein; adenylyl cyclase hormonal inhibition; tumour;
 KW plasma membrane regulation; antisense composition; treatment; prevent;
 KW delay; infection; inflammation; tumour formation; research; diagnose; ss.
 XX
 OS Synthetic.
 XX
 PN US6046321-A.
 XX
 PD 04-APR-2000.
 XX
 PF 09-APR-1999; 99US-0289377.
 XX
 PR 09-APR-1999; 99US-0289377.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Cowser LM;
 XX
 DR WPI; 2000-292434/25.
 XX
 PT New antisense compounds targeting nucleic acids encoding human
 PT G-alpha-il useful for modulating G-alpha-il expression and for treating
 PT diseases associated with G-alpha-il expression -
 XX
 PS Claim 3; Column 38; 31pp; English.
 XX
 CC Human G-alpha-il is a member of the Gi subfamily of G proteins which is
 CC involved in hormonal inhibition of adenylyl cyclase and in the
 CC regulation of plasma membrane enzymes. The expression of G-alpha-il is
 CC altered in some tumours. The present sequence is a G-alpha-il antisense
 CC oligonucleotide, which can be used to inhibit the expression of human
 CC G-alpha-il. The invention relates to antisense oligonucleotides
 CC represented in AAA10814-A10853, which can be used in the treatment of
 CC diseases or condition associated with the expression of G-alpha-il by

CC modulating the expression of G-alpha-11 in cells or tissues. The
 CC antisense compositions may also be used prophylactically, e.g. to
 CC prevent or delay infection, inflammation or tumour formation.
 CC Furthermore, the antisense oligonucleotides may also be useful in
 CC research and diagnostics, e.g. in detecting nucleic acids encoding
 CC G-alpha-11 by conjugation of an enzyme to the oligonucleotide, or
 CC radiolabelling the oligonucleotide. Kits using such detection means for
 CC detecting the level of G-alpha-11 in the sample may also be prepared.
 CC Antisense oligonucleotides, which are able to inhibit specific gene
 CC expression, are often used to elucidate the function of particular genes.
 CC These antisense compounds are also used to distinguish between functions
 CC of various members of a biological pathway.
 XX
 SQ Sequence 18 BP; 4 A; 5 C; 2 G; 7 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 250 TGAAGGACTTAGACAGGA 267
 DB 18 TGAATGACTTGGACAGAA 1

RESULT 1195

AAA05269/c
 ID AAA05269 standard; DNA; 18 BP.
 AC AAA05269;

DT 19-MAY-2000 (first entry)

XX PCR primer D-F used in Sox-2 amplicon generation.

DE PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; c-kit; Tryp-1;
 KW Pax-6; mutation detection; therapeutic target identification; mouse;
 KW mast cell growth factor; ss.

OS Mus sp.

PN US6015670-A.

PD 18-JAN-2000.

XX 14-NOV-1997; 97US-0970740.

XX 17-MAY-1996; 96US-0017824.

PR 16-MAY-1997; 97US-0857946.

XX (HEXA-) HEXAGEN TECHNOLOGY LTD.

XX Goodfellow PN;

XX WPI; 2000-181139/16.

XX Detecting mutations in selected genes, useful e.g. for identifying
 PT therapeutic targets or products, by analysing DNA in mutated embryonic
 PT stem cells without phenotypic characterization -

PS Example 6; Column 32; 66pp; English.

XX PCR primers AAA05245-A05406 are used to generate amplicons from the
 CC mouse Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Tryp-1 gene, Sry
 CC gene, MGF (mast cell growth factor) gene, c-kit gene, and the Pax-6 gene.
 CC The primers are used in a method for the identification of a mutation in
 CC a selected gene in a tissue without the prior observation of a
 CC phenotypic alteration in the mutated organism or cell. The method is used
 CC to identify mutations in a selected gene that encode products of
 CC potential therapeutic activity or that are potential targets,
 CC particularly where the gene of interest has been identified as a
 CC candidate gene by positional cloning. Other applications are determining
 CC functions of genes; detecting the range of phenotypes associated with
 CC different mutations in a particular gene and identification of

CC particular mutations. Animals containing an identified mutation are used
 CC as models for studying diseases or their treatment, and calls from them
 CC for in vitro assessment of drug action. Interbreeding of mutant mice is
 CC used to investigate genetic interaction in the overall phenotype.

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 TCCTCCAGGTGCAGAGG 50
 DB 18 TCCTTCATGTGCAGAGC 1

RESULT 1196

AAZ89730/c
 ID AAZ89730 standard; DNA; 18 BP.

XX AAZ89730;

XX 05-MAY-2000 (first entry)

XX Human RIP-1 antisense oligonucleotide ISIS# 23893.

XX RIP-1; RalBP; RLIP; antisense inhibitor; anti-inflammatory; cytostatic;
 KW anti-infective; diagnose; prevent; treatment; tumour formation; ss.

XX Homo sapiens.

XX US6020198-A.

XX 01-FEB-2000.

XX 25-SEP-1998; 98US-0161443.

XX 25-SEP-1998; 98US-0161443.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsett LM;

XX WPI; 2000-146889/13.

XX Antisense inhibition of human RIP-1 expression, useful for diagnosing,
 PT preventing and treating conditions such as inflammation -

XX Claim 3; Column 27; 26pp; English.

XX This sequence represents an antisense oligonucleotide which binds to the
 CC coding region of human RIP-1. RIP-1 (also known as RalBP1 and RLIP) is a
 CC GTPase activating protein (GAP) thought to be a downstream target of Ral.
 CC The invention relates to antisense phosphorothioate oligonucleotides with
 CC anti-infective, anti-inflammatory and cytostatic activity. The
 CC oligonucleotides are RIP-1 antisense inhibitors and are used in the
 CC diagnosis, prevention and treatment of conditions associated with RIP-1
 CC expression. Conditions associated with RIP-1 expression include various
 CC infections, inflammation and tumour formation.

XX Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 760 AGATGGCAGAACTGGACA 777
 DB 18 AGAGTGCAGAACTGGACA 1

RESULT 1197
 AAZ43284/c

ID AAZ43284 standard; DNA; 18 BP.
 XX AAZ43284;
 AC
 XX 11-FEB-2000 (first entry)
 DT
 XX Murine Sox2 gene PCR primer 7.
 DE
 XX Screening; mutation; treatment; disease; drug discovery;
 KW PCR primer; ss.
 KW
 XX Mus musculus.
 OS
 XX US5994075-A.
 XX
 XX 30-NOV-1999.
 PD
 XX
 XX 16-MAY-1997; 97US-0857946.
 PF
 XX 17-MAY-1996; 96US-0017824.
 PR
 XX (HEXA-) HEXAGEN TECHNOLOGY LTD.
 PA
 XX Goodfellow PN;
 PI
 XX WPI; 2000-038255/03.
 DR
 XX Identifying a mutation in a gene of interest in an organism useful for
 PT identifying genes encoding products which may have therapeutic benefits
 PT
 PT
 XX Example 7; Column 69-70; 70pp; English.
 PS
 XX This invention describes a novel mutational screening method based on
 CC genomic and genetic techniques to identify and characterize a mutation
 CC in a gene of interest without first selecting a phenotypic
 CC characteristic. The screening methods are useful for identifying genes
 CC encoding products which may have therapeutic benefit for treating human
 CC or animal diseases. The method can be used for the DNA mutation
 CC screening of a class or a family of genes providing a rapid assay for
 CC identifying mutant genes. The methods produce organisms which can be used
 CC for drug discovery e.g. providing a model for the study and treatment of
 CC a disease state, allow in vitro assessment of drug activity and
 CC interbreeding of mutants which allow investigation of gene interactions
 CC in the overall phenotype. A range of phenotypes associated with different
 CC mutations, and specified mutations in a gene of interest can be
 CC determined. The method can be adapted to screen for a mutation in two or
 CC more genes of interest in an organism. The methods allow mutations in a
 CC gene of interest to be identified without having to rely on matching a
 CC gene with a disease. AAZ43260-243421 represent PCR primers used in the
 CC method of the invention.
 XX
 SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 33 TCCTCCAGGTGCAGAGG 50
 Db 18 TCCTCATGTGCAGAGC 1
 RESULT 1198
 AAF89357
 ID AAF89357 standard; DNA; 18 BP.
 AC
 XX AAF89357;
 AC
 XX 10-DEC-2001 (first entry)
 DT
 XX Sample member clustering method related human DNA PCR primer #94.
 DE
 XX

KW Cluster; hierarchical clustering algorithm; population based study;
 KW clinical trial; DNA fingerprint; genetic profile analysis; PCR primer;
 KW SNP; single nucleotide polymorphism; ss.
 XX Homo sapiens.
 OS
 XX WO200129257-A2.
 PN
 XX 26-APR-2001.
 PD
 XX 20-OCT-2000; 2000WO-IB01632.
 PF
 XX 22-OCT-1999; 99US-0161231.
 PR
 XX 07-JUL-2000; 2000US-0216897.
 XX (GEST) GENSET.
 PA
 XX Schork N, Skierczynski B;
 PI
 XX WPI; 2001-316248/33.
 DR
 XX Genetic clustering by distributing members into optimal numbers of
 PT clusters determined by a hierarchical clustering algorithm or by
 PT paired-pair analysis of homozygous pairs in clusters got from
 PT non-hierarchical clustering -
 XX
 PS Claim 61; Page 93; 100pp; English.
 XX
 CC The present invention describes methods of clustering members of a
 CC sample, involving applying a hierarchical clustering algorithm to the
 CC sample members, determining the optimal number of clusters based on this
 CC and distributing the sample members into clusters using non-hierarchical
 CC clustering. The methods are useful in population based studies such as
 CC clinical trials, DNA fingerprinting and genetic profile analyses. The
 CC present sequence was used to demonstrate the method of the invention.
 XX
 SQ Sequence 18 BP; 5 A; 5 C; 3 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 865 ATGAGCCCACTCCATTG 882
 Db 1 ATGAAACCCAGTCCATTG 18
 RESULT 1199
 AAH55233/c
 ID AAH55233 standard; DNA; 18 BP.
 XX
 AC AAH55233;
 AC
 XX 03-SEP-2001 (first entry)
 DT
 XX Genomic DNA methylation parallel detection associated DNA fragment #135.
 DE
 XX DNA methylation; parallel detection; 5-unmethylated cytosine; CpG;
 KW CpNG; amplification; transcription regulation; genetic imprinting;
 KW tumorigenesis; primer; ss.
 XX
 XX Unidentified.
 OS
 XX WO200142493-A2.
 PN
 XX 14-JUN-2001.
 PD
 XX 06-DEC-2000; 2000WO-DE04381.
 PF
 XX 06-DEC-1999; 99DE-1059691.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX

PI Olek A, Piepenbrock C;
 XX WPI; 2001-381705/40.
 XX
 XX Parallel detection of the methylation pattern of many genomic DNA
 PT regions, useful for detecting aberrant methylation, includes multiple
 PT amplification of chemically modified DNA -
 XX
 XX Claim 18; Page 21; 63pp; German.
 XX
 CC This invention describes a novel method for the parallel detection of the
 CC methylation status of genomic DNA (I) which involves a (I) sample being
 CC treated chemically to convert 5-unmethylated cytosine to uracil,
 CC thymidine or some other base having hybridization behavior different from
 CC that of C, then amplifying simultaneously at least 10 different fragments
 CC (of fewer than 2 kb) using synthetic oligonucleotide (ON) primers. These
 CC primers are based on regulatory, transcribed and/or translated segments
 CC present in the sample after chemical treatment. The sequence context of
 CC all, or some, of the CpG and CpNpG motifs in the amplified products is
 CC then determined. The method is used to detect aberrant methylation
 CC patterns in the genome, these are implicated in regulation of
 CC transcription, genetic imprinting and tumorigenesis. Many target regions
 CC in the genome can be analyzed simultaneously and it is not essential to
 CC know the sequence context of all targeted regions. Primers may be
 CC designed for preferential amplification of particular segments of
 CC interest (e.g. promoters and exons).
 XX
 SQ Sequence 18 BP; 5 A; 0 C; 1 G; 12 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1080 TATTAAAAAATAAAAA 1097
 DB 18 TATTACTAAAAATAAAAA 1
 RESULT 1200
 AAH55234
 ID AAH55234 standard; DNA; 18 BP.
 XX
 XX AAH55234;
 XX
 DT 03-SEP-2001 (first entry)
 DE Genomic DNA methylation parallel detection associated DNA fragment #136.
 XX
 KW DNA methylation; parallel detection; 5-unmethylated cytosine; CpG;
 KW CpNpG; amplification; transcription regulation; genetic imprinting;
 KW tumorigenesis; primer; ss.
 XX
 OS Unidentified.
 XX
 XX WO200142493-A2.
 FN
 XX 14-JUN-2001.
 PD
 XX
 PF 06-DEC-2000; 2000WO-DE04381.
 XX
 XX 06-DEC-1999; 99DE-1059691.
 PR
 XX (EPITG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C;
 PI
 XX WPI; 2001-381705/40.
 XX
 XX Parallel detection of the methylation pattern of many genomic DNA
 PT regions, useful for detecting aberrant methylation, includes multiple
 PT amplification of chemically modified DNA -
 XX
 XX Claim 18; Page 21; 63pp; German.

XX This invention describes a novel method for the parallel detection of the
 CC methylation status of genomic DNA (I) which involves a (I) sample being
 CC treated chemically to convert 5-unmethylated cytosine to uracil,
 CC thymidine or some other base having hybridization behavior different from
 CC that of C, then amplifying simultaneously at least 10 different fragments
 CC (of fewer than 2 kb) using synthetic oligonucleotide (ON) primers. These
 CC primers are based on regulatory, transcribed and/or translated segments
 CC present in the sample after chemical treatment. The sequence context of
 CC all, or some, of the CpG and CpNpG motifs in the amplified products is
 CC then determined. The method is used to detect aberrant methylation
 CC patterns in the genome, these are implicated in regulation of
 CC transcription, genetic imprinting and tumorigenesis. Many target regions
 CC in the genome can be analyzed simultaneously and it is not essential to
 CC know the sequence context of all targeted regions. Primers may be
 CC designed for preferential amplification of particular segments of
 CC interest (e.g. promoters and exons).
 XX
 SQ Sequence 18 BP; 12 A; 1 C; 0 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1080 TATTAAAAAATAAAAA 1097
 DB 1 TATTACTAAAAATAAAAA 18
 RESULT 1201
 AAS01725/c
 ID AAS01725 standard; DNA; 18 BP.
 XX
 XX AAS01725;
 XX
 DT 12-SEP-2001 (first entry)
 DE Glucanase genomic DNA sequencing primer 1018.
 XX
 KW Glucanase; endochitinase; exochitinase; cell-wall degradation; fungus;
 KW transgenic plant; plant pathogen; bacteria; seafood waste; shell; ss;
 KW chitin; chemical modification; glucan; sequencing primer.
 XX
 OS Fusarium sporotrichoides.
 XX
 XX WO200116353-A1.
 FN
 XX 08-MAR-2001.
 PD
 XX 30-AUG-2000; 2000WO-US23802.
 PF
 XX 30-AUG-1999; 99US-0151582.
 PR 11-AUG-2000; 2000US-0224946.
 PR 28-AUG-2000; 2000US-0649747.
 XX
 XX (NOVO) NOVO NORDISK BIOTECH INC.
 PA (USDA) US SEC OF AGRIC.
 XX
 XX Okubara PA, Blechl AE, Hohn TM, Berka RW;
 PI
 XX WPI; 2001-218524/22.
 DR
 XX Fusarium nucleic acids encoding polypeptides having glucanase,
 PT endochitinase or exochitinase activity, useful for producing transgenic
 PT plants which are resistant to plant pathogens, particularly Fusarium
 PT species -
 XX
 PS Disclosure; Page 78; 216pp; English.
 XX
 CC The sequence represents a sequencing primer for DNA encoding the Fusarium
 CC fungal enzyme, glucanase. Glucanase, endochitinase and exochitinase
 CC are polypeptides with cell-wall degrading activity, derived from Fusarium
 CC fungal genes. The associated nucleic acids can be used to produce

CC transgenic plants which are resistant to plant pathogens, particularly
 CC Fusarium species. They can also be used to isolate homologous genes from
 CC fungi to obtain genes which protect host cells, including fungi, bacteria
 CC and plants against related fungal pathogens. The polypeptides, especially
 CC chitinases and glucanases, are useful for degrading seafood waste, such
 CC as shells that contain chitin, or for chemical modification of chitin or
 CC glucan.

XX SQ Sequence 18 BP; 4 A; 8 C; 2 G; 4 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 GTACTGGGTGCTGAAG 834
 DB 18 GTGCTGAGAGTCTGAAG 1

RESULT 1202

AAF61167/C
 ID AAF61167 standard; DNA; 18 BP.

XX AAF61167;

XX 18-MAY-2001 (first entry)

DE Human betal-adrenoreceptor primer #2.

XX Betal-adrenoreceptor; human; mutation; disease predisposition;
 KW cardiomyopathy; dilative; primer; ss.

XX Homo sapiens.

XX WO200111039-A2.

XX 15-FEB-2001.

XX 04-AUG-2000; 2000WO-DE02648.

XX 05-AUG-1999; 99DE-1038390.

XX (DELB-) DELBRUCK CENT MOLEKULARE MEDIZIN MAX.

XX Wallukat G, Podlowski S, Wenzel K, Mueller J;

XX WPI; 2001-202770/20.

XX New mutated gene for human betal-adrenoreceptor, useful for drug
 PT development and in genotyping for predisposition to cardiomyopathy -
 XX Disclosure; Page 6; 23pp; German.

CC This invention describes a novel human betal-adrenoreceptor gene (I)
 CC that comprises 1-7 or more mutations, excluding the sequence with the
 CC mutations Ala145Gly or Gly1165Cys. The invention also describes (1)
 CC a method for determining predisposition to disease by genotyping DNA of
 CC (i) at one or more exchanged position and comparison with a reference
 CC sequence; and (2) a new variant of the betal-adrenoreceptor (II) which
 CC include at least one of the amino acid changes Ser49Gly, Ala59Ser,
 CC Gly389Arg, Arg399Cys, His402Arg, Thr404Ala and/or Pro418Ala, but
 CC excluding the sequence with a single amino acid exchange at positions 49
 CC or 389. Genotyping of (I) is used to determine predisposition to
 CC cardiomyopathy, specifically the dilative form, also for prognosis and
 CC assessing severity of this condition. Gene (I) can be used for the
 CC following: (i) development of therapeutic agents, especially a new class
 CC of betal-adrenoreceptor (ant)agonists; (ii) construction of genes or
 CC vectors, especially for pharmaceutical development; and (iii) develop
 CC diagnostic kits, particularly for determining predisposition and
 CC individual responses to different betal-adrenoreceptor (ant)agonists,
 CC including predisposition to develop side effects and habituation.

XX SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 605 GGTGGACGTGGCCATCTC 622
 DB 18 GGTGATCGTGGCCATCGC 1

RESULT 1203

AAF94707
 ID AAF94707 standard; DNA; 18 BP.

XX AAF94707;

XX 23-MAY-2001 (first entry)

DE Rho C antisense phosphorothioate oligonucleotide SEQ ID 131.

XX Rho; GTP binding protein; phosphorothioate antisense oligonucleotide;
 KW RhoA; RhoB; RhoC; RhoG; Rac 1; cdc42; hyperproliferative condition;
 KW cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;
 KW ss.

XX Homo sapiens.

XX WO2001115739-A1.

XX 08-MAR-2001.

XX 18-AUG-2000; 2000WO-US22808.

XX 31-AUG-1999; 99US-0387341.

XX (ISIS-) ISIS PHARM INC.

XX Roberts ML, Cowser LM;

XX WPI; 2001-191677/19.

XX An antisense compound targeted to a nucleic acid molecule encoding a
 PT member of the human Rho family of small GTP binding proteins useful for
 PT treating e.g. cancer and ischaemia -

XX Example 16; Page 73; 156pp; English.

CC This invention relates to an antisense compound targeted to a nucleic
 CC acid molecule encoding a member of the human Rho family of small GTP
 CC binding proteins, where the antisense compound inhibits the expression of
 CC the member of the human Rho family. The invention includes antisense
 CC oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide
 CC sequence, AAF94645 - AAF94684 which target a RhoB nucleotide sequence,
 CC AAF94686 - AAF94725 which target a RhoC nucleotide sequence, AAF94727 -
 CC AAF94766 which target RhoG nucleotide sequence, AAF94769 - AAF94790 which
 CC target a Rac 1 nucleotide sequence and AAF94795 - AAF94809 which target
 CC cdc42 nucleotide sequence. The antisense compound is useful for treating
 CC hyperproliferative conditions, especially cancer, abnormal wound healing
 CC or clotting conditions and ischaemia/reperfusion or reoxygenation injury.
 CC The compound may also be used to diagnose the above conditions.

XX SQ Sequence 18 BP; 5 A; 8 C; 2 G; 3 T; 0 other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 614 GCCCATCTCAACACAGGC 631
 DB 1 GGCCATCTCAACACATCTC 18

RESULT 1204

AAC99280
 ID AAC99280 standard; DNA; 18 BP.
 XX
 AC AAC99280;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE Probe sequence used in probe array SEQ ID 40.
 XX
 KW Probe; probe array; probe-combined substrate; detection; ss.
 XX
 OS Synthetic.
 XX
 PN JP2000270896-A.
 XX
 PD 03-OCT-2000.
 XX
 PF 28-JAN-1999; 99JP-0019915.
 XX
 PR 28-JAN-1999; 99JP-0019915.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2001-027424/04.
 XX
 PT A preparation of a probe-combined substrate, a probe array, detection
 of a target substance, specification of the base sequence of a
 PT single-stranded nucleic acid in a sample, and determination of a target
 PT substance in a sample -
 XX
 PS Example 3; Page 17; 20pp; Japanese.
 XX
 CC This invention relates to a probe-combined substrate, a probe array, and
 a method for the detection of a target substance in a sample. The probe
 CC array can be used for detecting a target substance with high
 CC reliability. Sequences AAC99241 - AAC99305 represent probes used in an
 CC array in an example illustrating the invention.
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1025 GCTGGCGCTGGCTTTCAT 1042
 | | | | | | | | | | | | | | | | | |
 DB 1 GATGGCGCTGGCTTTCAT 18
 RESULT 1205
 AAH47615/C
 ID AAH47615 standard; DNA; 18 BP.
 XX
 AC AAH47615;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human Her-3 mRNA inhibiting antisense oligo ISIS # 19628.
 XX
 KW Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
 KW antiinflammatory; cytostatic; antibacterial; antisense; ss.
 XX
 OS Synthetic.
 XX
 OS Homo sapiens.
 XX
 PN US6277640-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 31-JUL-2000; 2000US-0630706.
 XX
 PR 31-JUL-2000; 2000US-0630706.
 XX

(ISIS-) ISIS PHARM INC.
 Bennett CF, Cowser LM;
 WPI; 2001-535134/59.
 Antisense compounds capable of modulating expression of human Her-3,
 member of epidermal growth factor family of receptor/tyrosine kinases,
 useful for preventing or delaying infection, inflammation or tumor
 formation -
 Claim 1; Column 43-44; 49pp; English.
 The invention provides antisense compounds capable of inhibiting the
 expression of human Her-3, a member of epidermal growth factor (EGF)
 family of receptor/tyrosine kinases. The antisense oligonucleotides are
 useful for inhibiting the expression of Her-3 in cells or tissues. They
 are commonly used as research reagents and in diagnostics for example, to
 elucidate the function of particular genes. The antisense compounds are
 also useful for distinguishing between functions of various members of a
 biological pathway and for research use. They are also utilized for
 diagnostics, therapeutics, prophylaxis and in kits. They are useful
 CC prophylactically, e.g. to prevent or delay infection, inflammation or
 CC tumor formation. Sequences AAH47592-47615 represent chimeric antisense
 CC phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,
 CC used for the inhibition of Her-3 mRNA expression.
 XX
 SQ Sequence 18 BP; 7 A; 3 C; 4 G; 4 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 977 TATAATCTCAGCCCTTGG 994
 | | | | | | | | | | | | | | | | | |
 DB 18 TGTAATCTCAGCACTTGG 1
 RESULT 1206
 ABX96552
 ID ABX96552 standard; DNA; 18 BP.
 XX
 AC ABX96552;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Human genomic DNA p53 codon 72 SNP primer #3.
 XX
 KW Human; allele-specific base detection; primer extension reaction;
 KW base-specific detection primer; allele-specific primer extension assay;
 KW AS; high throughput; single nucleotide polymorphism; SNP analysis;
 KW mutation detection; genetic variation; allele-specific extension;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200268694-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-GB00794.
 XX
 PR 23-FEB-2001; 2001GB-0004560.
 XX
 PR 23-FEB-2001; 2001US-0791190.
 XX
 PR 07-FEB-2002; 2002US-0071926.
 XX
 PA (PYRO-) PYROSEQUENCING AB.
 PA (DZIE/) DZIELEWSKA H.
 XX
 PI Lundeberg J, Ahmadian A, Nyren P;
 WPI; 2002-707012/76.
 XX

PT Detecting a base at a pre-determined position in a nucleic acid
 PT molecule, comprises performing primer extension reactions using
 PT base-specific detection primers in the presence of a
 PT nucleotide-degrading enzyme -
 XX
 PS Example 1; Page 26; 59pp; English.
 XX
 CC The present invention relates to a method for detecting a base at a
 CC pre-determined position in a nucleic acid molecule. The method
 CC comprises performing primer extension reactions using base-specific
 CC detection primers, each being specific for a particular base at the
 CC predetermined position. The allele-specific (AS) primer extension
 CC assay method of the invention is useful for detecting an
 CC allele-specific base at a pre-determined position in a nucleic acid
 CC molecule, for high throughput single nucleotide polymorphism (SNP)
 CC analysis, and for detecting mutations and genetic variations. The new
 CC method solves the deficiencies of previous methods by providing a
 CC method of allele-specific extension that allows accurate discrimination
 CC between matched and mismatched configurations, as well as reducing or
 CC eliminating false positive results observed in prior art. The use of
 CC two allele-specific primers increases the sensitivity by a factor of
 CC two because signals of two extensions are obtained. The present
 CC sequence represents a primer used in the examples of the present
 CC invention.
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 664 TGCAGCTGAAGTCCACAG 681
 Db 1 TCCAGATGAAGTCCACAG 18
 RESULT 1207
 ABT06253
 ID ABT06253 standard; DNA; 18 BP.
 XX
 AC ABT06253;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Synthetic DNA selling system - related oligonucleotide 58.
 XX
 KW synthetic DNA selling system; internet; ss; purchase order menu;
 KW major histocompatibility complex; MHC.
 XX
 OS Synthetic.
 XX
 PN JP2002074089-A.
 XX
 PD 12-MAR-2002.
 XX
 PF 29-AUG-2000; 2000JP-0259715.
 XX
 PR 29-AUG-2000; 2000JP-0259715.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2002-492955/53.
 XX
 XX Synthetic DNA selling system using the Internet, displays purchase
 PT order menu to orderer's terminal and initiates production of selected
 PT DNA for the successful bidder -
 XX
 PS Disclosure; Fig 5; 22pp; Japanese.
 XX
 CC The invention comprises a synthetic DNA selling system using the
 CC internet. The system displays a purchase order menu display, with the
 CC number of base sequences of DNA from which the orderer selects a DNA. The
 CC order information is transmitted to a successful bidder side server which

CC orders for production and delivery of selected synthetic DNA. The system
 CC of the invention is useful for marketing synthetic DNAs of different base
 CC sequences and concentrations according to the desire of the user,
 CC especially genes concerned with human major histocompatibility complex
 CC (MHC). Oligonucleotides ABT06196 - ABT06278 are used in the invention.
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1025 GCTGGGCGCTGGCTTCAT 1042
 Db 1 GATGGGCGCTGGCTTCAT 18
 RESULT 1208
 ABT04732
 ID ABT04732 standard; DNA; 18 BP.
 XX
 AC ABT04732;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE End-labelled probe array production method-related oligonucleotide 39.
 XX
 KW End-labelled probe array production; probe; ss; target substance capture.
 XX
 OS Unidentified.
 XX
 PN JP2002153284-A.
 XX
 PD 28-MAY-2002.
 XX
 PF 24-NOV-2000; 2000JP-0357446.
 XX
 PR 24-NOV-2000; 2000JP-0357446.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2002-552742/59.
 XX
 PT Preparation of an end-labelled probe array, for capturing a target
 PT substance -
 XX
 PS Example 1; Page 5; 25pp; Japanese.
 XX
 CC The invention comprises a method for the synthesis of an end-labelled
 CC probe array - in which part of a probe for capturing a target substance
 CC is fixed at a plural of the matrix sites on the surface of a probe array
 CC substrate. In the method of the invention the units for constituting the
 CC probe are combined successively and, at the final stage of the successive
 CC synthesis, a labelling substance is combined to the end of the probe and
 CC extended to a desired chain length. The method of the invention is useful
 CC for the production of a probe array. The present DNA sequence represents
 CC an oligonucleotide that was used in an example of the invention.
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1025 GCTGGGCGCTGGCTTCAT 1042
 Db 1 GATGGGCGCTGGCTTCAT 18
 RESULT 1209
 ABN99785
 ID ABN99785 standard; DNA; 18 BP.
 XX

AC ABN99785;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE DNA probe #39 for use in an oligonucleotide array.
 XX
 KW Human; probe; array; oligonucleotide detection; ss.
 XX
 OS Synthetic.
 XX
 FN JP2002065274-A.
 XX
 PD 05-MAR-2002.
 XX
 PF 31-AUG-2000; 2000JP-0263395.
 XX
 PR 31-AUG-2000; 2000JP-0263395.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2002-474199/51.
 XX
 PT Detection of an object component in a sample using an oligonucleotide
 as detecting probe -
 XX
 PS Example 3; Page 19; 25pp; Japanese.
 XX
 CC The invention relates to a novel method for detecting a complex formed
 between a probe and its complement. The method is used for detecting a
 complex formed between an oligonucleotide of known base sequence and a
 complementary probe, and for evaluating if the sequence is contained in
 liquid samples, or the level of binding by using the oligonucleotide as
 the detecting probe. The sequence represents a probe used in the
 invention.
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1025 GCTGGGCTGGCTTTCAT 1042
 Db 1 GATGGGCTCGGTTTCAT 18
 RESULT 1210
 ABK72477
 ID ABK72477 standard; DNA; 18 BP.
 AC
 XX ABK72477;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Sample oligonucleotide #39 for analysing nucleic acid base sequence.
 XX
 KW Nucleic acid base sequence analysis; DNA diagnosis; probe; ss.
 XX
 OS Synthetic.
 XX
 FN WO200233068-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 18-OCT-2000; 2000WO-JP07244.
 XX
 PR 18-OCT-2000; 2000WO-JP07244.
 XX
 PA (CANO) CANON KK.
 XX
 PI Yamamoto N, Okamoto T, Suzuki T;
 XX
 DR WPI; 2002-372310/40.

XX Screening an unknown base sequence at a defined site of a target
 PT single-stranded nucleic acid for use in DNA diagnosis and therapy,
 PT comprises a DNA chip, fluorescence yield and pattern-based method,
 XX
 PS Example 1; Page 13; 53pp; Japanese.
 XX
 CC The present invention relates to a method of analysing an unknown
 nucleic acid base sequence. The method comprises preparing a probe
 array, hybridising with the probe array, measuring the fluorescence
 yield in the reaction, obtaining a template pattern, producing a sample
 pattern, and comparing the sample pattern with the template pattern.
 CC The method is useful for specifying an unknown base sequence at a
 defined site of a target single-stranded nucleic acid, which is useful
 for analysing a nucleic acid base sequence. The method is applicable
 in DNA diagnosis and therapy, and is useful in medicine and biology.
 CC Measuring the fluorescence yield allows the detection of a one-base
 mismatch which can be considered to produce high detection accuracy.
 CC The hybrid pattern of the DNA probe is used so the difference in
 thermostability is less important, and the judgement on each spot can
 be reliably carried out. ABK72439-ABK72502 represent sample
 CC originucleotides used in the present invention.
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;
 Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1025 GCTGGGCTGGCTTTCAT 1042
 Db 1 GATGGGCTCGGTTTCAT 18
 RESULT 1211
 ABL59674
 ID ABL59674 standard; DNA; 18 BP.
 XX
 AC ABL59674;
 XX
 DT 18-JUL-2002 (first entry)
 XX
 DE Oligonucleotide probe SEQ ID NO:39.
 XX
 KW Simultaneous determination; probe; ss.
 XX
 OS Synthetic.
 XX
 FN JP2002065299-A.
 XX
 PD 05-MAR-2002.
 XX
 PF 31-AUG-2000; 2000JP-0263505.
 XX
 PR 31-AUG-2000; 2000JP-0263505.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2002-397662/43.
 XX
 PT Simultaneous testing of the reactivity of a sample with other different
 samples, comprises applying to the two samples to a substrate
 comprising divided matrices -
 XX
 PS Example 1; Page 11; 24pp; Japanese.
 XX
 CC The present invention describes a method for determining simultaneously
 the reactivity of a first sample with other samples, in which the second
 to the 2 plus nth (n is not less than 1) samples having different
 properties are arranged independently on a substrate, on whose surface
 the first sample is already present, and the reactivities between the
 first sample and each of the second to the 2 plus n-th samples are
 determined. Also described is a tissue sample matrix in which several

CC samples from different sources are present on each matrix divided on a
 CC substrate. The method is used for determining simultaneously the
 CC reactivity of a first sample with several other differing samples.
 CC ABL59636 to ABL59701 represent oligonucleotide probes used in an example
 CC from the present invention.

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;
 SQ

Query Match 1.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1025 GCTGGCGCTCGCTTCAT 1042
 Db 1 GATGGCGCTCGCTTCAT 18

RESULT 1212

ABL58280/C
 ID ABL58280 standard; DNA; 18 BP.

XX ABL58280;

DT 15-JUL-2002 (first entry)

DE Probe #4 used in a hybridisation assay.

KW Liquid discharge; nucleic acid analysis; gene examination; probe;
 KW hybridisation; ss.

XX Synthetic.

XX EP1188475-A2.

XX 20-MAR-2002.

XX 18-SEP-2001; 2001EP-0307932.

XX 19-SEP-2000; 2000JP-0284046.

XX 19-FEB-2001; 2001JP-0042344.

XX (CANO) CANON KK.

PI Okamoto T, Yamamoto N, Watanabe H, Suzuki T;

DR WPI; 2002-364388/40.

PT Producing probe supports for use in base sequence analysis of gene
 PT deoxyribonucleic acid, involves providing liquid discharging device for
 PT two-dimensionally arranging and fixing probe arrays on solid-phase
 PT substrates -

XX Example 5; Page 22; 53pp; English.

CC The invention relates to producing a probe support. The method involves
 CC (a) providing a liquid discharging device including reservoirs for
 CC containing liquids containing the probes and discharge nozzles connecting
 CC with the corresponding reservoirs; (b) aligning the discharge nozzles and
 CC the support relatively; and (c) discharging the liquids containing the
 CC probes from the discharge nozzles to different positions on the support.
 CC The number of reservoirs and discharge nozzles are the number of probes.
 CC The method is useful for producing probe supports useful in base sequence
 CC analysis of gene deoxyribonucleic acids (DNAs) and gene examination. The
 CC present sequence represents a probe used in a hybridisation assay.

SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 other;

Query Match

Best Local Similarity 1.2%; Score 13.2; DB 1; Length 18;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1025 GCTGGCGCTCGCTTCAT 1042
 | | | | | | | | | | | | | | | |

Db 18 GATGGCGCTCGCTTCAT 1

RESULT 1213

ABL95898

ID ABL95898 standard; DNA; 18 BP.

XX ABL95898;

DT 19-JUN-2002 (first entry)

DE Probe d for assaying nucleic acids.

KW Probe; polymorphism detection; mutation detection;
 KW disease diagnosis; microbial identification; ss.

XX Unidentified.

XX WO200208414-A1.

XX 31-JAN-2002.

XX 27-JUN-2001; 2001WO-IB01147.

XX 27-JUN-2000; 2000JP-0193133.

XX 03-AUG-2000; 2000JP-0236115.

XX 26-SEP-2000; 2000JP-0292483.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (KANK-) KANKYO ENG CO LTD.

PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;

XX WPI; 2002-195876/25.

PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids
 PT and their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification -

XX Example 12; Page 60; 152pp; Japanese.

CC The present invention relates to nucleic acid probes, which are useful
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in
 CC which a single-stranded oligonucleotide is labelled with a fluorescent
 CC substance and a quencher in a manner that the fluorescence intensity of
 CC the hybridisation reaction system is increased after completion of the
 CC hybridisation but no stem loop structure is formed. The probes are useful
 CC for assaying nucleic acids and their polymorphism and mutation,
 CC particularly useful for e.g. analytical applications, disease diagnosis
 CC and microbial identification. The present sequence was used to illustrate
 CC the invention.

SQ Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 other;

Query Match

Best Local Similarity 1.2%; Score 13.2; DB 1; Length 18;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1080 TATTATAAAAAAAAAAAAAA 1097

Db 1 TATTATAAAAAAAAAAAAAA 18

RESULT 1214

ABL54939

ID ABL54939 standard; DNA; 18 BP.

XX ABL54939;

DT 18-JUN-2002 (first entry)

XX

PT complementary base sequences against template by the LAMP method,
PT applicable in identifying genetic diseases, cancerization and
PT microorganisms -

XX Example 3; Page 66; 107pp; Japanese.

XX The invention relates to a novel method for synthesizing a target base
CC sequence-containing nucleic acids. The method comprises the formation of
CC single-stranded nucleic acids; synthesis of complementary strand by
CC annealing; and producing single-stranded nucleic acid from a target base
CC sequence by the synthesis of a complementary strand by annealing of a
CC complementary base sequence. The method is useful for synthesizing a
CC target base sequence-containing nucleic acids, which is applicable in
CC detecting SNP (single nucleotide polymorphism) in genes, identifying
CC genetic diseases, cancer and microorganisms. Such a method can be
CC easily, rapidly and freely carried out without being influenced by
CC contamination or complicated temperature control, but with improved
CC reaction specificity, high accuracy and efficiency, operable at low cost.
CC This polynucleotide sequence represents a PCR primer used in the
CC synthesizing method of the invention.

XX Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 other;

SQ

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 603 CGGTGGAGTGGCCATC 620
DB 1 CGTGTGGATGAGGCCATC 18

RESULT 1217
ABZ21485/c
ID ABZ21485 standard; DNA; 18 BP.
XX
AC ABZ21485;
XX
DT 28-MAR-2003 (first entry)
XX
DE Synthetic probe SEQ ID NO 5.
XX
KW Probe array; probe; ss.
XX
OS Synthetic.
XX
FN JP2002253251-A.
XX
PD 10-SEP-2002.
XX
PF 28-FEB-2001; 2001JP-0055972.
XX
PR 28-FEB-2001; 2001JP-0055972.
XX
PA (CANO) CANON KK.
XX
DR WPI; 2003-096532/09.
XX
PT A process for preparation of a high density array of probes, used for
PT DNA analysis and screening, comprising solution dropped on a carrier to
PT form multiple spots at high speed -
XX
PS Example 3; Page 14; 19pp; Japanese.

XX The invention relates to preparation of a probe array by high speed and
CC accurate dropping of the probe solution to improve quality of the probe
CC array. The probe array is useful in the analysis of base sequences of
CC DNA and reliable genetic screening of multiple items. The present
CC sequence is that of a probe used in examples of the invention.

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 other;

SQ

Query Match 1.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1025 GCTGGGCTGCTTCAT 1042
DB 18 GATGGGCTCGCTTCAT 1

RESULT 1218
AAQ34018/c
ID AAQ34018 standard; DNA; 13 BP.
XX
AC AAQ34018;
XX
DT 25-MAR-2003 (updated)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA420.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
FN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 337; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100.
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved in the determination of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1

RESULT 1219

AAQ34128
 ID AAQ34128 standard; DNA; 13 BP.
 XX
 AC AAQ34128;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-FEB-1993 (first entry)
 XX
 DE Sequence of a microsatellite from clone TGLA70A.
 XX
 KW PCR; selection; primers; OPRIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US00340.
 XX
 PR 15-JAN-1991; 91US-0642342.
 XX
 PA (GENM-) GENMARK.
 XX
 PI Georges M, Massey JM;
 XX
 DR WPI; 1992-284684/34.
 XX
 PT Polymorphic bovine DNA markers - used in genetic identification,
 PT gene mapping, and selective breeding
 XX
 PS Table 7; Page 382; 517pp; English.
 XX
 CC The sequence is that of a bovine microsatellite sequence obtd.
 CC by screening a library of bovine MboI DNA fragments of between
 CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
 CC One out of 50 clones cross-hybridised. Assuming independent
 CC distribution of microsatellites and MboI sites, the frequency of
 CC (T6)n > 9 microsatellites in the bovine genome is estimated at >100,
 CC 000. The sequence information for ca. 230 such bovine microsatellites
 CC is summarised in the specification and indexed herein (see below).
 CC The sequences upstream and downstream of the microsatellite sequence
 CC were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRIM). The microsatellites may be used to identify individuals,
 CC for parentage testing, and in the genetic mapping of economic trait
 CC loci, or genes involved in the determination of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AAQ33501-34437.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 13 BP; 13 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1084 AAAAAAAAAAAAAA 1096
 Db 1 AAAAAAAAAAAAAA 13
 RESULT 1220
 AAQ54278/c
 ID AAQ54278 standard; DNA; 13 BP.
 XX
 AC AAQ54278;
 XX
 DT 17-JUN-1994 (first entry)
 XX
 DE Antineoplastic oligonucleotide #5.
 XX

KW Polyborane; carborane; antineoplastic; antisense; property;
 KW 10B neutron capture; tumour therapy; antisense agent; transcription;
 KW translation; replication; ss.
 XX
 OS Synthetic.
 XX
 FH Key
 FT misc_feature
 FT 1..2
 FT /tag= a
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 2..3
 FT /tag= b
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 3..4
 FT /tag= c
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 4..5
 FT /tag= d
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 5..6
 FT /tag= e
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 6..7
 FT /tag= f
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 7..8
 FT /tag= g
 FT /note= "N-methyl-N-{2-(1,2-dicarbonidoundecaboranyl)
 FT ethyl}}]-phosphoramidate linkage"
 FT
 FT 8..9
 FT /tag= h
 FT /note= "N-butyl-N-(6-{{1-propyl}}1,12-dicarbocloso-
 FT dodecaboranyl))-hexyl-phosphoramidate linkage"
 FT
 FT 9..10
 FT /tag= i
 FT /note= "N-butyl-N-(6-{{1-propyl}}1,12-dicarbocloso-
 FT dodecaboranyl))-hexyl-phosphoramidate linkage"
 FT
 FT 10..11
 FT /tag= j
 FT /note= "N-butyl-N-(6-{{1-propyl}}1,12-dicarbocloso-
 FT dodecaboranyl))-hexyl-phosphoramidate linkage"
 FT
 FT 11..12
 FT /tag= k
 FT /note= "N-butyl-N-(6-{{1-propyl}}1,12-dicarbocloso-
 FT dodecaboranyl))-hexyl-phosphoramidate linkage"
 FT
 FT 12..13
 FT /tag= l
 FT /note= "N-butyl-N-(6-{{1-propyl}}1,12-dicarbocloso-
 FT dodecaboranyl))-hexyl-phosphoramidate linkage"
 FT
 FT 13..14
 FT /tag= k
 FT /note= "N-butyl-N-(6-{{1-propyl}}1,12-dicarbocloso-
 FT dodecaboranyl))-hexyl-phosphoramidate linkage"
 FT
 XX US5272250-A.
 XX
 XX 21-DEC-1993.
 XX
 PF 10-JUL-1992; 92US-0911218.
 XX
 PR 10-JUL-1992; 92US-0911218.
 XX
 PA (SOOD/) SOOD A.
 PA (SPIE/) SPIELVOGEL B F.
 XX
 PI Sood A, Spielvogel BF;
 XX

DR WPI; 1993-413470/51.
 XX New phosphoramidate opds. contg. poly.borane or carborane gp.
 PT including oligo-nucleotide derivs. - useful as antitumour and
 PT anti-sense agents, e.g. di:ethyl N-methyl N-(O-carboranyl methyl)
 PT phosphoramidate
 XX
 XX Claim 15; Column 15; 10pp; English.
 XX
 CC The sequences given in AAQ52474-79 are oligonucleotides which contain
 CC a polyborane or carborane group. These oligonucleotides exhibit
 CC antineoplastic and antisense properties. They may be useful in 10B
 CC neutron capture tumour therapy, and as antisense agents for blocking
 CC transcription, translation or replication of nucleic acid sequences
 CC in cells.
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1036
 Db 13 AAAAAAAAAAAAAA 1
 RESULT 1221
 AAV03386/c
 ID AAV03386 standard; DNA; 13 BP.
 XX AC AAV03386;
 XX
 DT 17-APR-1998 (first entry)
 DE Enhanced specificity anchor primer 13.
 XX
 KW Enhanced specificity anchor primer; polyA tail;
 KW gene expression difference; cell type; ss.
 XX
 OS Synthetic.
 XX
 FN WO9737045-A1.
 XX
 PD 09-OCT-1997.
 XX
 PF 02-APR-1997; 97WO-US05814.
 XX
 FR 03-APR-1996; 96US-0014666.
 XX
 PA (JOHJ) JOHNSON & JOHNSON CONSUMER PROD.
 XX
 PI Combates N, Pardinias JR, Parimoo S, Prouty SM, Stenn KS;
 XX
 DR WPI; 1997-503123/46.
 XX
 PT Method for comparing mRNA from different nucleic acid samples - by
 PT reverse transcription and amplification using oligo-T primers
 XX
 PS Disclosure; Fig 4B; 44pp; English.
 XX
 CC Primers AAV03374-421 are enhanced specificity anchor primers that bind
 CC to the polyA tail of mRNA and cDNA. The primers are of the general
 CC formula: T12MNN, where M is A, G or C and N is A, G, C or T. The primers
 CC are used in the method of the invention. This method compares the
 CC presence or level of individual mRNA molecules in at least 2 nucleic acid
 CC samples. The method comprises contacting each of the nucleic acid
 CC samples with a oligodeoxynucleotide primer that hybridises to a first
 CC site in mRNAs in the nucleic acid samples, reverse transcribing the mRNAs
 CC to which the primer hybridises to produce a population of DNA strands
 CC that are complementary to the mRNAs in the 2 samples. The amount of cDNA
 CC produced is quantified. The populations of cDNA are contacted with a
 CC second oligodeoxynucleotide primer (e.g. present primer) that hybridises

CC to a second site in the cDNA populations, the contact being performed
 CC under conditions in which the second primer hybridises with at least
 CC some of the DNA strands in the 2 populations. Portions of the DNA
 CC strands are amplified to produce a second population of amplification
 CC products. The presence or level of individual amplification products in
 CC the first and second populations of amplification products are compared
 CC and contaminating cDNAs are subtracted from the re-amplified product.
 CC The method can be used for screening differences in gene expression
 CC between various cell types or between cells in different stages of
 CC development or cells under different pharmacological conditions.
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 0 G; 11 T; 0 other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1081 AAAAAAAAAAAAAA 1093
 Db 13 AAAAAAAAAAAAAA 1
 RESULT 1222
 AAV43768/c
 ID AAV43768 standard; DNA; 13 BP.
 XX AC AAV43768;
 XX
 DT 16-NOV-1998 (first entry)
 DE Cancer associated gene primer 37.
 XX
 KW ss; cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer; primer; amplification.
 XX
 OS Synthetic.
 XX
 FN WO9837187-A1.
 XX
 PD 27-AUG-1998.
 XX
 PF 18-FEB-1998; 98WO-JP00667.
 XX
 PR 21-FEB-1997; 97JP-0052508.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 XX
 DR WPI; 1998-467552/40.
 XX
 PT Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 XX
 PS Disclosure; Page 79; 92pp; Japanese.
 XX
 CC The primers AAV43732-V43776 were to produce cancer associated gene
 CC fragments which can be used to detect cancer cells in tissue samples or
 CC biological fluids. They are detected by monitoring the change in mRNA
 CC expression as compared to normal tissue of one or more cancer-associated
 CC genes whose cDNA stringently hybridises to the nucleic acid fragments.
 CC The change in expression may be an increase or a decrease compared to
 CC normal tissue. The mRNA expression may be determined by PCR, Northern
 CC blotting or ribonuclease protection assay, or by determining the change
 CC in the amount of protein encoded by the gene(s) as compared to normal
 CC tissue, for example by using a labelled antibody recognising the
 CC protein. Detection of cancer cells for cancer diagnosis, including
 CC detection of metastatic cancer cells in tissues other than the primary
 CC tumour site.
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 0 G; 11 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1094
 Db 13 TTAATAAAAAAAAAA 1

RESULT 1223
 AAX78231/C
 ID AAX78231 standard; DNA; 13 BP.
 AC
 XX
 DT 23-AUG-1999 (first entry)
 DE MALDI-analysis oligo dt probe.
 XX
 KW Matrix-assisted laser desorption/ionisation mass spectrometry;
 KW MALDI analysis; specifically hybridised probe; identification;
 KW laser beam; probe; ss.
 XX
 OS Synthetic.
 XX
 PN WO9929898-A2.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-EP07911.
 XX
 PR 05-DEC-1997; 97EP-0121471.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Berlin K, Gut IG, Lehrach H;
 XX
 WPI; 1999-394983/33.
 XX
 PT Matrix-assisted laser desorption-ionisation mass spectrometry
 XX
 PS Disclosure; Page 29; Sipp; German.
 XX
 CC This invention describes a novel method for the analysis of specifically
 CC hybridized probes of varying mass for identification of nucleic acid
 CC molecules by matrix-assisted laser desorption/ionisation mass
 CC spectrometry (MALDI). The method comprises (i) hybridizing a nucleic
 CC acid molecule with a predetermined probe having a different mass; (ii)
 CC separating unhybridized probes, (iii) contacting the hybridized probe
 CC with a matrix, which supports desorption/ionisation of the probe by a
 CC laser beam, (iv) analyzing the hybridized probe in the surrounding
 CC matrix with an electrical conductive material consisting of a probe
 CC carrier, in a mass spectrometer and (v) determining the sequence of the
 CC nucleic acid molecule, where the position of the probe on the carrier
 CC defines the order of the hybridized nucleic acid molecule. The method
 CC is useful for the simultaneous characterization of several unknown
 CC nucleic acid molecules with a set of various probes.

Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1224
 AAX77992/C
 ID AAX77992 standard; DNA; 13 BP.
 XX

AC AAX77992;
 XX
 DT 16-AUG-1999 (first entry)
 DE Electrospray mass spectrometry oligo dt primer.
 XX
 KW Nucleic acid detection; electrospray mass spectrometry; probe;
 KW hybridisation; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9929897-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-EP07909.
 XX
 PR 12-DEC-1997; 97EP-0121983.
 XX
 PR 05-DEC-1997; 97EP-0121470.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Berlin K, Gut IG, Lehrach H;
 XX
 WPI; 1999-371355/31.
 XX
 PT Electrospray mass spectrometry for the simultaneous characterization
 PT of several unknown nucleic acid molecules
 XX
 PS Example 7; Page 23; 46pp; German.
 XX
 CC This invention describes a novel method for the analysis of specifically
 CC hybridized probes in solvents by electrospray mass spectrometry for
 CC identification of nucleic acid molecules. The method involves (i)
 CC hybridization of a nucleic acid molecule with a predetermined probe,
 CC where each probe has a different mass and separation of unhybridized
 CC probes, (ii) removal of the specifically hybridized probes in a solvent,
 CC (iii) analysis of the hybridized probe in the solvent by electrospray
 CC mass spectrometry and (iv) determination of the nucleic acid molecule
 CC through the hybridized probe. The method is useful for the simultaneous
 CC characterization of several unknown nucleic acid molecules with a set of
 CC various probes.

Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1225
 AAX32598
 ID AAX32598 standard; DNA; 13 BP.
 AC AAX32598;
 XX
 DT 09-FEB-2000 (first entry)
 DE DNA oligomer A-13S used in the preparation of an optically active probe.
 XX
 KW Probe; A-13S; YOA-13S; optically active phosphorus atom; extract; detect;
 KW fluorescent intercalated dye; identify; Genetic engineering; diagnose;
 KW treatment; phosphonic diester linkage; ss.
 XX
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 PN misc_feature 5..6
 FT /*tag= a
 FT

FT XX /note= "Location of phosphonic diester linkage"

PN EP959077-Al.

XX 24-NOV-1999.

PD XX

PF XX 06-MAY-1999; 99EP-0303552.

XX XX

PR 06-MAY-1998; 98JP-0123298.

PR 28-JUL-1998; 98JP-0212569.

XX XX

PA (TOXU) TOSOH CORP.

XX XX

PI Horie R, Ishiguro T;

XX XX

DR WPI; 2000-015275/02.

XX XX

PT Novel DNA probes used to obtain oligonucleotides which can be used for

PT identification, extraction and control of expression of target genes -

XX XX

PS Example 6; Page 10; 39pp; English.

XX XX

CC This oligomer is used in the construction of the DNA probe of the

CC invention. This sequence is used in the preparation of the DNA probe

CC YOA-138. The probe contains an optically active phosphorus atom, DNA and

CC a fluorescent intercalated dye. The invention also relates to a method

CC of selective cleavage of a trialkylsilyl ether linkage used for preparing

CC the probe. The DNA probes are used to obtain oligonucleotides which can

CC be used to identify, extract and control expression of a target gene,

CC useful in genetic engineering, clinical diagnosis and medical treatment.

CC When the probe binds to its complementary oligo-dT the fluorescence

CC intensity of the probe increases.

XX XX

SQ Sequence 13 BP; 13 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096

Db 1 AAAAAAAAAAAAAA 13

RESULT 1226

AAZ34665/C

ID AAZ34665 standard; DNA; 13 BP.

XX AC AAZ34665;

XX XX

DT 15-FEB-2000 (first entry)

XX XX

DE RT primer A0 used in DDRT-PCR identification of ERAB.

XX XX

KW Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;

KW Leydig cell; differential display RT-PCR; DDRT-PCR;

KW short chain alcohol dehydrogenase; SCAD; testis; marker;

KW spermatogenesis; primer; ss.

XX XX

OS Synthetic.

XX XX

PN WO9954347-A2.

XX XX

PD 28-OCT-1999.

XX XX

PF 19-APR-1999; 99WO-EF02610.

XX XX

PR 17-APR-1998; 98US-0082257.

XX XX

PA (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.

XX XX

PI Ivell R, Spiess A, Balvers M, Jaehner D, Hansis C;

XX XX

DR WPI; 2000-052699/04.

XX XX

PT Novel differential display reverse transcription PCR method used to

PT detect genes expressed in mutant tissues -

XX XX

PS Disclosure; Page 26; 40pp; English.

XX XX

CC This sequence represents a T1IN oligonucleotide (A0) used in a

CC novel differential display RT-PCR (DDRT-PCR) method of detecting

CC genes expressed in tissues, especially mutant tissue. The

CC oligonucleotide was used to prime a reverse transcription reaction

CC on RNA isolated from adult male w/wv azoospermic mutant mice

CC testes. 324 PCRs were performed on the resulting cDNA using 3'

CC clamp primers and variable decamer 5' primers (see AAZ34667-95).

CC Differentially expressed clones were used as probes in northern

CC hybridisation, and a novel gene product that was preferentially

CC upregulated in w/wv mouse testis was identified, and termed

CC Alzheimer-associated beta-amyloid binding protein (ERAB, see

CC AAZ32239).

XX XX

SQ Sequence 13 BP; 1 A; 0 C; 0 G; 12 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1095

Db 13 TAAAAAAAAAAAAA 1

RESULT 1227

AAH25467/C

ID AAH25467 standard; DNA; 13 BP.

XX AC AAH25467;

XX XX

DT 22-AUG-2001 (first entry)

XX XX

DE 3' PCR primer used for isolation of rubisco cDNA clones.

XX XX

KW Rubisco; small subunit gene promoter; storage reserve; seed;

KW transgenic plant; PCR primer; ss.

XX XX

OS Brassica campestris.

XX XX

PN WO200141559-Al.

XX XX

PD 14-JUN-2001.

XX XX

PF 08-DEC-2000; 2000WO-FI01081.

XX XX

PR 10-DEC-1999; 99FI-0002659.

XX XX

PA (UNIC-) UNICROP LTD.

XX XX

PI Kuvshinov V, Kanerva A, Koivu K, Pehu E;

XX XX

DR WPI; 2001-381420/40.

XX XX

PT Novel process of converting storage reserves of dicot seeds into

PT compositions comprising desired gene products, based on source-sink

PT principle -

XX XX

PS Example 2; Page 25; 54pp; English.

XX XX

CC PCR primers AAH25459-72 were used for isolation and cloning of rubisco

CC cDNA clones. The rubisco small subunit gene promoter is used in the

CC process of the invention. The specification describes a process for

CC converting storage reserves (such as protein, carbohydrate and lipid

CC reserves) in dicot plant seeds into compositions of dicot seeds into

CC compositions comprising one or more desired gene products, based on a

CC source-sink principle. The process comprises harnessing the regulatory

CC sequences of transient proteins accumulating during the initiation of
CC germination for the production of desired gene products. The method
CC provides a more feasible, cost-effective, environmentally friendly
CC process and production system for producing gene products, especially
CC proteinaceous gene products in the cotyledons of transgenic dicot
CC seeds.
XX
SQ Sequence 13 BP; 2 A; 0 C; 0 G; 11 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1094
DB 13 TTAATAAAAAAAAAA 1

RESULT 1228
AAF99662/C
ID AAF99662 standard; DNA; 13 BP.

AC AAF99662;

DT 12-JUN-2001 (first entry)

Immunostimulatory nucleic acid #778.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
immunostimulatory; tumour; viral infection; bacterial infection;
fungal infection; parasitic infection; cancer; asthma;
infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 99US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids -

XX Claim 101; Page 55; 338pp; English.

XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Th2 to a Th1 immune response and to activate immune cells.
XX Note: the present sequence may have a phosphorothioate backbone.

XX Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1

RESULT 1229

AAF99663/C

ID AAF99663 standard; DNA; 13 BP.

AC AAF99663;

DT 12-JUN-2001 (first entry)

Immunostimulatory nucleic acid #779.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
immunostimulatory; tumour; viral infection; bacterial infection;
fungal infection; parasitic infection; cancer; asthma;
infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 99US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids -

XX Claim 101; Page 55; 338pp; English.

XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Th2 to a Th1 immune response and to activate immune cells.
XX Note: the present sequence may have a phosphorothioate backbone.

XX Sequence 13 BP; 0 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1096
DB 13 AAAAAAAAAAAAAA 1

Query Match 1.3%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1099
 DB 19 TTAATAAAAAAAAAATAA 2

RESULT 866
 ABK93683/c
 ID ABK93683 standard; DNA; 19 BP.
 XX AC ABK93683;
 XX DT 26-AUG-2002 (first entry)
 XX XX Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #30.
 XX Human; ss; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 XX cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 XX pancreatic cancer; embryonic development; viral pathogenesis;
 XX autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 XX lupus erythematosus; herpes virus infection; pox virus infection;
 XX adenovirus infection; proliferative disease.
 XX OS Homo sapiens.
 XX FN WO200226968-A2.
 XX PD 04-APR-2002.
 XX PF 27-SEP-2001; 2001WO-CA01379.
 XX PR 28-SEP-2000; 2000US-0672717.
 XX XX (UYOT-) UNIV OTTAWA.
 XX XX (ABGE-) AEGERA THERAPEUTICS INC.
 XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX WPI; 2002-479562/51.
 XX PS Novel antisense inhibitor of apoptosis nucleic acid useful for
 XX enhancing apoptosis in a cell, for treating cancer and other
 XX proliferative diseases -
 XX Claim 8; Page 33; 135pp; English.

The invention relates to an inhibitor of apoptosis (IAP) antisense
 nucleic acid (I) that inhibits IAP biological activity, regardless of
 length of the antisense nucleic acid, the IAP proteins may be mouse
 or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 composition comprising a mammalian IAP antisense molecule and a method of
 enhancing apoptosis in a cell, comprising administering a negative
 regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 antisense inhibitor is useful for enhancing apoptosis in a cell in a
 mammal diagnosed with a proliferative disease. The method is useful for
 treating a patient diagnosed with a proliferative disease like cancer.
 The IAP antisense molecule is useful to treat, ameliorate, improve,
 sustain or prevent proliferative diseases (e.g. ovarian cancer,
 adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 conditions where apoptosis is involved or implicated (e.g. embryonic
 development, viral pathogenesis, autoimmune disorders, neurodegenerative
 diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 virus, pox virus and adenovirus). The present sequence is an IAP
 antisense molecule of the invention.

Sequence 19 BP; 6 A; 6 C; 3 G; 4 T; 0 other;
 Query Match 1.3%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 657 GTTCTCATGCGCTGAAG 674
 DB 18 GTTGTCTATGACGCTGTAG 1

RESULT 867
 ABL58468/c
 ID ABL58468 standard; DNA; 19 BP.
 XX AC ABL58468;
 XX DT 30-JUL-2002 (first entry)
 XX XX Mouse GPR4 cDNA amplifying primer.
 XX G protein coupled receptor; GPCR; GPR4; TDAG8; lysophosphatidylcholine;
 XX LPC; sphingosylphosphorylcholine; nootropic; antiatherosclerotic; SPC;
 XX antiarthritic; dermatological; hepatotropic; cytostatic; neuroprotective;
 XX gynaecological; OGR1; G2A; PCR; primer; ss.
 XX OS Mus sp.
 XX FN WO200224222-A2.
 XX PD 28-MAR-2002.
 XX PF 20-SEP-2001; 2001WO-US29446.
 XX PR 20-SEP-2000; 2000US-234249P.
 XX PA (CLEV-) CLEVELAND CLINIC FOUND.
 XX PI Xu Y, Zhu K;
 XX WPI; 2002-401952/43.
 XX PT Treating a disease condition e.g. Niemann-Pick disease type A and
 XX atopic dermatitis in a patient, by administering an antagonist of
 XX G-protein coupled receptors, GPR4 or TDAG8 -
 XX Example 1; Page 17; 46pp; English.

The invention provides methods for treating a disease condition in a
 patient or suppressing tumour cell growth. One method (M1) involves
 administering an antagonist of G protein coupled receptors, GPR4 or
 TDAG8, or contacting the tumour cell with an antagonist of GPR4 or TDAG8.
 A second method (M2) involves administering an agent which interferes
 with GPR4 or TDAG8 binding to lysophosphatidylcholine (LPC); A third
 method (M3) involves measuring the level of sphingosylphosphorylcholine
 (SPC) in the patient. (M1) is useful for treating a disease such as
 Niemann-Pick disease type A and atopic dermatitis, and for suppressing
 tumour cell growth in vivo in a human. (M2) is useful for treating or
 preventing an inflammatory disease conditions, atherosclerosis, liver
 cirrhosis, arthritis, endometriosis, cancer or Alzheimer's disease in a
 human. (M3) is useful for determining the progress of and detecting the
 presence of a disease condition, in particular ovarian cancer. A
 composition comprising a synthetic peptide capable of binding to SPC, is
 capable of interfering with the binding of SPC to a GPCR such as OGR1,
 G2A, GPR4 or TDAG8. The present sequence represents a PCR primer specific
 for the mouse GPR4 cDNA.

Sequence 19 BP; 2 A; 6 C; 5 G; 6 T; 0 other;
 Query Match 1.3%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACGGCCACAGCCAGCTA 20
 DB 19 ATGAGCCACAGCCAGGTA 2

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RESULT 868
ABZ84260/c
ID ABZ84260 standard; DNA; 19 BP.
XX AC ABZ84260;
XX DT 14-MAY-2003 (first entry)
XX DE Toxicologically relevant rat PCR primer #1419.
XX KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX OS Rattus sp.
XX OS Synthetic.
XX PN W02003016500-A2.
XX PD 27-FEB-2003.
XX PF 16-AUG-2002; 2002WO-US26514.
XX PR 16-AUG-2001; 2001US-313080P.
XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;
XX PI Allen P;
XX DR WPI; 2003-268322/26.
XX PT Determining a toxicological response to an agent, useful for screening
XX PT of drugs, comprises comparing the expression profile of one or more
XX PT human toxic response genes to a reference gene expression profile
XX PT indicative of toxicity -
XX PS Claim 1; Page 338; 455pp; English.
XX CC The present invention describes a method (M1) for determining a
XX CC toxicological response to an agent, which comprises comparing the
XX CC expression profile of one or more human toxic response genes to a
XX CC reference gene expression profile indicative of toxicity, and so
XX CC determining the presence of a toxic response to the agent. Also
XX CC described: (1) an array comprising one or more polynucleotides selected
XX CC from the genes corresponding to the partial sequences given in ABZ82842
XX CC to ABZ84764, or their fragments of at least 20 nucleotides, or
XX CC homologues; and (2) determining if a gene putatively identified to be a
XX CC toxic response gene plays a role on toxic response pathways by
XX CC determining the expression profile of the gene after exposure of cells
XX CC or a human subject to a known toxic pharmaceutical or industrial agent,
XX CC comprising: (a) exposing cells to an agent; (b) obtaining the test gene
XX CC expression profile for a putatively identified toxic response gene after
XX CC exposure to a known toxic pharmaceutical or industrial agent; and
XX CC (c) comparing the test profile to the expression profile of a gene with
XX CC a similar function or comparing the test profile to the expression
XX CC profile of that gene after exposure to other known toxic compounds. The
XX CC methods are useful for predicting and determining toxicological responses
XX CC on a cellular, organ or system level. The arrays comprising the human
XX CC genes are useful for toxicological screening of drugs, pharmaceutical
XX CC compounds and chemicals.
XX SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;
Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 852 CCCCCCACTGGTGATGAG 869
|||||
Db 19 CCCCCCACTGGTGAGAG 2
|||||

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RESULT 869
AAQ53923
ID AAQ53923 standard; DNA; 20 BP.
XX AC AAQ53923;
XX DT 25-MAR-2003 (updated)
XX DT 21-JUN-1994 (first entry)
XX DE TYR 1 PCR primer for amplifying TYR locus used in detection method.
XX KW PCR; polymerase chain reaction; detection; amplification; ASPE;
XX KW allele specific primer extension; discrimination; ss.
XX OS Synthetic.
XX PN W09325563-A1.
XX PD 23-DEC-1993.
XX PF 17-JUN-1992; 92WO-US05133.
XX PR 17-JUN-1992; 92AU-0022511.
XX PR 17-JUN-1992; 92WO-US05133.
XX PA (CITY ) CITY OF HOPE.
XX PI Wallace RB;
XX DR WPI; 1994-007441/01.
XX PT New primer for detecting specific target nucleic acid in sample -
XX PT has 3' end complementary to target which is adjacent to
XX PT nucleotide and 5' end complementary to preselected sequence
XX PS Example 2; Page 11; 40pp; English.
XX CC Two primers TYR 1 and 2 (AAQ53923-24) were used to amplify the TYR
XX CC locus for use as a template. An allele specific primer (AAQ53925) was
XX CC then used to amplify the template molecule, the first base
XX CC incorporated into the extension products being radioactively
XX CC labelled. Individuals homozygous for the TYR allele gave two
XX CC extension products. The extension products for the allele gave two
XX CC by hybridisation with one synthetic oligonucleotide to which the 5'
XX CC end of the allele specific primer was made complementary. See
XX CC AAQ53926-47 for grid oligonucleotides.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 510 GCCAGTTTGCAATTGGG 527
|||||
Db 1 GCAAGTTTGCTTTGGG 18
|||||
RESULT 870
AAZ05409/c
ID AAZ05409 standard; DNA; 20 BP.
XX AC AAZ05409;
XX DT 07-OCT-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX KW paratrachoma; inclusion conjunctivitis; genital disease; perinephritis;
XX KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;

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KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX Synthetic.

OS Chlamydia trachomatis.

XX WO9928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98WO-IB01939.

XX 04-NOV-1998; 98US-0107077.

XX 28-NOV-1997; 97FR-0015041.

XX 17-DEC-1997; 97FR-0016034.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis

XX Disclosure; Page 1769; 1755pp; English.

XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAZ36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal urethritis, epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis; pneumonia in breast feeding infants; CC and venereal lymphogranulomatosis. The polypeptides of the CC invention may be of use in treating these diseases.

XX Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 5.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 269 CACCTTCAGAAAGTTGTT 286

Db 20 CTCCTTCAGAAAGTTGTT 3

RESULT 871

AAAX34805

ID AAX34805 standard; DNA; 20 BP.

AC AAX34805;

XX 06-JUL-1999 (first entry)

DE Human ZSIG-11 DNA amplifying primer ZC11874.

XX Secretory protein; ZSIG-11; ligand polypeptide; testis; endoprotease;

XX Prohormone convertase; fertility; therapeutic; human; PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9916870-A1.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-US20449.

XX 19-MAY-1998; 98US-0085966.

XX 29-SEP-1997; 97US-0060327.

PR 29-SEP-1997; 97US-0939897.

PR 19-MAY-1998; 98US-0081310.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO;

XX WPI; 1999-263692/22.

XX Polynucleotide encoding a human secretory protein, ZSIG-11.

XX Example 1; Page 106; 113pp; English.

XX The invention relates to a human secretory protein, ZSIG-11. Host cells containing a vector comprising the ZSIG-11 nucleic acid are used for the recombinant expression of the protein. ZSIG-11 is a novel ligand polypeptide and specific antibodies can be used to detect its presence in a biological sample. Probes derived from ZSIG-11 nucleotide sequences can also be used in detection of ZSIG-11 RNA. ZSIG-11 is expressed at high levels in testis, and could be used to identify/study prohormone convertases or endoproteases that exhibit testis specificity. Antagonists, including antibodies, are useful for inhibiting or eliminating the function of ZSIG-11. It is possible that ZSIG-11 and its antagonists will be useful as fertility inducing therapeutics. CC Sequences AAX34800-21 represent PCR primers for amplifying the ZSIG-11 DNA.

XX Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 5.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 409 TCCAGCAGGCTCTCGGC 426

Db 1 TCCAGCAGACTCTCCAGC 18

RESULT 872

AAAX5978/c

ID AAX5978 standard; DNA; 20 BP.

XX AAX5978;

XX 05-SEP-2000 (first entry)

XX Human G713 PCR primer SEQ ID NO:17.

XX Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia; biallelic marker; polymorphism; central nervous disease; detection; neuroleptic; G713 gene expression inhibitor; genotyping; PCR primer; brain disorder; psychiatric disorder; bipolar disorder; ss.

XX Homo sapiens.

XX WO200022122-A2.

XX 20-APR-2000.

XX 12-OCT-1999; 99WO-IB01730.

XX 13-OCT-1998; 98US-0103955.

XX 30-OCT-1998; 98US-0106457.

XX (GEST) GENSET.

XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen D, Essioux L;

XX WPI; 2000-317979/27.

XX Novel polynucleotide of human G713 gene useful for diagnosis and prophylactic treatment of brain, psychiatric disorders like schizophrenia and bipolar disorders -

XX Disclosure; Page 26; 271pp; English.

XX The present invention describes an isolated, purified or recombinant

CC polynucleotide (PN) (I) comprising a contiguous span of 8 to 50

CC nucleotides, where the span includes a G713 or chromosome 13q31-q33

CC related biallelic marker. (I) has neuroleptic activity and can be used

CC as a G713 gene expression inhibitor. (I) can be used genotyping to

CC estimate the frequency of an allele of a G713 or chromosome 13q31-q33

CC related biallelic marker in a population, and of a haplotype for a set

CC of biallelic markers in a population. (I) is also useful in detecting

CC an association between a haplotype and a trait. The frequency is used

CC for detecting an association between a genotype and a trait being

CC schizophrenia. The genotype is used to determine whether an individual

CC is at risk of developing schizophrenia. (I) can also be used as a

CC medicament against several disorders preferably brain, psychiatric

CC disorders such as schizophrenia and bipolar disorder. Early

CC identification of risk of developing schizophrenia is possible, which

CC would enable early and/or prophylactic treatment. AAA55964 to AAA55966

CC represent human G713 genomic DNA sequences; AAA55967 encodes the human

CC G713 protein AAY90362; AAA55968 encodes the murine G713 protein

CC AAY90363; AAA55992 to AAA56030 represent human chromosome 13q31-q33 locus

CC biallelic markers A12 to A49; AAA55969 to AAA55991, and AAA56031 and

CC AAA56032 represent PCR primers used in the exemplification of the present

CC invention.

XX Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 other;

SQ Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 5.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1079 CTATTAAAAA AAAA 1096

Db 18 CTGTCAAAAA AAAA 1

RESULT 873

AAA15595/c

ID AAA15595 standard; DNA; 20 BP.

XX AAA15595;

AC AAA15595;

XX 01-AUG-2000 (first entry)

DT Reverse PCR primer for hPMP70 gene amplification.

DE PCR primer; adrenoleukodystrophy; 4-phenyl butyrate; 4-PBA; X-ALD;

XX peroxisome proliferation; fatty acid reduction; treatment; human;

KW peroxisomal membrane half-transporter protein; hPMP70; ss.

XX Homo sapiens.

OS WO200018394-A1.

XX 06-APR-2000.

XX 28-SEP-1999; 99WO-US22415.

XX 28-SEP-1998; 98US-0102186.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Smith KD;

XX WPI; 2000-292995/25.

XX Novel method for treating adrenoleukodystrophy comprises administering

XX an agent which causes peroxisome proliferation -

XX Example 7; Page 23; 50pp; English.

XX This sequence represents a PCR primer used to amplify the hPMP70 gene

CC that encodes a peroxisomal membrane half-transporter protein. The PCR

CC product is used in a method for testing the effect of 4-Phenyl butyrate

CC (4-PBA) treatment on cells derived from patients with X-linked

CC adrenoleukodystrophy (X-ALD). The invention relates to a treatment for a

CC patient with adrenoleukodystrophy. The treatment comprises administering

CC an agent which causes peroxisome proliferation (e.g. 4-PBA). Peroxisome

CC proliferation causes a reduction in the level of C24:0 or C26:0 fatty

CC acids in the central nervous system of the patient. Adrenoleukodystrophy

CC is associated with defective peroxisomal beta-oxidation of saturated long

CC chain fatty acids. The methods are useful for treating a patient with

CC adrenoleukodystrophy, and screening for candidate therapeutic agents for

XX treating adrenoleukodystrophy.

SQ Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 5.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 CCAGTTTGGCATTGGGA 528

Db 19 CCAGTTTGGCATTGGGA 2

RESULT 874

AAA15597/c

ID AAA15597 standard; DNA; 20 BP.

XX AAA15597;

AC AAA15597;

XX 01-AUG-2000 (first entry)

DT Reverse PCR primer for mPMP70 gene amplification.

DE PCR primer; adrenoleukodystrophy; 4-phenyl butyrate; 4-PBA; X-ALD;

XX peroxisome proliferation; fatty acid reduction; treatment; mouse;

KW peroxisomal membrane half-transporter protein; mPMP70; ss.

XX Mus sp.

OS WO200018394-A1.

XX 06-APR-2000.

XX 28-SEP-1999; 99WO-US22415.

XX 28-SEP-1998; 98US-0102186.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Smith KD;

XX WPI; 2000-292995/25.

XX Novel method for treating adrenoleukodystrophy comprises administering

XX an agent which causes peroxisome proliferation -

XX Example 7; Page 23; 50pp; English.

XX This sequence represents a PCR primer used to amplify the mPMP70 gene

CC that encodes a peroxisomal membrane half-transporter protein. The PCR

CC product is used in a method for testing the effect of 4-Phenyl butyrate

CC (4-PBA) treatment on cells derived from mice with X-linked

CC adrenoleukodystrophy (X-ALD). The invention relates to a treatment for a

CC patient with adrenoleukodystrophy. The treatment comprises administering

CC an agent which causes peroxisome proliferation (e.g. 4-PBA). Peroxisome

CC proliferation causes a reduction in the level of C24:0 or C26:0 fatty

CC acids in the central nervous system of the patient. Adrenoleukodystrophy

CC is associated with defective peroxisomal beta-oxidation of saturated long

CC chain fatty acids. The methods are useful for treating a patient with

CC adrenoleukodystrophy, and screening for candidate therapeutic agents for

XX treating adrenoleukodystrophy.

SQ Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 5.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 511 CCAGTTTGGCATTGGGA 528
 ||||| ||||| ||||| |||||
 Db 19 CCAGTTTGGCATTGGGA 2
 RESULT 875
 AAF74118/C
 ID AAF74118 standard; DNA; 20 BP.
 XX AC
 XX AAF74118;
 DT 30-APR-2001 (first entry)
 DE Primer #52.
 XX Solute carrier family 6 neurotransmitter transporter; serotonin 4;
 KW SLC6A4; genotyping; allele specific oligonucleotide; ss.
 XX Homo sapiens.
 OS
 XX WO200109161-A1.
 PN 08-FEB-2001.
 XX 31-JUL-2000; 2000WO-US20638.
 PF 29-JUL-1999; 99US-0146290.
 PR (GENA-) GENAISSANCE PHARM INC.
 PA Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
 PI WPI; 2001-123317/13.
 DR New isolated polynucleotide comprising a polymorphic variant for the
 PT solute carrier family 6 neurotransmitter transporter, serotonin member
 PT 4 gene for identifying drugs for treating disorders related to
 PT expression of the protein -
 XX Example 1; Page 36; 152pp; English.
 XX The present invention relates to a polymorphic variant of a reference
 CC sequence for the solute carrier family 6 neurotransmitter
 CC transporter, serotonin member 4 (SLC6A4) gene or a fragment of it
 CC or a sequence complementary to the first sequence.
 CC The invention is used in producing a recombinant organism
 CC that can be used to express SLC6A4 for protein structure analysis and
 CC binding studies. A composition comprising a genotyping oligonucleotide
 CC is used to detect a polymorphism in the SLC6A4 gene.
 XX Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 5.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 991 TTGGAGTCTGAGGCTGG 1008
 ||||| ||||| ||||| |||||
 Db 19 TTGGAGTCTGAGGCTGG 2
 RESULT 876
 AAF55880/C
 ID AAF55880 standard; DNA; 20 BP.
 XX AC
 XX AAF55880;
 XX

DT 12-APR-2001 (first entry)
 XX Linker #5.
 DE Vaccine; immunostimulator; interleukin-2; IL-2; ss.
 KW Unidentified.
 XX WO200104271-A2.
 PN 18-JAN-2001.
 XX 12-JUL-2000; 2000WO-US19042.
 PF 13-JUL-1999; 99US-0143425.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Collins PL, Bukreyev A, Murphy BR, Whitehead SS;
 PI WPI; 2001-091926/10.
 DR Recombinant respiratory syncytial virus (RSV) incorporating a
 XX heterologous polynucleotide encoding an immune modulatory molecule is
 PT used as a vaccine to provide an immune response to RSV -
 PT Disclosure; Page 27; 154pp; English.
 PS The present invention relates to an infectious recombinant Respiratory
 CC Syncytial Virus (RSV), comprising a recombinant RSV genome or antigenome,
 CC incorporating a heterologous polynucleotide encoding an immune modulatory
 CC molecule (e.g. interleukin-2; IL-2), a major nucleocapsid protein,
 CC nucleocapsid phosphoprotein, large polymerase protein and a RNA
 CC polymerase elongation factor. The RSV elicits a protective immune
 CC response to RSV in a vaccinated host. The present sequence is a linker
 CC used in the construction of the RSV of the present invention.
 XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 5.1e-02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 157 CATACTTGACCATCCCG 174
 ||||| ||||| ||||| |||||
 Db 20 CATATTGCCCATCCCG 3
 RESULT 877
 AAC92901
 ID AAC92901 standard; DNA; 20 BP.
 XX AAC92901;
 XX 27-MAR-2001 (first entry)
 DT Human P13 kinase p55 gamma antisense oligonucleotide, SEQ ID NO:84.
 DE Human phosphatidylinositol 3-kinase p55 gamma regulatory subunit;
 KW P13 kinase p55 gamma; p55-gamma; p55-gamma; PIK3R3; p55PIK;
 KW signal transduction; downstream effector; receptor tyrosine kinase;
 KW insulin receptor; IR; insulin-like growth factor receptor; IGFIR;
 KW cell growth; differentiation; apoptosis; developmental regulation;
 KW alternative splicing; tumour formation; cancer; inflammation;
 KW infection; expression inhibition; phosphorothioate;
 KW antisense oligonucleotide; ss.
 XX Homo sapiens.
 OS US6165790-A.
 XX 26-DEC-2000.
 PD XX

PT Novel isolated HY2 family bilin reductase having bilin reductase
PT activity, useful for converting biliverdin to phytyobilin, and for
PT producing a photoactive holophytochrome and/or phytofluor -
XX PS Example 1; Page 49; 102pp; English.

XX CC The present sequence is that of a primer that was used, with the
CC primer given in ABA91743, in the PCR amplification of the cleaved
CC amplified polymorphic sequence (CAPS) marker CMZB10.18 of chromosome
CC 3 of Arabidopsis thaliana. The primer pair includes a Ddel
CC restriction endonuclease site. An hy2-1 mutant of ecotype
CC Landsberg erecta was outcrossed with wild-type ecotype Columbia,
CC and a mapping population was selected from F2 families with a long
CC hypocotyl phenotype. PCR primer pairs (see ABA91735-48) for 7 CAPS
CC markers were used in a map-based cloning of the HY2 gene. The HY2
CC locus was initially mapped to an interval of about 66 kb between the
CC markers CMZB10 and CF3124. Fine mapping localised the HY2 gene (see
CC ABA91766) to 2 overlapping bacterial artificial chromosome clones,
CC MZB10.18 and F3124.1. The HY2 gene encodes a ferredoxin-dependent
CC biliverdin reductase, phytychromobilin synthase (see AAM50863), that
CC is related to a family of proteins found in oxygenic photosynthetic
CC bacteria. HY2 is an example of HY bilin reductases of the
CC invention, which are useful e.g. for the conversion of biliverdin
CC to phytyobilin and the assembly of holophytochromes or phytofluors.
XX SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 309 CATGGGAAAGACTGTCAGA 326
Dd 2 CATGGGAAAGTCTGCAA 19

RESULT 880

ID ABX50049 standard; DNA; 20 BP.
XX AC ABX50049;
XX DT 13-FEB-2003 (first entry)
XX DE Thale cress HY2 DNA PCR primer #10.
XX KW Thale cress; PCR: primer; ss; nucleus; phytyochrome; apoprotein;
KW cytoplasm; heterologous transactivator; heterologous repressor;
XX light response.
XX OS Arabidopsis thaliana.
XX PN WO200297137-A1.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US17266.
XX PR 29-MAY-2001; 2001US-294463P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Lagarias JC, Kochi T, Frankenberg N, Gambetta GA, Montgomery BL;
XX WPI; 2003-041421/03.
XX DR

XX PT Transporting a polypeptide into the nucleus of a cell comprises using
PT light to transport a polypeptide attached to the apoprotein component
PT of a phytyochrome into the nucleus -
XX Example 1; Page 53; 102pp; English.

XX CC The invention relates to a method for transporting a polypeptide into the

CC nucleus of a cell, comprising expressing a phytyochrome comprising the
CC polypeptide attached to the apoprotein component of the phytyochrome in a
CC cell, and exposing the cell to light where the phytyochrome migrates from
CC the cytoplasm of the cell into the nucleus which transports the
CC polypeptide into the nucleus. The invention also relates to regulating a
CC phytyochrome containing a heterologous transactivator or repressor
CC attached to an apoprotein component of the phytyochrome in a cell, and
CC exposing the cell to light where the phytyochrome migrates from the
CC cytoplasm of the cell into the nucleus and the transactivator or
CC repressor alters expression of a gene in the nucleus. The methods are
CC used to transport a polypeptide into the nucleus of a cell or to regulate
CC the transcription of a gene in response to light. This sequence
CC represents a PCR primer used to amplify DNA used in the scope of the
CC invention.

XX SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 309 CATGGGAAAGACTGTCAGA 326
Dd 2 CATGGGAAAGTCTGCAA 19

RESULT 881

AAQ24704/C
ID AAQ24704 standard; DNA; 21 BP.
XX AC AAQ24704;
XX DT 25-MAR-2003 (updated)
DT 17-DEC-2001 (updated)
DT 10-NOV-1992 (first entry)
XX V-beta-a primer.
XX KW Inv(7); PCR; polymerase chain reaction; ataxiatelangiectasia; AT;
KW lymphoid malignancy; pesticide; herbicide; Nijmegen breakage syndrome;
XX ss.
XX OS Synthetic.
XX PN USN7683685-N.
XX PD 18-FEB-1992.
XX PF 11-APR-1991; 91US-0683685.
XX PR 11-APR-1991; 91US-0683685.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX PI Kirsch IR, Lipkowitz S, Stern MH;
XX WPI; 1992-166775/20.
XX PT Identifying individuals at increased risk of lymphoid leukemia
PT and lymphoma - using DNA from immune receptor locus capable of
PT displaying genomic instability
XX PS Disclosure; Page 15; 55pp; English.
XX CC The sequences given in AAQ24701-Q24713 are a set of PCR primers which
CC are complementary to a sequence within a 2000bp inversion of chromosome
CC 7. This inversion (inv(7)(p14q35)) is found in normal people but
CC patients suffering from the disease ataxiatelangiectasia (AT) have a
CC 70-100 fold increase of the T-lymphocyte specific inversion inv(7).
CC Using these sequences a screening test has been developed which can
CC accurately measure lymphocyte-specific genomic instability and by
CC extrapolation thus identifies individuals at increased risk for the

CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
 CC disease, and graft versus host disease. The method can be used to
 CC remove malignant cells from bone marrow transplants. AAZ25912-Z26825
 CC represent human polymorphic sites described in the method of the
 CC invention.

XX
 SQ Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 5.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAA 1100
 |||||
 Db 4 TAACATAAAAA 21

RESULT 884
 AAX60141
 ID AAX60141 standard; DNA; 21 BP.
 XX
 AC AAX60141;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE PCR primer used to amplify Mycoplasma hyopneumoniae P102 protein DNA.
 XX
 KW P102 protein; vaccine; antigen; diagnosis; swine; immunisation;
 KW enzootic pneumonia; PCR primer; ss.
 XX
 OS Synthetic.

XX
 PN WO9926664-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 24-NOV-1998; 98WO-US25044.
 XX
 PR 26-NOV-1997; 97US-0066565.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Hsu T, Minion FC;
 XX
 DR WPI; 1999-357741/30.
 XX
 PT Recombinant antigenic Mycoplasma hyopneumoniae protein
 XX
 PS Example 2; Page 23; 45pp; English.

XX
 CC PCR primers AAX60140-41 were used to amplify DNA encoding a Mycoplasma
 CC hyopneumoniae P102 protein clone. The P102 protein and its fragments
 CC are used in vaccines to protect against enzootic pneumonia,
 CC particularly in swine. Recombinant P102 polypeptides may be used as
 CC antigens for diagnostic purposes to determine whether or not a
 CC biological test sample contains M. hyopneumoniae antigens or
 CC antibodies. The P102 polypeptides or DNA sequences may also be used
 CC for immunising or protecting non-human animals, preferably swine,
 CC against M. hyopneumoniae infections, particularly enzootic pneumonia.

XX
 SQ Sequence 21 BP; 8 A; 2 C; 5 G; 6 T; 0 other;
 Query Match 1.3%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 5.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 905 TTTTAAGTGAAGACAC 922
 |||||
 Db 1 TTGTAAGTGAAGACAC 18

RESULT 885
 ABS97869/c

ID ABS97869 standard; DNA; 21 BP.
 XX
 AC ABS97869;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human UDP-glucuronosyl transferase 24B gene PCR primer #6.
 XX
 KW Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 O2E; CYP450O2E1; LTF;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile;
 KW STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological.

XX Homo sapiens.

XX WO200257410-A2.

XX 25-JUL-2002.

XX 28-NOV-2001; 2001WO-US44838.

XX 28-NOV-2000; 2000US-0724389.

XX (DNAS-) DNA SCI LAB INC.

XX Guida M, Hall J;

XX WPI; 2002-698522/75.

XX Isolated nucleic acid molecules having polymorphisms in known human
 PT genes e.g. cytochrome P450 and cathepsin S useful as genetic linkage
 PT markers for locating, identifying and characterizing the genes
 PT responsible for disorder-related traits -

XX Example 18; Page 133; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 O2E1 (CYP450O2E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase
 CC activating protein (FLAP), glutathione-S-transferase 12 (GST12),
 CC histamine-N-methyl transferase (HNMT), kallikrein 2 (KLK2), nicotinamide
 CC -N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance
 CC 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated
 CC protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine
 CC muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or
 CC CHMR5) sequence. The polymorphisms in the human genes cited in the
 CC invention are useful as genetic linkage markers for locating and
 CC characterising the genes that are responsible for specific traits within
 CC the genome and eventually identifying the genes responsible for a
 CC variety of disorder-related traits as a result of their e.g.,
 CC overexpression, constitutive expression, mutation or underexpression,
 CC which may be used in diagnosing and/or treating the disorders. The
 CC nucleic acid molecules comprising the polymorphic sequences contained
 CC in CYP450A1, CYP450A2, CYP450O2E1, ARNT, EPHX2, GST12, NNMT, NQO2,

CC	NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful
CC	for screening individuals for altered drug metabolism. The polymorphic
CC	sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may
CC	also be used to screen individuals for susceptibility to cancer.
CC	Polymorphic sequences in ADRL1 or CHMR2 are used to screen for altered
CC	cardiovascular function, in COX2 for altered susceptibility to
CC	colorectal tumours, in DBI or CHMR1 for altered central nervous system
CC	function, in FIAP and HNMT for altered pulmonary, immunological or
CC	haematological function, in KLK2 for altered serine protease activity in
CC	the prostate, in LTF for altered immunological or haematological
CC	function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral
CC	nervous system function. The present sequence represents a PCR
CC	primer used to amplify the sequences of the invention.
XX	
XX	Sequence 21 BP; 3 A; 1 C; 4 G; 13 T; 0 other;
XX	
XX	Query Match 1.3%; Score 14.8; DB 1; Length 21;
XX	Best Local Similarity 88.9%; Pred. No. 5.3e+02;
XX	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX	
Qy	1079 CTATTAAAAA 1096
Db	20 CTCCTCAAAAAA 3
XX	
XX	RESULT 886
XX	ABK51692/C
ID	ABK51692 standard; DNA; 21 BP.
XX	
AC	ABK51692;
XX	
DT	30-JUL-2002 (first entry)
XX	
DE	Human corticotropin releasing hormone (CRH) antisense PCR primer.
XX	
XX	Human; nuclear receptor; NURR; inflammatory immune disease; arthritis;
KW	corticotropin releasing hormone; receptor; CRH; rheumatoid arthritis;
KW	chronic inflammatory joint disease; psoriatic arthritis; thyroiditis;
KW	sarcoid arthritis; ulcerative colitis; PCR; primer; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO200187923-A1.
PD	
PD	22-NOV-2001.
XX	
PF	11-MAY-2001; 2001WO-US15311.
XX	
PR	12-MAY-2000; 2000US-203645P.
XX	
XX	(BAYU) BAYLOR COLLEGE MEDICINE.
PA	
PI	Murphy E, Conneely OM, Fitzgerald O, Bresihan B;
XX	
DR	WPI; 2002-075311/10.
XX	
PT	Treating inflammatory immune disease such as arthritis, comprises
PT	suppressing expression level of NURR subfamily of nuclear transcription
PT	factors, or corticotropin releasing hormone receptor -
XX	
PS	Example 27; Page 84; 123pp; English.
XX	
CC	The present invention relates to a new method of treating an organism
CC	for an inflammatory immune disease. The method of the invention comprises
CC	reducing expression of a NURR subfamily nucleic acid sequence or
CC	corticotropin releasing hormone (CRH) receptor nucleic acid sequence,
CC	inhibiting transcriptional activity of a NURR superfamily member/CRH
CC	receptor amino acid sequence, or reducing the level of NURR superfamily
CC	member/CRH receptor sequence. The method is useful for treating an
CC	organism for an inflammatory immune diseases such as chronic inflammatory
CC	joint disease, preferably arthritis, selected from rheumatoid arthritis,
CC	psoriatic arthritis and sarcoid arthritis, ulcerative colitis and
CC	thyroiditis. The method is also useful for screening a compound that

CC	interferes with interaction of a NURR subfamily polypeptide with a
CC	ligand, or identifying a compound for the treatment of an inflammatory
CC	immune response. The agonist of the invention is useful for inhibiting
CC	transcriptional activity of nuclear receptor polypeptide and the
CC	antagonist is useful for decreasing the expression of a NURR subfamily
CC	member. The present nucleic acid sequence represents the human
CC	corticotropin releasing hormone (CRH) antisense PCR primer that was used
CC	in the methods of the invention for amplification of human CRH.
XX	
XX	Sequence 21 BP; 8 A; 3 C; 8 G; 2 T; 0 other;
XX	
XX	Query Match 1.3%; Score 14.8; DB 1; Length 21;
XX	Best Local Similarity 88.9%; Pred. No. 5,3e+02;
XX	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps
QY	983 CTCAGCCCTTGGAGTCT 1000
DB	
DB	21 CTCAGCCCTTGGATTCT 4
RESULT 887	
ABN87920/C	
ID	ABN87920 standard; DNA; 15 BP.
XX	
AC	ABN87920;
XX	
DT	12-AUG-2002 (first entry)
XX	
DE	Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
XX	
XX	Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;
KW	gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
KW	primer; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	misc_feature 14
FT	/*tag= a
FT	/note= "polymorphic base"
XX	
PN	WO200242320-A2.
XX	
PD	30-MAY-2002.
XX	
XX	13-NOV-2001; 2001WO-US46473.
PF	
XX	
PR	10-NOV-2000; 2000US-247202P.
XX	
PA	(GENA-) GENAISANCE PHARM INC.
XX	
PI	Bieglecki KM, Sanchis A, Sausker EA, Sun X;
XX	
DR	WPI; 2002-471719/50.
XX	
PT	New genetic variants of Glutathione reductase isogenes, useful for
PT	improving efficiency and reliability in drug development for treating
PT	hemolytic anemia -
XX	
PS	Claim 14; Page 14; 137pp; English.
XX	
CC	The present invention describes genetic variants of the human glutathione
CC	reductase (GSR) gene (1). (1) has antianaemic activity and can be used in
CC	gene therapy. (1) can be used in screening for drugs targeting (1) that
CC	are useful for treating haemolytic anaemia. Methods from the present
CC	invention can be used: for improving the efficiency and reliability of
CC	several steps in the discovery and development of drugs for treating
CC	diseases associated with GSR activity; for haplotyping, which is also
CC	used by the pharmaceutical research scientist to validate GSR as a
CC	candidate target for treating a specific condition or disease predicted
CC	to be associated with GSR activity, e.g. haemolytic anaemia, and in the
CC	design of clinical trials for treating a specific condition of disease
CC	associated with GSR activity; and/or screening compounds targeting GSR

CC (I) is useful in studying the expression and function of GSR, and in
 CC expressing GSR protein for use in screening for candidate drugs to treat
 CC diseases related to GSR activity. (I) is also useful in studying the
 CC effect of the variation on the biological activity of GSR as well as on
 CC the binding affinity of candidate drugs targeting GSR for the treatment
 CC of haemolytic anaemia. The present sequence represents an allele specific
 CC oligonucleotide (ASO) primer for the human GSR gene, which is given in
 CC the amplification of the present invention.
 CC N.B. The polymorphic base (showing a single nucleotide polymorphism) in
 CC the ASO primer is shown using an IUPAC ambiguity code (as given in the
 CC present invention).
 XX Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 1 other;

Query Match 1.3%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 4.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1096
 DB 15 TGAATAAAAAAAAAA 1

RESULT 888
 AAX18362/c
 ID AAX18362 standard; DNA; 16 BP.
 XX AAX18362;
 AC
 DT 11-MAY-1999 (first entry)
 DE
 DE RT-PCR primer of the invention SEQ ID 3.
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX Synthetic.
 XX JP11032765-A.
 XX 09-FEB-1999.
 XX 18-JUL-1997; 97JP-0208312.
 XX 18-JUL-1997; 97JP-0208312.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in
 XX RT-PCR

XX Disclosure; Page 10; 19pp; Japanese.
 XX This sequence represents a primer of the invention. The invention relates
 XX to sequences of at least two nucleotides of formula:
 XX (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 XX X = a labelled compound and/or a nucleotide with voluntary sequence;
 XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 XX of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 XX N = adenine, guanine, cytosine or thymine; gamma = thymine;
 XX k = natural number of 3 or over indicating the repetition of gamma, in
 XX which thymine expressed by gamma is composed of 1/3 or less of adenine,
 XX guanine and/or cytosine. The new nucleotides are useful as primers for
 XX RT-PCR and determination of base sequences. The new sequences allow for
 XX reproductive and highly efficient analysis of gene sequences.
 XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 4.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1097
 DB 16 TGAATAAAAAAAAAA 1

RESULT 889
 AAX18363/c
 ID AAX18363 standard; DNA; 16 BP.

XX AAX18363;
 AC
 DT 11-MAY-1999 (first entry)
 DE
 DE RT-PCR primer of the invention SEQ ID 4.
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.
 XX JP11032765-A.
 XX 09-FEB-1999.
 XX 18-JUL-1997; 97JP-0208312.
 XX 18-JUL-1997; 97JP-0208312.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in
 XX RT-PCR

XX Disclosure; Page 10; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates
 XX to sequences of at least two nucleotides of formula:
 XX (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 XX X = a labelled compound and/or a nucleotide with voluntary sequence;
 XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 XX of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 XX N = adenine, guanine, cytosine or thymine; gamma = thymine;
 XX k = natural number of 3 or over indicating the repetition of gamma, in
 XX which thymine expressed by gamma is composed of 1/3 or less of adenine,
 XX guanine and/or cytosine. The new nucleotides are useful as primers for
 XX RT-PCR and determination of base sequences. The new sequences allow for
 XX reproductive and highly efficient analysis of gene sequences.

XX Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 4.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1099
 DB 16 AGAAAAAAAAAAAAAAAAA 1

RESULT 890
 AAX18366/c
 ID AAX18366 standard; DNA; 16 BP.

XX AAX18366;
 AC
 DT 11-MAY-1999 (first entry)
 DE
 DE RT-PCR primer of the invention SEQ ID 7.
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.


```

DR WFI; 1999-264040/22.
XX
XX Uniquely tagged molecules identifiable by a unique property or
PT characteristic
PT
XX Example 8; Page 104; 138pp; English.
PS
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag
CC that is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification
CC of a large subset of targets out of a very large collection of similar
CC or dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
CC example from the present invention.
XX
XX Sequence 17 BP; 2 A; 2 C; 10 G; 3 T; 0 other;
SQ
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 40 GGTGCGAGGCGCGTA 55
DB 1 GGTGCGAGGCGCGTA 16
RESULT 896
AAK54277
ID AAK54277 standard; DNA; 17 BP.
AC AAK54277;
XX
XX 05-JUL-1999 (first entry)
XX
XX Endothelial nitric oxide synthase antisense oligonucleotide.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX Synthetic.
XX OS
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US19419.
XX
XX 09-JUN-1998; 98US-0093972.
XX
XX 17-SEP-1997; 97US-0059160.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX

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```

XX
XX Nyce JW;
PI
XX WFI; 1999-229400/19.
DR
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
PT
XX Disclosure; Page 61; 120pp; English.
PS
XX
CC The specification describes antisense oligonucleotides (AAK52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAK55272-74. These multiple target
CC oligonucleotides (specifically AAK55180-271) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC respiration, respiratory distress syndrome, pain, cystic fibrosis, chronic
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
XX Sequence 17 BP; 0 A; 7 C; 6 G; 4 T; 0 other;
SQ
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 378 GCCGTCCTGCTGGCG 393
DB 1 GCCGTCCTGCTGGCG 16
RESULT 897
AAF19843
ID AAF19843 standard; DNA; 17 BP.
XX
XX AAF19843;
AC
XX
XX 14-MAR-2001 (first entry)
XX
XX Human endothelial nitric oxide synthase polynucleotide fragment #1410.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX cancer; ss.
XX
XX Homo sapiens.
XX OS
XX WO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US08020.
XX
XX 06-APR-1999; 99US-0127958.
XX

```

PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PI Nyce JW;
 XX WPI; 2000-679539/66.
 XX
 XX
 XX Low adenine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 251; 1592pp; English.
 XX
 XX The present invention describes low adenine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impaired respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 17 BP; 0 A; 7 C; 6 G; 4 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 378 GCGGTCTCTGCTGCGG 393
 Db 1 GCGGTCTCTGCTGCGG 16
 RESULT 898
 AAA33721
 ID AAA33721 standard; DNA; 17 BP.
 XX
 XX AAA33721;
 AC
 XX 28-JUL-2000 (first entry)
 XX
 XX Low adenine antisense oligonucleotide SEQ ID NO:1410.
 XX
 XX Human; adenosine receptor; low adenine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.
 XX WO200009525-A2.
 XX 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US17712.
 XX 03-AUG-1998; 98US-0095212.
 XX (UYEC-) UNIV EAST CAROLINA.
 XX Nyce JW;
 XX WPI; 2000-205971/18.
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 XX Claim 18; Page 441; 1343pp; English.
 XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC the ONS reduces side effects. The reduction of the adenosine content of
 CC the release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 2815, and then the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1880
 CC (AAA32323 to AAA33992) are specifically claimed ONS from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.
 XX
 SQ Sequence 17 BP; 0 A; 7 C; 6 G; 4 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 378 GCGGTCTCTGCTGCGG 393
 Db 1 GCGGTCTCTGCTGCGG 16
 RESULT 899
 AAA25454/c
 ID AAA25454 standard; DNA; 17 BP.
 XX
 XX AAA25454;
 AC
 XX 19-JUL-2000 (first entry)
 XX
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphothioate; endonuclease;

KW anticancer; breast cancer; endometrium cancer; ss.
 XX Homo sapiens.
 OS WO9954459-A2.
 PN 28-OCT-1999.
 PD 19-APR-1999; 99WO-US08547.
 PF 20-APR-1998; 98US-0082404.
 PR 23-JUN-1998; 98US-0103636.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX WPI; 2000-013248/01.
 DR New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -
 XX Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodi(thioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA3503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1083 TAAATAAAAAAAAAA 1098
 DB 16 TACAAAAAAAAAAAAA 1

RESULT 900
 ID ABA77189 standard; DNA; 17 BP.
 AC ABA77189;
 XX 24-JAN-2002 (first entry)
 DT Adenosine deaminase deficiency correcting oligo SEQ ID NO: 35.
 DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;

KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antitickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX Homo sapiens.
 OS WO200173002-A2.
 PN 04-OCT-2001.
 PD 27-MAR-2001; 2001WO-US09761.
 PF 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192179P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX Claim 7; Page 43; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin, APC,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.

XX Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 725 GGAGCTGCGGTACAGT 740
 DB 1 GGAGCTGCGGTACAGT 16

RESULT 901
 ID ABA77190/c
 XX ABA77190 standard; DNA; 17 BP.
 AC ABA77190;
 XX 24-JAN-2002 (first entry)
 DT Adenosine deaminase deficiency correcting oligo SEQ ID NO: 36.
 DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytoskeletal; antitickling; antianaemic; haemostatic;
 KW antileptic; ss.
 OS Homo sapiens.
 PN WO200173002-A2.
 PD 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-US09761.
 XX 27-MAR-2000; 2000US-192176P.
 XX 27-MAR-2000; 2000US-192179P.
 XX 01-JUN-2000; 2000US-208538P.
 XX 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC;
 PI WPI; 2001-639230/73.
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 XX treating cystic fibrosis, comprises at least one mismatch and chemical
 XX modification -
 XX Claim 7; Page 43; 294pp; English.
 XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 725 GGAGCTGCGGTACAGT 740
 DB 17 GGAGGTGCGGTACAGT 2
 RESULT 902
 ABA77193
 ID ABA77193 standard; DNA; 17 BP.
 AC ABA77193;
 XX 24-JAN-2002 (first entry)
 DT Adenosine deaminase deficiency correcting oligo SEQ ID NO: 39.
 DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;

KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytoskeletal; antitickling; antianaemic; haemostatic;
 KW antileptic; ss.
 OS Homo sapiens.
 PN WO200173002-A2.
 PD 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-US09761.
 XX 27-MAR-2000; 2000US-192176P.
 XX 27-MAR-2000; 2000US-192179P.
 XX 01-JUN-2000; 2000US-208538P.
 XX 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC;
 PI WPI; 2001-639230/73.
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 XX treating cystic fibrosis, comprises at least one mismatch and chemical
 XX modification -
 XX Claim 7; Page 43; 294pp; English.
 XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 725 GGAGCTGCGGTACAGT 740
 DB 1 GGAGGTGCGGTACAGT 16
 RESULT 903
 ABA77194/c
 ID ABA77194 standard; DNA; 17 BP.
 AC ABA77194;
 XX 24-JAN-2002 (first entry)
 DT Adenosine deaminase deficiency correcting oligo SEQ ID NO: 40.
 DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;

KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antiskilling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192176P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 DR
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 PS Claim 7; Page 43; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCAL, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 725 GGAGCTGGGTACAGT 740
 |||||
 DB 17 GGAGTGGGTACAGT 2
 |||||
 RESULT 904
 ABA77197
 ID ABA77197 standard; DNA; 17 BP.
 XX
 AC ABA77197;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Adenosine deaminase deficiency correcting oligo SEQ ID NO: 43.
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;

KW retinoblastoma; BRCAL; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antiskilling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192176P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 DR
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX
 PS Claim 7; Page 43; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCAL, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 725 GGAGCTGGGTACAGT 740
 |||||
 DB 2 GGAGTGGGTACAGT 17
 |||||
 RESULT 905
 ABA77198/c
 ID ABA77198 standard; DNA; 17 BP.
 XX
 AC ABA77198;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Adenosine deaminase deficiency correcting oligo SEQ ID NO: 44.
 KW

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MHL1; APOB; mismatch repair; MSH2; MSH6; hyperlipidemia; apolipoprotein E; LDLR; familial hypercholesterolemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antitickling; antianaemic; haemostatic; antileptic; ss.

OS Homo sapiens.
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09761.
 XX
 PR 27-MAR-2000; 2000US-192176P.
 XX
 PR 27-MAR-2000; 2000US-192179P.
 XX
 PR 01-JUN-2000; 2000US-208538P.
 XX
 PR 30-OCT-2000; 2000US-244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kniec EB, Gamper HB, Rice MC;
 XX
 DR WPI; 2001-639230/73.
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification -
 XX
 PT
 XX
 PS Claim 7; Page 43; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MHL1, MSH2, MSH6, apolipoprotein E (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and presenilin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolemia, thalassemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention.
 XX
 SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 725 GGAGTGGCGGTACAGT 740
 DB 16 GGAGTGGCGGTACAGT 1
 RESULT 906
 AAX34987/c
 ID AAX34987 standard; DNA; 18 BP.
 XX
 AC AAX34987;
 XX
 XX 30-JUN-1999 (first entry)
 DT
 DE Antisense oligonucleotide targeted to protein kinase A-RI-alpha gene.

Human protein kinase A-RI-alpha gene; antisense oligonucleotide; carcinostatic; leukemia; large intestinal cancer; rectal cancer; colon cancer; lung cancer; stomach cancer; hepatic cancer; melanoma; malignant lymphoma; tongue cancer; oesophagus cancer; breast cancer; uterus cancer; pharynx cancer; brain tumour; malignant myoma; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX WO9616976-A1.
 XX
 PD 06-JUN-1996.
 XX
 PF 01-DEC-1995; 95WO-JP02452.
 XX
 PR 02-DEC-1994; 94JP-0324006.
 XX
 XX (POKK) POLA CHEM IND INC.
 XX
 XX Geiser TG, Tsuchiya M;
 XX
 XX WPI; 1996-277711/28.
 XX
 XX Oligonucleotide contg. human protein kinase A gene sequence - useful as carcinostatic agent
 PT
 PT
 XX
 PS Claim 7; Page 16; 24pp; Japanese.
 XX
 CC The present sequence represents an antisense oligonucleotide directed against the human protein kinase A-RI-alpha gene. The antisense oligonucleotides is useful as a carcinostatic agent, e.g. for treating leukemia, large intestinal cancer, rectal cancer, colon cancer, cancer of the lung or stomach, hepatic cancer, malignant lymphoma, tumour, melanoma, or malignant myoma.
 XX
 SQ Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 5.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 477 CTTGGCATTCCTCAGG 492
 DB 16 CTTGGCATTCCTCAGG 1
 RESULT 907
 AAX34992
 ID AAX34992 standard; DNA; 18 BP.
 XX
 AC AAX34992;
 XX
 XX 30-JUN-1999 (first entry)
 DT
 DE Antisense oligonucleotide targeted to protein kinase A-RI-alpha gene.
 XX
 XX Human protein kinase A-RI-alpha gene; antisense oligonucleotide; carcinostatic; leukemia; large intestinal cancer; rectal cancer; colon cancer; lung cancer; stomach cancer; hepatic cancer; melanoma; malignant lymphoma; tongue cancer; oesophagus cancer; breast cancer; uterus cancer; pharynx cancer; brain tumour; malignant myoma; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX WO9616976-A1.
 XX
 PD 06-JUN-1996.
 XX
 PF 01-DEC-1995; 95WO-JP02452.
 XX

PR 02-DEC-1994; 94JP-0324006.

XX (POK) POLA CHEM IND INC.

PI Geiser TG, Tsuchiya M;

XX WPI; 1996-277711/28.

XX Oligo:nucleotide contg. human protein kinase A gene sequence -
PT useful as carcinostatic agent

XX Claim 9; Page 18; 24pp; Japanese.

XX The present sequence represents an antisense oligonucleotide directed
CC against the human protein kinase A-R1-alpha gene. The antisense
CC oligonucleotides is useful as a carcinostatic agent, e.g. for treating
CC leukaemia, large intestinal cancer, rectal cancer, colon cancer,
CC cancer of the lung or stomach, hepatic cancer, malignant lymphoma,
CC cancer of the tongue, oesophagus, breast, uterus or pharynx, brain
CC tumour, melanoma, or malignant myoma.

XX Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 477 CTGGCATCTCTCAGG 492

DB 3 CATGGCATCTCTCAGG 18

RESULT 908

ID AAA58577

XX AAA58577 standard; DNA; 19 BP.

AC AAA58577;

20-OCT-2000 (first entry)

PCR primer ZC24271 used to amplify human BCMA gene fragment.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli;
XX PCR primer; ss.

OS Homo sapiens.

XX WO200040716-A2.

PN 13-JUL-2000.

PF 07-JAN-2000; 200WO-US00396.

XX 07-JAN-1999; 99US-0226533.

PR (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises

PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX Example 5; Page 164; 175pp; English.

XX PCR primers AAA58577-78 were used to amplify a human BCMA gene fragment.
CC BCMA is a B cell protein related to transmembrane activator and
CC CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
CC or BCMA (a related B cell protein) receptor contain a cysteine rich
CC domain, and are used for inhibiting ztnf4 activity. ztnf4 is a TNF
CC receptor-ligand engagement associated with activated or resting
CC B lymphocytes, effector T-cells, or with antibody production. The
CC antibody production is associated with an autoimmune disease selected
CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
CC and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
CC receptor-ligand engagement is associated with asthma, bronchitis,
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas,
CC lymphomas, light chain neuropathy, amyloidosis, moderating immune
CC response, immunosuppression, graft rejection, graft versus host disease,
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease,
CC joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
CC polypeptides, fusions, antibodies, agonists or antagonists can be used
CC to treat hypertension, renal artery stenosis, or occlusion, and
XX cholesterol or renal emboli.

SQ Sequence 19 BP; 5 A; 1 C; 5 G; 8 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 5.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 TTGTAATGCAACTGTG 87

DB 4 TTGTAATGCAAGTGTG 19

RESULT 909

AAV22586/C
ID AAV22586 standard; DNA; 20 BP.

XX AAV22586;

XX 08-JUL-1998 (first entry)

XX Antisense oligonucleotide designed to target the R1 message.

XX R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;
XX antisense; growth; inhibition; sensitivity; hydroxyurea;
XX chemotherapeutic drug; methotrexate; PALA; treatment; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9805769-A2.

XX 12-FEB-1998.

PF 01-AUG-1997; 97WO-CA00540.

XX 07-MAR-1997; 97US-0039959.

PR 02-AUG-1996; 96US-0023040.

XX (GENE-) GENESENSE TECHNOLOGIES INC.

XX Wright JA, Young AH;

XX WPI; 1998-145609/13.

XX Antisense oligonucleotides to ribonucleotide reductase genes - used
PT to modulate tumour growth and inhibit tumour cell proliferation

PS Claim 8; Page 49; 79pp; English.

CC AAV2531-89 represent antisense oligonucleotides which are targeted

CC against the mRNA of the R1 subunit sequence of ribonucleotide reductase.

CC Aberrant expression of the R2 gene, which encodes the second subunit of

CC the ribonucleotide reductase gene, can determine the malignant

CC characteristics of cells. Suppression of R2 and R1 gene expression was

CC found to reduce transformed properties of R2 and R1 gene expression was

CC oligonucleotides can be used for modulating tumour cell growth, or for

CC inhibiting tumour cell proliferation. They can also be used for

CC increasing the sensitivity of neoplastic cells to chemotherapeutic drugs

CC (especially to hydroxyurea, methotrexate (MTX), and PAIA). The antisense

CC oligonucleotides may be used to treat proliferative disorders including

CC leukaemias, lymphomas, sarcomas, melanomas, various other forms of

CC cancer, papillomas, arthrosclerosis, psoriasis, polythemia,

CC mastocytosis, autoimmune diseases, angiogenesis, bacterial infections and

CC viral infections (including HIV hepatitis, or herpes infections).

XX

SQ Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 5.9e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099

Db 20 AAAAAAAAAAAAAA 5

RESULT 910

AAC73668/c

ID AAC73668 standard; DNA; 20 BP.

XX AAC73668;

AC

XX

DT 02-FEB-2001 (first entry)

XX

DE Murine IL-5 antisense oligonucleotide ISIS #16994.

XX

XX Mouse; interleukin-5; IL-5; signal transduction;

KW antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;

KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;

KW inflammation; cancer; ss.

XX

OS Mus musculus.

OS Synthetic.

XX

PN WO200058512-A1.

XX

PD 05-OCT-2000.

XX

PF 17-MAR-2000; 2000WO-US07318.

XX

PR 26-MAR-1999; 99US-0280799.

XX

XX (ISIS-) ISIS PHARM INC.

XX

XX Dean NM, Karras JG, McKay R;

XX

DR WPI; 2000-594648/56.

XX

XX Antisense oligonucleotide compound used to treat asthma and

PT eosinophilic syndrome in humans modulates interleukin-5 signal

PT transduction -

XX

PS Example 2; Page 48; 156pp; English.

XX

CC The present sequence is an oligonucleotide used for antisense

CC modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides

CC were designed to target nucleic acids encoding IL-5 and IL-5

CC receptor-alpha. The antisense oligonucleotides may be used for the

CC treatment of diseases associated with IL-5 signal transduction, IL-5

CC expression or IL-5 receptor-alpha expression. Such diseases include

CC asthma and eosinophilic syndrome. The oligonucleotides are also useful

CC for research uses and to prevent or delay infection, inflammation or

CC tumour formation.

XX

SQ Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 5.9e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 TCGAAGCTCAGGCTG 1007

Db 18 TCGAAGCTCAGGCTG 3

RESULT 911

AAA90815/c

ID AAA90815 standard; DNA; 20 BP.

XX

XX AAA90815;

AC

XX

DT 20-DEC-2000 (first entry)

XX

DE Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.

XX

XX Antisense oligonucleotide; ribonucleotide reductase; R1 protein;

KW R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.

XX

OS Synthetic.

XX

XX WO200047733-A1.

PN

XX

PD 17-AUG-2000.

XX

PF 09-FEB-2000; 2000WO-CA00120.

XX

XX 11-FEB-1999; 99US-0249730.

PR

XX (GENE-) GENESENSE TECHNOLOGIES INC.

XX

XX Wright JA, Young AH;

PI

XX WPI; 2000-558216/51.

DR

XX

XX New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting

PT tumor cell growth -

PT

XX

PS Example 3; Page 32; 137pp; English.

XX

XX The present sequence is an antisense oligonucleotide directed against the

CC mRNA encoding the R1 component of mammalian ribonucleotide reductase.

CC Ribonucleotide reductase catalyses the conversion of ribonucleotides to

CC their corresponding deoxyribonucleotides and thus plays an important role

CC in DNA synthesis and cell proliferation. Regulation of ribonucleotide

CC reductase is altered in cultured malignant cells and increased levels of

CC R2 protein and R2 mRNA have been found in pre-malignant and malignant

CC tissues as compared to normal control tissue samples. The present

CC antisense sequence is therefore useful for inhibiting tumourigenicity of

CC neoplastic cells and inhibiting metastasis of tumour cells. It is also

CC useful for increasing sensitivity of neoplastic cells to chemotherapeutic

CC drugs, thus allowing chemotherapeutic treatments to be used in patients

CC who have become resistant or less sensitive to chemotherapy. The sequence

CC may be RNA or DNA and may comprise a modified backbone and/or nucleotide

CC analogues.

XX

SQ Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 5.9e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099

```
Db      20 AAAAAAAAAAAAAA 5
RESULT 912
RAC82924/c
ID AAB82924 standard; DNA; 20 BP.
XX
XX AC AAB82924;
XX
XX DT 21-MAR-2001 (first entry)
XX
XX DE Human S-9 derived oligonucleotide #8.
XX
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX OS Homo sapiens.
XX
XX PN DE19923966-A1.
XX
XX PD 30-NOV-2000.
XX
XX PF 25-MAY-1999; 99DE-1023966.
XX
XX PR 25-MAY-1999; 99DE-1023966.
XX
XX PA (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
XX WPI; 2001-050938/07.
XX
XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
XX PT least one recognition unit comprising a region with a defined structure
XX PT adjacent to a region with a randomized structure -
XX
XX PS Examples; Fig 1; 8pp; German.
XX
XX CC This invention describes a novel recognition system comprising at least
XX CC 1 recognition unit bound to a support, each recognition unit comprising a
XX CC region A with a defined structure adjacent to a region B with a
XX CC randomized structure. The recognition system is useful for screening,
XX CC identifying, or characterizing at least 1 component of a sample,
XX CC especially nucleic acids and/or proteins, and for screening for and/or
XX CC identifying cellular or synthetic binding partners, preferably proteins,
XX CC peptides, nucleic acids, chemical agents, preferably organic compounds,
XX CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX CC teratogens, herbicides, fungicides or pesticides.
XX
XX SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAATAAAAAAAAAA 1097
DB 16 TTAATAAAAAAAAAA 1
RESULT 913
ABZ72209/c
ID ABZ72209 standard; DNA; 20 BP.
XX
XX AC ABZ72209;
XX
XX DT 03-APR-2003 (first entry)
XX
XX DE Gene 216 SSCP sequencing primer SEQ ID NO 181.
XX
XX KW Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
XX KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
obesity; inflammatory bowel disease; primer; ss.
Synthetic.
WO200178994-A2.
25-OCT-2001.
13-APR-2001; 2001WO-US12245.
13-APR-2000; 2000US-0548797.
(GENO-) GENOME THERAPEUTICS CORP.
Keith T;
WPI; 2001-639428/73.
Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
proteins they encode, useful for the prevention, diagnosis and
treatment of asthma, obesity and inflammatory bowel disease -
Example 10; Page 150; 520pp; English.
The invention relates to isolated genes (Gene 216) from human chromosome
20p13-p12 and the proteins they encode. The nucleic acids and proteins
may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate Gene 216 expression. For example, the
nucleic acids (or vectors) and proteins may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of Gene 216 by expressing
inactive proteins or to supplement the patients own production of Gene
216 proteins. Additionally, the nucleic acids may be used to produce the
secreted Gene 216 protein, by inserting the nucleic acids into a host
cell and culturing the cell to express the protein. The nucleic acids
and complementary sequences may also be used as DNA probes in diagnostic
assays to detect and quantitate the presence of similar nucleic acid
sequences in samples and therefore which patients may be in need of
restorative therapy. The Gene 216 protein may also be used as antigens in
the production of antibodies against Gene 216 and in assays to identify
modulators of Gene 216 expression and activity. The anti-Gene 216
antibodies and antagonists may also be used to down regulate expression
and activity. The anti-Gene 216 antibodies may also be used as diagnostic
agents for detecting the presence of Gene 216 proteins in samples (e.g.
by enzyme linked immunosorbant assay or ELISA). Disorders that may be
prevented, diagnosed and/or treated by the above methods include, for
example asthma, obesity and inflammatory bowel disease. The present
invention is that of a Gene 216 related primer used in examples of the
invention. The primers are used in the physical mapping of the gene
(ABZ72067-ABZ72088), polymorphism identification using single strand
conformational polymorphism (SSCP) analysis (ABZ72091-ABZ72184),
sequencing (ABZ72185-ABZ72268) and genotyping (ABZ72317-ABZ72362).
Sequence 20 BP; 9 A; 6 C; 3 G; 2 T; 0 other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 821 TGTGGGTGCTGAAGCT 836
DB 18 TGTGGGTGCTGAAGCT 3
RESULT 914
ABT13907/c
ID ABT13907 standard; DNA; 20 BP.
XX
XX AC ABT13907;
XX
XX DT 13-FEB-2003 (first entry)
XX
XX DE Human helicase-moi inhibiting oligonucleotide #32.
```

```

XX KW Human; antisense gene therapy; phosphorothioate backbone;
XX KW antisense oligonucleotide; helicase-moi gene; inflammation; ss;
XX KW helicase-moi-associated condition; infection; tumour formation;
XX KW 2'-MOE nucleotide; 2'-methoxyethyl nucleotide.
XX OS Homo sapiens.
XX PN US6444466-B1.
XX PD 03-SEP-2002.
XX PF 10-MAY-2001; 2001US-0853768.
XX PR 10-MAY-2001; 2001US-0853768.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Watt AT;
XX DR WPI; 2002-749291/81.
XX PT Novel antisense compound for modulating expression of human
XX PT helicase-moi and for treating inflammation, specifically hybridizes to
XX PT a specific region in nucleic acid molecule encoding the human
XX PT helicase-moi
XX PS Claim 3; Column 45-46; 52pp; English.
XX CC The invention comprises antisense oligonucleotides which are targeted to
XX CC the coding region of the human helicase-moi gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of human helicase-moi in cells or tissues, and for treating a
XX CC helicase-moi-associated condition. The antisense oligonucleotides of the
XX CC invention may also be used to delay infection, inflammation and tumour
XX CC formation. The present DNA sequence represents a human helicase-moi gene
XX CC antisense oligonucleotide of the invention.
XX CC NOTE: The present DNA sequence has a phosphorothioate backbone, bases 1-5
XX CC and 16-20 are 2'-methoxyethyl (2'-MOE) nucleotides.
XX SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 310 ATGGGAAGACTGCAG 325
Db ||||||| |||||
16 ATGGGAAGTCTGCAG 1

RESULT 915
AAD39496
ID AAD39496 standard; DNA; 20 BP.
XX AC AAD39496;
XX DT 04-OCT-2002 (first entry)
XX DE Human calreticulin antisense oligonucleotide, ISIS 109289.
XX KW Human; calreticulin; antisense compound; hyperproliferative disorder;
XX KW cancer; autoimmune disease; viral infection; cardiovascular disease;
XX KW antisense therapy; cytostatic; immunosuppressive; virucide; antisense;
XX KW phosphorothioate backbone; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER

Human; antisense gene therapy; phosphorothioate backbone;
antisense oligonucleotide; helicase-moi gene; inflammation; ss;
helicase-moi-associated condition; infection; tumour formation;
2'-MOE nucleotide; 2'-methoxyethyl nucleotide.
Homo sapiens.
US6444466-B1.
03-SEP-2002.
10-MAY-2001; 2001US-0853768.
10-MAY-2001; 2001US-0853768.
(ISIS-) ISIS PHARM INC.
Ward DT, Watt AT;
WPI; 2002-749291/81.
Novel antisense compound for modulating expression of human
helicase-moi and for treating inflammation, specifically hybridizes to
a specific region in nucleic acid molecule encoding the human
helicase-moi
Claim 3; Column 45-46; 52pp; English.
The invention comprises antisense oligonucleotides which are targeted to
the coding region of the human helicase-moi gene. The antisense
oligonucleotides of the invention are useful for inhibiting the
expression of human helicase-moi in cells or tissues, and for treating a
helicase-moi-associated condition. The antisense oligonucleotides of the
invention may also be used to delay infection, inflammation and tumour
formation. The present DNA sequence represents a human helicase-moi gene
antisense oligonucleotide of the invention.
NOTE: The present DNA sequence has a phosphorothioate backbone, bases 1-5
and 16-20 are 2'-methoxyethyl (2'-MOE) nucleotides.
Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 310 ATGGGAAGACTGCAG 325
Db ||||||| |||||
16 ATGGGAAGTCTGCAG 1

Claim 3; Page 82; 109pp; English.

The invention relates to antisense compounds, compositions and methods
for modulating the expression of calreticulin. The compositions comprise
antisense compounds, particularly antisense oligonucleotides, targeted
to nucleic acids encoding calreticulin. The antisense compound is useful
for inhibiting the expression of calreticulin in human cells or tissues.
It is also useful for treating a human having a disease or condition
associated with calreticulin, e.g., hyperproliferative disorder e.g.
cancer, autoimmune disease, viral infection or cardiovascular disease,
by inhibiting expression of calreticulin. It is useful for diagnostics,
therapeutics, prophylaxis and as research reagents and kits. It is also
used in antisense therapy. The present sequence is an antisense compound
targeted to human calreticulin. This sequence is used to study the
antisense inhibition of calreticulin expression-phosphorothioate 2'-MOE
gapmer oligonucleotides.

Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
FT 6..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
FT 1
FT /*tag= d
FT /mod_base= m5c
FT 4
FT /*tag= e
FT /mod_base= m5c
FT 11
FT /*tag= f
FT /mod_base= m5c
FT 12
FT /*tag= g
FT /mod_base= m5c
FT 17
FT /*tag= h
FT /mod_base= m5c
FT 18
FT /*tag= i
FT /mod_base= m5c
FT 20
FT /*tag= j
FT /mod_base= m5c

WO200236743-A2.
10-MAY-2002.
30-OCT-2001; 2001WO-US49045.
30-OCT-2000; 2000US-0702327.
(ISIS-) ISIS PHARM INC.
Bennett CF, Cowser LM;
WPI; 2002-479759/51.
Novel antisense compound targeted to nucleic acid encoding
calreticulin, useful for treating a human having disease or condition
associated with calreticulin e.g. cancer, viral infection, autoimmune
disease
Claim 3; Page 82; 109pp; English.

The invention relates to antisense compounds, compositions and methods
for modulating the expression of calreticulin. The compositions comprise
antisense compounds, particularly antisense oligonucleotides, targeted
to nucleic acids encoding calreticulin. The antisense compound is useful
for inhibiting the expression of calreticulin in human cells or tissues.
It is also useful for treating a human having a disease or condition
associated with calreticulin, e.g., hyperproliferative disorder e.g.
cancer, autoimmune disease, viral infection or cardiovascular disease,
by inhibiting expression of calreticulin. It is useful for diagnostics,
therapeutics, prophylaxis and as research reagents and kits. It is also
used in antisense therapy. The present sequence is an antisense compound
targeted to human calreticulin. This sequence is used to study the
antisense inhibition of calreticulin expression-phosphorothioate 2'-MOE
gapmer oligonucleotides.

Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```


ABX75062/c
 ID ABX75062 standard; DNA; 20 BP.
 XX AC ABX75062;
 XX DT 25-MAR-2003 (first entry)
 XX DE Human gene 216 polymorphism detection PCR primer #119.
 XX DE Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;
 XX KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism;
 XX KW SNP; gene therapy; respiratory disease; asthma; obesity; PCR;
 XX KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;
 XX KW adult respiratory distress syndrome; inflammatory bowel syndrome.
 XX OS Homo sapiens.
 XX PN WO200283077-A2.
 XX PD 24-OCT-2002.
 XX PF 15-APR-2002; 2002WO-US12063.
 XX PR 13-APR-2001; 2001US-0834597.
 XX PR 13-APR-2001; 2001WO-US12245.
 XX PA (SCHE) SCHERING CORP.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Keith T, Little RD, Van Berdewegh P, Dupuis J, Del Mastro RG;
 XX PI Simon J, Allen K, Pandit S;
 XX PR WPI; 2003-092960/08.
 XX PT New isolated gene 216 nucleic acids, useful for diagnosing, preventing
 XX PT or treating a disorder, such as asthma, bronchial hyper-responsiveness,
 XX PT chronic obstructive pulmonary disease, obesity or inflammatory bowel
 XX PT syndrome -
 XX PS Example 10; Page 156; 650pp; English.
 XX CC This invention relates to a novel isolated nucleic acid, gene 216,
 XX CC identified from human chromosome 20p13-p12. The invention also discloses
 XX CC regions of the 216 gene that contain single nucleotide polymorphisms
 XX CC (SNP's) which may be used as markers for disease susceptibility or
 XX CC severity. The nucleotides of the invention may have antiasthmatic,
 XX CC antiinflammatory or anorectic activities and may be used in gene
 XX CC therapy. The nucleic acids, antibodies or its fragments are useful for
 XX CC diagnosing, preventing or treating a disorder, such as respiratory
 XX CC diseases (e.g. asthma, bronchial hyper-responsiveness, chronic
 XX CC obstructive pulmonary disease or adult respiratory distress syndrome),
 XX CC obesity, or inflammatory bowel syndrome. The nucleic acids are also
 XX CC useful for identifying increased susceptibility of a subject to the
 XX CC disorders mentioned. The nucleic acids can also be used as primers and
 XX CC templates for the recombinant production of disorder-associated
 XX CC peptides or polypeptides, for chromosome and gene mapping, or for
 XX CC tissue distribution studies. The present sequence represents a gene
 XX CC 216 specific PCR primer used in the scope of the invention.
 XX Sequence 20 BP; 9 A; 6 C; 3 G; 2 T; 0 other;
 SQ Query Match 1.3%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 5.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 821 TGTGGTCTGAGCT 836
 Db 18 TGTGGTCTGAGCT 3

ABX15031;
 14-MAR-2003 (first entry)
 Human matrix metalloproteinase 9, MMP9, sequencing primer C.
 ss; primer; matrix metalloproteinase 9; MMP9; myocardial ischaemia;
 myocardial necrosis; B-type natriuretic peptide; BNP; myocardial injury;
 constricting chest pain; acute coronary syndrome; ACS.
 Synthetic.
 WO200289657-A2.
 14-NOV-2002.
 04-MAY-2002; 2002WO-US14219.
 04-MAY-2001; 2001US-288871P.
 28-AUG-2001; 2001US-315642P.
 (BIOS-) BIOSITE INC.
 Valkirs GE, Dahlen JR, Kirchick H, Buechler KF;
 WPI; 2003-120494/11.
 Diagnosing myocardial ischemia or myocardial necrosis in a patient
 comprises determining a level of B-type natriuretic peptide (BNP) or
 BNP-related marker to the presence or absence of myocardial ischemia in
 the patient
 Example 2; Page 60; 105pp; English.
 The invention relates to diagnosing myocardial ischaemia or myocardial
 necrosis in a patient comprising determining a level of a diagnostic
 indicator in a sample obtained from the patient, and correlating the
 level of B-type natriuretic peptide (BNP) or BNP-related marker
 (e.g. matrix metalloproteinase 9, MMP9) to the presence or
 absence of myocardial ischaemia in the patient. Also included are
 diagnosing an acute coronary syndrome comprising analysing a test
 sample obtained from a patient for the presence or amount of one or
 more specific markers for myocardial injury and one or more
 non-specific markers for myocardial injury, screening a patient
 experiencing constricting chest pain for an acute coronary
 syndrome, monitoring a course of treatment in a patient, determining
 a prognosis of a patient diagnosed with acute coronary syndrome and
 determining a prognosis of a patient diagnosed with acute coronary
 syndrome. The method is useful for diagnosing myocardial ischaemia or
 myocardial necrosis, for early detection and differentiation of acute
 coronary syndrome (ACS), and in the identification of individuals at
 risk for adverse events upon presentation with ACS symptoms. The method
 may be used to facilitate the treatment of ACS patients and the
 development of additional diagnostic indicators. The markers are useful
 in diagnosing and treating a patient and/or in monitoring the course of
 a treatment regimen, and for screening compounds and pharmaceutical
 compositions that might provide a benefit in treating or preventing
 such conditions. The present sequence is a primer used to verify the
 correct cloning of a coding sequence for human MMP9 which is used to
 express MMP9 protein for use in raising anti-MMP9 antibodies.
 Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 other;
 1.3%; Score 14.4; DB 1; Length 20;
 397 GTCGAGGCTGGAGAA 1012
 Pred. No. 5.9e+02;
 Mismatches 1; Indels 0; Gaps 0;
 16 GTCGAGGCTGGAGAA 1

RESULT 919
 ABX15031/c
 ID ABX15031 standard; DNA; 20 BP.

RESULT 920
ABX04322/c
ID ABX04322 standard; DNA; 20 BP.
XX
XX
AC ABX04322;
XX
XX
DT 13-JAN-2003 (first entry)
XX
DE Mouse Interleukin 5 antisense oligonucleotide ISIS 16994.
XX
XX Mouse; ss; antisense; interleukin 5; IL-5; IL-5 receptor;
XX
XX antiasthmatic; immunosuppressant; eosinophilic syndrome; asthma.
XX
OS Mus musculus.
XX
XX US2002128216-A1.
XX
XX
PD 12-SEP-2002.
XX
XX 07-MAR-2001; 2001US-0800629.
XX
XX 26-MAR-1999; 99US-0280799.
XX
XX 17-MAR-2000; 2000WO-US07318.
XX
XX (DEAN/) DEAN N M.
XX
XX (KARR/) KARRAS J G.
XX
XX (MCKA/) MCKAY R.
XX
XX (MANO/) MANOHARAN M.
XX
XX Dean NM, Karras JG, McKay R, Manoharan M;
XX
XX WPI; 2003-039602/03.
XX
XX Novel antisense compound for treating disease/condition e.g.
XX
XX eosinophilic syndrome or asthma associated with interleukin-5 or IL-5
XX
XX receptor expression or IL-5 signal transduction, modulates IL-5 signal
XX
XX transduction -
XX
XX Example 10; Page 14; 77pp; English.
XX
XX The invention relates to an antisense compound of 8-30 nucleobases in
XX
XX length, which modulates interleukin (IL)-5 signal transduction.
XX
XX Also include are a pharmaceutical composition comprising the antisense
XX
XX oligonucleotide and a pharmaceutically acceptable carrier or diluent, and
XX
XX a diagnostic kit for detecting the expression level of the membrane form
XX
XX versus soluble form of IL-5 receptor a. The antisense compound is useful
XX
XX for modulating IL-5 signal transduction, modulating expression of
XX
XX mammalian IL-5 or modulating the expression of mammalian IL-5 receptor a,
XX
XX in cells or tissues, for altering the ratio of the isoforms of mammalian
XX
XX IL-5 receptor a in mammalian cells or tissues, treating a mammalian
XX
XX having a disease or condition associated with IL-5 signal transduction,
XX
XX IL-5 expression or IL-5 receptor a expression, where the disease or
XX
XX condition include eosinophilic syndrome or asthma. An antisense compound
XX
XX which alters splicing of an RNA encoding IL-5 receptor a is also useful
XX
XX for treating a mammal having a disease or condition. The present sequence
XX
XX is an antisense oligonucleotide targeting mouse IL5.
XX
XX Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 other;
XX
XX
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 992 TGGAGGCTGAGGCTG 1007
XX
XX 18 TGGAGGCTGAGGCTG 3
XX
XX
RESULT 921
AAA47676/c
ID AAA47676 standard; cDNA; 15 BP.
XX
XX AAA47676;
AC

XX
XX 08-NOV-2000 (first entry)
XX
XX Oligo d(T) primer for human DDAH1.
XX
XX Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
XX
XX arginine deaminase; hyperlipidemia; renal failure; hypertension;
XX
XX restenosis; atherosclerosis; schizophrenia; multiple sclerosis;
XX
XX cancer; ischemia reperfusion injury; septic shock;
XX
XX multi organ failure; arthritis; skin disorders;
XX
XX inflammatory cardiac disease; migraine; infection; ss.
XX
OS Homo sapiens.
XX
XX WO200004888-A2.
XX
XX
XX 03-AUG-2000.
XX
XX 26-JAN-2000; 2000WO-GB00226.
XX
XX 26-JAN-1999; 99GB-0001705.
XX
XX 04-JUN-1999; 99GB-0013066.
XX
XX (UNLO) UNIV COLLEGE LONDON.
XX
XX Vallance PUT, Leiper JM, Whitley GSW, Charles IG;
XX
XX WPI; 2000-543392/49.
XX
XX Novel methylarginase polypeptides and polynucleotides, used to identify
XX
XX modulators of them, which are used in the treatment of e.g. cancer,
XX
XX hypertension, and bacterial infections
XX
XX Example 1; Page 33; 68pp; English.
XX
XX Nucleotides encoding methylarginase polypeptides, vectors comprising
XX
XX these nucleotides and the polypeptides themselves can be used in
XX
XX medicaments for the treatment of hyperlipidemia, renal failure,
XX
XX hypertension, restenosis after angioplasty, atherosclerosis, or
XX
XX complications of heart failure, schizophrenia, multiple sclerosis or
XX
XX cancer. Modulators of the enzyme can be used in medicaments
XX
XX for the treatment of ischemia-reperfusion injury of the brain or heart,
XX
XX cancer, lethal hypertension in severe inflammatory conditions such as
XX
XX septic shock or multi-organ failure, or local and systemic inflammatory
XX
XX disorders including arthritis skin disorders, inflammatory cardiac
XX
XX disease, migraine, or microbial or bacterial infection. The
XX
XX sequence of human DDAH1 was obtained by data base searching. The
XX
XX EST's used in the process are given in GENESEQ records AAA47661-A47677.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 other;
XX
XX
Query Match 1.3%; Score 14.2; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1083 TAAAAAATAAAAAA 1097
XX
XX :|||||||
XX
XX 15 BAAAAAATAAAAAA 1
XX
XX
RESULT 922
AAD44150
ID AAD44150 standard; DNA; 15 BP.
XX
XX AAD44150;
XX
XX
XX 13-DEC-2002 (first entry)
XX
XX
XX Oligo-AT PCR primer #1 used to illustrate the method of the invention.
XX
XX Sequential consensus region-directed amplification; gene expression;
XX
XX disease diagnosis; gene analysis; human; matrix metalloproteinase;
XX
XX PCR; primer; ss.

```

XX OS Unidentified.
XX PN US6277571-B1.
XX XX
XX PD 21-AUG-2001.
XX PF 30-SEP-1998; 98US-0163485.
XX PR 03-OCT-1997; 97US-108152P.
XX PA (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX PI Fillmore H, Broadus W, Gillies G;
XX DR WPI; 2002-412824/44.
XX PT Sequential consensus region-directed amplification for sorting mixture
XX of DNAs into 2 or more subsets or distinguishing gene expression
XX patterns in 2 samples, useful for disease diagnosis and gene analysis -
XX Example; Fig 1D; 19pp; English.
XX CC The invention relates to a method of sequential consensus region-directed
XX amplification for sorting a mixture of DNAs into 2 or more subsets or
XX distinguishing gene expression patterns in 2 samples. The methods, kits
XX and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
XX more subsets or distinguishing gene expression patterns in 2 samples
XX e.g. for disease diagnosis and gene analysis. The present sequence is
XX oligo AT PCR primer used to illustrate the method of the invention.
XX SQ Sequence 15 BP; 14 A; 0 C; 0 G; 0 U; 1 other;

Query Match 1.3%; Score 14.2; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 1 AAAAAAAAAAAAAA 15

RESULT 923
AAAX18387/C
ID AAAX18387 standard; DNA; 16 BP.
AC AAAX18387;
DT 11-MAY-1999 (first entry)
DE RT-PCR primer of the invention SEQ ID 28.
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX Synthetic.
XX JP11032765-A.
XX 09-FEB-1999.
XX 18-JUL-1997; 97JP-0208312.
XX 18-JUL-1997; 97JP-0208312.
XX (TAKI ) TAKARA SHUZO CO LTD.
XX WPI; 1999-183822/16.
XX Peptides having at least two new nucleotides - useful as primers in
XX RT-PCR
XX Example 1; Page 12; 19pp; Japanese.

```

```

CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula:
CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
CC X = a labelled compound and/or a nucleotide with voluntary sequence;
CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
CC k = natural number of 3 or over indicating the repetition of gamma, in
CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
CC guanine and/or cytosine. The new nucleotides are useful as primers for
CC RT-PCR and determination of base sequences. The new sequences allow for
CC reproductive and highly efficient analysis of gene sequences.
XX SQ Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 2 other;

Query Match 1.3%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1097
DB 15 BAAAAAAAAAAAAA 1

RESULT 924
AAAN90485
ID AAAN90485 standard; DNA; 19 BP.
XX AAAN90485;
AC AAAN90485;
DT 03-NOV-1989 (first entry)
DE Escherichia coli 23S rRNA oligo probe.
XX Escherichia coli; oligonucleotide probe; periodontal
XX disease; mouth diseases; 23S rRNA; species-specific.
XX Os Escherichia coli.
XX WO8906704-A.
XX 27-JUL-1989.
XX 09-JAN-1989; 89WO-US000072.
XX 11-JAN-1988; 88US-0142106.
XX (MICR-) MICROPROBE CORP.
XX Schwartz DE, Kanemoto RH, Watanabe SM, Dix K;
XX WPI; 1989-233857/32.
XX Oligonucleotide probes for detection of periodontal pathogens
XX - comprising a segment of nucleic acid capable of hybridising to
XX bacterial ribosomal RNA.
XX Claim 38; page 51; 53pp; English.
XX 23S rRNA oligonucleotide probe (23UPF) specific for Escherichia
XX coli, and corresp. to bases 1685-1703 of E. coli. It is a universal
XX primer. See AAAN90418-87.
XX SQ Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 216 CCCTCTCCGAGGTGACGG 234
DB 1 CCTTCTCCGAGGTACGG 19

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RESULT 925
AAZ75077/c
ID AAZ75077 standard; DNA; 19 BP.
XX
AC AAZ75077;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9433.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -
XX
XX Claim 8; Page 2242; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX Sequence 19 BP; 4 A; 7 C; 3 G; 5 T; 0 other;
XX
XX Query Match 1.3%; Score 14.2; DB 1; Length 19;
XX Best Local Similarity 84.2%; Pred. No. 6.1e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 999 CTGAGCTGGAGATGGGA 1017
DB 19 CTGAGACTGGAGTATGGCA 1
XX
RESULT 926
AAZ73056
ID AAF23056 standard; DNA; 19 BP.
XX
AC AAF23056;
XX
DT 20-MAR-2001 (first entry)
XX
DE C. trachomatis 23S rRNA specific sequence #2.
XX
XX Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
XX Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
XX Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
XX bacterium; ss.
XX
OS Chlamydia trachomatis.
XX
XX US6150517-A.
XX

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```

DT 20-MAR-2001 (first entry)
XX
DE Legionella 23S rRNA specific sequence #2.
XX
XX Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
XX Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
XX Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
XX bacterium; ss.
XX
OS Legionella sp.
XX
XX US6150517-A.
XX
XX 21-NOV-2000.
XX
XX 30-MAY-1995; 95US-0454063.
XX
XX 22-FEB-1994; 94US-0200866.
XX
XX 24-NOV-1987; 87US-0295208.
XX
XX 24-NOV-1987; 87WO-US03009.
XX
XX 11-DEC-1991; 91US-0808929.
XX
XX 24-NOV-1986; 86US-0934244.
XX
XX 07-AUG-1987; 87US-0083542.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX
XX WPI; 2001-060029/07.
XX
XX Preparing a probe for nucleic acid hybridization assays comprises
XX constructing a nucleotide polymer sufficiently complementary to
XX hybridize to an rRNA region that distinguishes non-viral target from
XX non-viral non-target species -
XX
XX Example 10; Column 34; 75pp; English.
XX
XX The present invention provides novel methods of producing probes for use
XX in the identification of a number of microorganisms. These include E.
XX coli, Mycobacterium, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
XX Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
XX bacteria.
XX
XX Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 other;
XX
XX Query Match 1.3%; Score 14.2; DB 1; Length 19;
XX Best Local Similarity 84.2%; Pred. No. 6.1e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 216 CCTCTCTCCAGAGTGACGG 234
DB 1 CCTTCTCCCGAGTTACGG 19
XX
RESULT 927
AAZ73065
ID AAF23065 standard; DNA; 19 BP.
XX
XX AAF23065;
XX
DT 20-MAR-2001 (first entry)
XX
DE C. trachomatis 23S rRNA specific sequence #2.
XX
XX Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
XX Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
XX Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
XX bacterium; ss.
XX
OS Chlamydia trachomatis.
XX
XX US6150517-A.
XX

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PD XX 21-NOV-2000.
PF XX
PF XX 30-MAY-1995; 95US-0454063.
XX XX
PR XX 22-FEB-1994; 94US-0200866.
PR XX 24-NOV-1987; 87US-0295208.
PR XX 24-NOV-1987; 87WO-US03009.
PR XX 11-DEC-1991; 91US-0806929.
PR XX 24-NOV-1986; 86US-0934244.
PR XX 07-AUG-1987; 87US-0083542.
XX XX
PA (GENP-) GEN-PROBE INC.
XX XX
PI McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX XX
DR WPI; 2001-060029/07.
XX XX
PT Preparing a probe for nucleic acid hybridization assays comprises
PT constructing a nucleotide polymer sufficiently complementary to
PT hybridize to an rRNA region that distinguishes non-viral target from
PT non-viral non-target species -
XX XX
XX Example 11; Column 37; 75pp; English.
XX XX
CC The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
CC bacteria.
XX XX
SQ Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 other;
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
OY 216 CCTCTCCGAGTACGG 234
Db 1 CCTCTCCGAGTACGG 19
RESULT 928
AAF23108
ID AAF23108 standard; DNA; 19 BP.
XX XX
AC AAF23108;
XX XX
DT 20-MAR-2001 (first entry)
XX XX
DE Fungal 28S rRNA specific sequence #1.
XX XX
KW Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
KW Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
KW Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
KW bacterium; ss.
XX XX
OS Fungi.
XX XX
PN US6150517-A.
XX XX
PD 21-NOV-2000.
XX XX
PF 30-MAY-1995; 95US-0454063.
XX XX
PR 22-FEB-1994; 94US-0200866.
PR 24-NOV-1987; 87US-0295208.
PR 24-NOV-1987; 87WO-US03009.
PR 11-DEC-1991; 91US-0806929.
PR 24-NOV-1986; 86US-0934244.
PR 07-AUG-1987; 87US-0083542.
XX XX
PA (GENP-) GEN-PROBE INC.
XX XX
PI McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX XX
DR WPI; 2001-060029/07.
XX XX
PT Preparing a probe for nucleic acid hybridization assays comprises
PT constructing a nucleotide polymer sufficiently complementary to
PT hybridize to an rRNA region that distinguishes non-viral target from
PT non-viral non-target species -
XX XX
XX Example 11; Column 37; 75pp; English.
XX XX
CC The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
CC bacteria.
XX XX
SQ Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 other;
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
OY 216 CCTCTCCGAGTACGG 234
Db 1 CCTCTCCGAGTACGG 19
RESULT 928
AAF26629
ID AAF26629 standard; DNA; 19 BP.
XX XX
AC AAF26629;
XX XX
DT 27-MAR-2001 (first entry)
XX XX
DE Universal probe 1028R.
XX XX
KW Bacterial protection; thermal shock; osmotic shock; pH shock;
KW oxidative stress; chemical stress; nutritional stress; UV-stress;
KW cold stress; fermentation; milk product; Bifidobacterium; lactobacillus;
KW prophylaxis; treatment; gastrointestinal infection; probe; ss.
XX XX
OS Synthetic.
XX XX
PN WO200077186-A2.
XX XX
PD 21-DEC-2000.
XX XX
PF 09-JUN-2000; 2000WO-EP05403.
XX XX
PR 11-JUN-1999; 99US-0138946.
XX XX
PA (NEST ) SOC PROD NESTLE SA.
XX XX
PI Schmidt G, Zink R;
XX XX
DR WPI; 2001-112222/12.
XX XX
PT New bacterial cells having protection against stress and adverse
PT conditions obtained by subjecting cells to sublethal stress level
PT treatment are useful in large-scale processes e.g. production of
PT fermented products -
XX XX
PS Disclosure; Page 9; 23pp; English.
XX XX
CC The present invention describes a bacterial cell having protection
CC against conditions lethal to an unprotected bacterial cell, and which
CC is obtained by subjecting a bacterial cell to treatment with a sublethal
CC level of stress. Also described are: (1) a nutritive composition
CC comprising bacteria having protection against conditions lethal to
CC unprotected bacteria; and (2) a method of protecting a bacterial cell
CC against stress by treating a bacterial cell with a sublethal level of
```

CC stress consisting of thermal shock, osmotic shock, pH shock, oxidative
 CC stress, chemical stress, nutritional stress, UV-stress or cold stress.
 CC The new cells having protection against lethal conditions are useful in
 CC the production of fermented products and starter cultures, and in the
 CC fermentation of milk products. Bifidobacteria and lactobacilli may be
 CC used in prophylaxis or treatment of ailments including gastrointestinal
 CC infections. The protected bacterial cells are more advantageous for use
 CC in large-scale processes than those unprotected cells. The present
 CC sequence represents a universal probe which is used in the
 CC exemplification of the present invention.

XX Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 6.1e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 216 CCTCTCCGAGTACGG 234

DB 1 CCTCTCCGAGTACGG 19

RESULT 930

ABA97625

ID ABA97625 standard; DNA; 19 BP.

XX AC ABA97625;

XX DT 11-APR-2002 (first entry)

XX DE Probe d.

XX KW ss; fluorochrome; nucleic acid probe; fluorescence.

XX OS Unidentified.

XX PN JP2001286300-A.

XX PD 16-OCT-2001.

XX PF 20-APR-2000; 2000JP-0120097.

XX PR 20-APR-1999; 99JP-0111601.

XX PR 24-AUG-1999; 99JP-0236666.

XX PR 30-AUG-1999; 99JP-0242693.

XX PR 01-FEB-2000; 2000JP-0028896.

XX PA (BIOI-) BIOINDUSTRY KYOKAI SH.

XX PA (KANK-) KANKYO ENG KK.

XX PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.

XX DR WPI; 2002-134193/18.

XX PT Measurement of nucleic acids, using a nucleic acid probe and analysis

XX PT of the obtained data -

XX PS Example 5; Page 17; 34pp; Japanese.

XX CC This invention relates to a method for measuring nucleic acids using a

XX CC nucleic acid probe labelled with a fluorochrome. The nucleic

XX CC acid probe decreases the fluorescence of the fluorochrome when

XX CC hybridised with a target nucleic acid, the decrease in the fluorescence

XX CC is measured. The method can be used for measuring a target nucleic acid.

XX SQ Sequence 19 BP; 15 A; 0 C; 0 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 6.1e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1098

DB 1 TATATATAAAAAA 19

RESULT 931
 AAD52991/c
 ID AAD52991 standard; DNA; 19 BP.
 XX AC AAD52991;
 XX DT 14-MAY-2003 (first entry)
 XX DE Bacteriophage N4 VRNAP gene terminator signal sequence #4.
 XX KW Virion RNA polymerase; nuclear magnetic resonance; NMR; microinjection;
 XX OS VRNAP; ds.
 XX OS Bacteriophage N4.
 XX PN WO200295002-A2.
 XX PD 28-NOV-2002.
 XX PF 22-MAY-2002; 2002WO-US16295.
 XX PR 22-MAY-2001; 2001US-292845P.
 XX PA (UYCH-) UNIV CHICAGO.
 XX PI Kazmierczak KM, Davydova EK, Rothman-Denes LB;
 XX DR WPI; 2003-140368/13.
 XX PT New nucleic acid encoding an N4 virion RNA polymerase for e.g.
 XX PT synthesizing RNAs of a desired sequence, RNAs for use as probes in
 XX PT hybridization studies or Southern or Northern blot analysis, and
 XX PT RNA:DNA hybrids -
 XX PS Example 4; Page 164; 165pp; English.

XX CC The invention relates to bacteriophage N4-coded virion RNA polymerase
 XX CC (VRNAP) and its nucleic acid. The nucleic acid is used to make an N4
 XX CC VRNAP which is useful in the synthesis of RNAs of a desired sequence,
 XX CC RNAs for use as probes in hybridisation studies or Southern or Northern
 XX CC blot analysis, and RNA:DNA hybrids for nuclear magnetic resonance (NMR)
 XX CC structure determination; for in vitro studies of spliceosome assembly,
 XX CC splicing reactions and antisense experiments; for in vitro translation
 XX CC or microinjection; and for nucleic acid amplification. The present
 XX CC sequence is Bacteriophage N4 VRNAP gene terminator signal sequence.

XX SQ Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 6.1e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 326 AGAAGCTGTGGAGCACTT 344

DB 19 AAAAGCTGGGAGCAGCTT 1

RESULT 932

AAQ20027/c

ID AAQ20027 standard; DNA; 20 BP.

XX AC AAQ20027;

XX DT 01-APR-1992 (first entry)

XX DE Cross-linking oligomer 112 for targeting HUMIL1B.

XX KW deoxyribonucleic acid; major groove; ethanoino group; IL-1;

XX KW aziridinylcytosine; cross-linking group; o-xyloso linking group;

XX KW human interleukin-1 beta; inverted polarity region; ss.

OS Synthetic.

XX Key Location/Qualifiers

PH modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "N4N4-ethanocytosine"

FT modified_base 4

FT /*tag= b

FT /mod_base= m5c

FT misc_feature 14..20

FT /*tag= c

FT /label= inverted_polarity_region

FT /note= "see comments"

FT modified_base 14

FT /*tag= d

FT /mod_base= m5c

FT modified_base 18

FT /*tag= e

FT /mod_base= m5c

FT modified_base 19

FT /*tag= f

FT /mod_base= OTHER

FT /note= "N-methyl-8-oxo-2'-deoxyadenine"

XX WO9118997-A.

PN 12-DEC-1991.

PD 24-MAY-1991; 91WO-1003680.

PF 14-JAN-1991; 91US-0640654.

PR 25-MAY-1990; 90US-0529346.

XX (GILE-) GILEAD SCIE INC.

XX Matteucci MD, Krawczyk S;

PI WPI; 1992-007480/01.

DR New sequence-specific non-photo-activated crosslinking agents -

XX bind to the major groove of duplex DNA and are esp. useful for

XX treating latent infections e.g. HIV

XX Example 4; Page 25; 42pp; English.

XX This oligomer contains an inverted polarity region formed from an

XX o-xylosa dimer synthon. Residues 13 and 14 are linked via an

XX o-xylosa group (i.e. nucleotides that have xylose sugar linked via

XX the o-xylosa ring). The sequence is designed to target the Human

XX interleukin-1 beta gene beginning at nucleotide 7378 and will

XX covalently cross-link to it via the N4N4-ethanocytosine group.

XX See also AAQ20026-Q20030.

XX Sequence 20 BP; 1 A; 4 C; 0 G; 15 T; 0 other;

SQ Query Match 1..3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAA 1099

DB 20 ATGAAAGAAAAAAGAA 2

RESULT 933

AAQ30371/C

ID AAQ30371 standard; DNA; 20 BP.

XX AAQ30371;

AC AAQ30371;

XX 25-MAR-2003 (updated)

DT 07-DEC-1992 (first entry)

XX Oligomer HUM beta 111 for forming triplex with IL-1 target duplex.

DE Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;

XX HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.

XX Synthetic.

XX Key Location/Qualifiers

PH modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT modified_base 4

FT /*tag= b

FT /mod_base= m5c

FT modified_base 14

FT /*tag= c

FT /mod_base= m5c

FT modified_base 18

FT /*tag= d

FT /mod_base= m5c

FT modified_base 19

FT /*tag= e

FT /mod_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT misc_feature 14..20

FT /*tag= f

FT /label= inverted_polarity_region

FT /note= "see comments"

FT misc_feature 13..14

FT /*tag= g

FT /note= "O-xylosa dimer synthon linkage"

XX WO9209705-A1.

PN 11-JUN-1992.

PD 25-NOV-1991; 91WO-US08811.

PF 23-NOV-1990; 90US-0617907.

PR 18-JAN-1991; 91US-0643382.

PR 08-APR-1991; 91US-0683420.

PR 17-APR-1991; 91US-0686544.

PR 17-APR-1991; 91US-0686546.

PR 17-APR-1991; 91US-0686547.

PR 27-SEP-1991; 91US-0766733.

XX (GILE-) GILEAD SCI INC.

XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;

XX WPI; 1992-217083/26.

XX New oligomers contg. modified bases - which form a triplex with

PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,

PT hepatitis, herpes, malignancy and inflammation

XX Claim 12; Page 70; 77pp; English.

XX The synthetic oligomer is capable of forming a triplex at

CC physiological pH with a purine rich target sequence by coupling

CC into the major groove of the duplex. The specific target sequence

CC of this oligomer is the human interleukin -1 beta gene beginning at

CC nucleotide 7378 contg. a purine rich sequence concd. on one strand

CC of the duplex. The oligomer, and others like it are useful in

CC diagnosis and therapy of diseases characterised by specific DNA

CC duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant

CC tumours and inflammation. The triple helices form under mild conditions

CC thus assays may be carried out without subjecting the test specimen to

CC harsh conditions. The oligomer contains an inverted polarity region

CC formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa

CC (nucleotides have the 3' positions of xylose sugars linked via the

CC o-xylene ring). Two nucleotides are coupled through a xylene residue
 CC to form the dimer synthon. This additional modifications may render
 CC the oligomer stable to nuclease activity. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems.
 CC See also AAQ25452-25501 and AAQ30226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 0 G; 15 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1081 ATTAAAAAATAAAAAA 1099
 Db 20 ATGAAGAAGAAAAAAGAA 2
 RESULT 934
 AAQ30372/c
 ID AAQ30372 standard; DNA; 20 BP.
 XX
 AC AAQ30372;
 XX
 XX 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)
 XX
 DE Oligomer HUM beta 112 for forming triplex with IL-1 target duplex.
 XX
 KW Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
 KW HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 FT modified_base 4
 FT /*tag= b
 FT /mod_base= m5c
 FT modified_base 14
 FT /*tag= c
 FT /mod_base= m5c
 FT modified_base 18
 FT /*tag= d
 FT /mod_base= m5c
 FT modified_base 19
 FT /*tag= e
 FT /mod_base= OTHER
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
 FT misc_feature 14..20
 FT /*tag= f
 FT /label= inverted_polarity_region
 FT /note= "see comments"
 FT misc_feature 13..14
 FT /*tag= g
 FT /note= "o-xylene dimer synthon linkage"
 XX
 W09209705-A1.
 XX
 PD 11-JUN-1992.
 XX
 XX 25-NOV-1991; 91WO-US08811.
 PF
 XX 23-NOV-1990; 90US-0617907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0686544.
 PR 17-APR-1991; 91US-0686546.
 PR 17-APR-1991; 91US-0686547.
 PR 27-SEP-1991; 91US-0766733.

XX (GILE-) GILEAD SCI INC.
 PA Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 PI WPI; 1992-217083/26.
 XX
 XX New oligomers contg. modified bases - which form a triplex with
 FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 FT hepatitis, herpes, malignancy and inflammation
 XX
 PS Claim 12; Page 70; 77pp; English.
 XX
 CC The synthetic oligomer is capable of forming a triplex at
 CC physiological pH with a purine rich target sequence by coupling
 CC into the major groove of the duplex. The specific target sequence
 CC of this oligomer is the human interleukin -1 beta gene beginning at
 CC nucleotide 7378 contg. a purine rich sequence concd. on one strand
 CC of the duplex. The oligomer, and others like it are useful in
 CC diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV; HER; HIV; hepatitis B, herpes, malignant
 CC tumours and inflammation. The triple helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions. The oligomer contains an inverted polarity region
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
 CC (nucleotides have the 3' positions of xylose sugars linked via the
 CC o-xylene ring). Two nucleotides are coupled through a xylene residue
 CC to form the dimer synthon. This additional modifications may render
 CC the oligomer stable to nuclease activity. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems.
 CC See also AAQ25452-25501 and AAQ30226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 1 A; 4 C; 0 G; 15 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1081 ATTAAAAAATAAAAAA 1099
 Db 20 ATGAAGAAGAAAAAAGAA 2
 RESULT 935
 AAQ53128
 ID AAQ53128 standard; DNA; 20 BP.
 XX
 AC AAQ53128;
 XX
 DT 03-JUN-1994 (first entry)
 XX
 DE Gene detection sequence 52.
 XX
 KW Gene detection; radio-isotopes; target gene; electrode;
 KW detection; optical fibre; hybridise; hybridisation; electrochemical;
 KW photochemical; electrolysis; probe; ss.
 XX
 OS Synthetic.
 XX
 PN JP05285000-A.
 XX
 PD 02-NOV-1993.
 XX
 XX 10-SEP-1992; 92JP-0242397.
 PF
 XX 13-FEB-1992; 92JP-0025621.
 PR
 PA (TOKE) TOSHIBA KK.
 XX
 XX WPI; 1993-382240/48.
 XX
 PT Detection method of gene without using radio-isotope - by

PT hybridisation of nucleic acid probe which is single strand having
 PT complementary sequence of gene and single strand denatured sample
 PT DNA

XX Disclosure; Page 23; 26pp; Japanese.

XX The sequences (AAQ53077-Q53136) are used in the invention to detect
 CC specific genes without the use of radio-isotopes. Detection
 CC is carried out by hybridisation of denatured (ss) sample DNA with a
 CC (ss) nucleic acid probe, complementary to the target sequence.
 CC Hybridisation occurs on the surface of an electrode or optical fibre
 CC and detection is visualised by the addition of an entity that
 CC recognises (ds) hybridised DNA and is electrochemically /
 CC photochemically active.

XX Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 AGAAGCTGGAGAGAGAGTGT 785
 Db 1 ACAGCTGGAGAGAGAGT 19

RESULT 936

AAQ58461/C

ID AAQ58461 standard; DNA; 20 BP.

XX AAQ58461;

XX AC

XX AAQ58461;

XX AC

XX 22-SEP-1994 (first entry)

DE Antisense oligonucleotide to the IL-1 beta gene.

XX Antisense; interleukin-1-beta; IL-1 beta; phospho-oligonucleotide;
 KW inhibit; chronic inflammatory disease; rheumatism; ss.

XX Synthetic.

OS

XX JP06041185-A.

XX PD

XX 15-FEB-1994.

XX 16-JUL-1992; 92JP-0213519.

XX 16-JUL-1992; 92JP-0213519.

XX (LTTK-) LTT KENKYUSHO KK.

XX WPI; 1994-089330/11.

XX New anti-sense phospho-oligo:nucleotide - esp. corresp. to

PT interleukin-1-beta sense sequence, useful to inhibit chronic

PT inflammatory diseases

XX Claim 2; Page 2; 6pp; Japanese.

XX Sequences (AAQ58558-61) are antisense oligonucleotides that are used

CC to inhibit the production of interleukin-1-beta (AAQ58462). The

CC oligonucleotides are useful for the inhibition of inflammatory

CC diseases such as chronic joint rheumatism.

XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 other;

Query Match

Best Local Similarity 1.3%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 744 GCCTTGGTCTTAAGAGA 762

Db 19 GCCTTGGGCTCAGGAAA 1

RESULT 937

AAQ98660

ID AAQ98660 standard; DNA; 20 BP.

XX AAQ98660;

XX AC

XX 25-MAR-2003 (updated)

DT 10-APR-1996 (first entry)

XX Human papilloma virus PAP88 specific internal PCR primer MY48.

DE Human papilloma virus; primer; detection; diagnosis; genital;

XX oral; carcinomas; research; PAP88; specific; MY48; internal;

XX typing; PCR; ss.

XX Synthetic.

OS US5447839-A.

XX 05-SEP-1995.

XX 20-APR-1993; 93US-0050743.

XX 14-NOV-1990; 90US-0613142.

XX 09-SEP-1988; 88US-0243486.

XX 10-MAR-1989; 89US-0322550.

XX 09-SEP-1989; 89WO-US03747.

XX 20-APR-1993; 93US-0050743.

XX (HOFF) HOFFMANN LA ROCHE INC.

XX Bauer HM, Greer CE, Manos MM, Resnick RM, Ting Y;

XX WPI; 1995-319884/41.

XX Detection of human papilloma virus DNA by amplification - using

PT specific consensus primer pairs and pref. detection with generic or

PT type specific probes for use in research and diagnosis

XX Disclosure; Columns 9-10; 36pp; English.

XX The human papilloma virus (HPV) specific primers AAQ98655-Q98662 were

CC used to amplify HPV nucleic acid sequences. The amplified sequences

CC were then screened using labelled probes, which detected and/or

CC typed the HPV sequences for research or diagnostic purposes, e.g.

CC to identify HPV that are implicated in genital or oral carcinomas.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 316 AAGACTGCAGAGAGCTGT 334

Db 2 AGGTCTGCAGAAAGCTGT 20

RESULT 938

AAAT01233/C

ID AAAT01233 standard; DNA; 20 BP.

XX AAAT01233;

XX 25-MAR-2003 (updated)

DT 07-DEC-1995 (first entry)

XX Human chromosome 13 gene based 13-STS7 antisense primer.

DE Normalised cDNA library; directionally cloned cDNA library;

XX

KW screening; hybridisation; human chromosome 13; exon mapping; STS;
 KW sequence tagged site; ss.

OS Synthetic.

PN WO9508647-A1.

PD 30-MAR-1995.

XX 23-SEP-1994; 94WO-US10821.

XX 24-SEP-1993; 93US-0126594.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Efstratiadis A, Soares MB;

XX WPI; 1995-139615/18.

XX New normalised directional cDNA libraries - used for isolating
 PT novel cDNA's, including tissue-specific and development-specific
 PT DNA.

PS Disclosure; Page 125; 186pp; English.

XX To initiate exon-mapping of human chromosome 13, cDNAs present in a
 CC normalised library were hybridised to arrayed chromosome-specific
 CC phage lambda clones. Part of the procedure involved PCR
 CC amplification of chromosome 13 sequences using primer pairs based
 CC on the 3' (and/or exceptionally the 5') terminal 300 nucleotides of
 CC each cDNA. (see AAT01228-T01257).

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 2 A; 9 C; 2 G; 7 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1001 GAGGCTGAGAAATGGGAG 1019

DB 19 GAGGCTGAGAAAGGTGAAG 1

RESULT 939

AAAT44752

ID AAT44752 standard; DNA; 20 BP.

XX AC AAT44752;

XX 25-MAR-2003 (updated)

DT 29-JAN-1997 (first entry)

XX Internal PCR primer MY48 to generate generic probe.

DE Probe; primer; PCR; polymerase chain reaction; amplification;

XX human papillomavirus; consensus; ss.

XX Synthetic.

XX US5527898-A.

XX 18-JUN-1996.

XX 07-JUN-1995; 95US-0474542.

XX 24-SEP-1993; 93US-0126452.

XX 09-SEP-1988; 88US-0243486.

XX 10-MAR-1989; 89US-0322550.

XX 09-SEP-1989; 89WO-US03747.

XX 14-NOV-1990; 90US-0613142.

XX 20-APR-1993; 93US-0050743.

XX 07-JUN-1995; 95US-0474542.

XX PA

XX (HOFF) HOFFMANN LA ROCHE INC.

XX PI

XX Bauer HM, Gravitt PE, Greer CE, Manos MM, Resnick RM;

XX PI

XX Zhang TY;

XX DR

XX WPI; 1996-299903/30.

XX XX

XX Nucleic acid hybridisation probes - specific for selected human

XX PT

XX papilloma virus types

XX PS

XX Disclosure; Column 19; 96pp; English.

XX CC

XX The invention relates to new oligonucleotide probes and primers used
 CC for the detection of human papillomaviruses (HPV) which are not genital
 CC types 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are
 CC esp. used to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and
 CC 68. The primers can be used to detect these HPV types in conjunction with
 CC the consensus primers and typing probes AAT44733-T44906, which are based
 CC on and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
 CC sequences. Detection of the amplification products is done with probes
 CC derived from consensus sequences found in all characterised HPV
 CC sequences. Primers AAT44751-2 are used to amplify a fragment of the
 CC highly divergent isolate HPV PAP88 L1 region for use as a generic probe
 CC to determine whether the HPV sequences have been successfully amplified
 CC in the reaction.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ

Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 316 AAGACTGCAGAGAGCTGT 334

DB 2 AGGCTGCAGAAAAGCTGT 20

RESULT 940

AAV01932/C

ID AAV01932 standard; DNA; 20 BP.

XX AC AAV01932;

XX 20-APR-1998 (first entry)

XX DE

XX Auxotrophic ORF TRP4 20mer tag.

XX KW

XX ADE1; auxotrophic yeast gene; probe array; tag; detection; VLSTPS;

XX very large scale immobilised polymer synthesis; parallel analysis; ss.

XX OS

XX Synthetic.

XX EN

XX EP799897-A1.

XX XX

XX 08-OCT-1997.

XX PF

XX 03-APR-1997; 97EP-0302313.

XX PR

XX 04-APR-1996; 96US-0626285.

XX PA

XX (APFY-) AFFYMETRIX INC.

XX PI

XX Davis RW, Mittmann MP, Morris MS, Schoemaker DD;

XX XX

XX WPI; 1997-482677/45.

XX DR

XX Selection of sets of tag nucleic acids and generation of probe
 PT arrays - for simultaneous detection of large numbers of nucleic
 PT acids in a sample

XX PS

Example 3; Fig 4; 46pp; English.

CC A method has been developed of selecting tag nucleic acids (TNA) with
 CC minimal hybridization to a nucleic acid. A composition has also been
 CC developed comprising a set of TNA with a constant region and a variable
 CC region, optionally with < 2 C nucleotides, where the variable region
 CC for each TNA has a similar Tm, G:C:A:T ratio and length, does not
 CC cross-hybridise to a probe NA, and preferably contains an even number
 CC of A+G nucleotides, each TNA when aligned with any other TNA of the set
 CC has at least 2 nucleotides different. An array of oligonucleotide probes
 CC comprising several experimental oligonucleotide probe sets attached to
 CC a solid substrate, where each set hybridises to a different target NA
 CC under stringent hybridisation conditions, each oligonucleotide probe in
 CC the set comprises a variable region, and where the NA probes do not
 CC cross hybridise in the array, is also new. The present sequence
 CC represents an autotrophic ORF 20mer tag, which is used in an example of
 CC the present invention. The method of synthesising the TNA's and probes
 CC are designated Very Large Scale Immobilised Polymer Synthesis
 CC (VLSIPS (RTM)). They permit massive parallel analysis of all the
 CC components, especially nucleic acids, in a mixture in a single assay.

CC Sequence 20 BP; 7 A; 6 C; 5 G; 2 T; 0 other;
 CC
 CC Query Match 1.3%; Score 14.2; DB 1; Length 20;
 CC Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 CC Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 507 TTGGCCAGTTTGGCATTTG 525
 Db 20 TTGGACGGTTTGGCATCTG 2

RESULT 941
 AAV01248/c
 ID AAV01248 standard; DNA; 20 BP.
 AC AAV01248;
 DT 23-MAR-1998 (first entry)
 DE Retinoblastoma 1 PCR primer for universal mammalian STS's.
 KW PCR primer; polymerase chain reaction; amplification; UM-STS;
 KW universal mammalian sequence tagged site; genomic map; clone; ss.
 OS Synthetic.
 PN WO9731012-A1.
 PD 28-AUG-1997.
 PF 18-FEB-1997; 97WO-US02403.
 PX 22-FEB-1996; 96US-0012061.
 PY (UNMI) UNIV MICHIGAN.
 PA (UNMS) UNIV MICHIGAN STATE.
 PI Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
 DR WPI; 1997-435083/40.
 XX New oligonucleotide primers amplifying gene regions conserved among
 PT mammals - useful for developing genomic maps, isolating clones and
 PT making cross-species comparisons
 XX Claim 1; Page 11; 26pp; English.

CC The present sequence represents a specifically claimed oligonucleotide
 CC PCR primer. The oligonucleotide can be used for polymerase chain
 CC reaction (PCR) amplification of DNA, specifically regions of specific
 CC genes that are conserved among mammalian species, i.e. pairs of
 CC oligonucleotides from the present specification represent universal
 CC mammalian sequence-tagged site (UM-STS) primers. The primers are used

CC to develop genomic maps, to isolate clones from libraries, to make
 CC cross-species comparisons and to develop additional genetic markers.
 CC UM-STS allow genomic comparisons to be made between more species.

CC Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 other;
 CC
 CC Query Match 1.3%; Score 14.2; DB 1; Length 20;
 CC Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 CC Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 115 AGAAACGGGAGAAAGGAT 133
 Db 19 AGAACTGGCAGAAATGAT 1

RESULT 942
 AAT48684/c
 ID AAT48684 standard; DNA; 20 BP.

XX AAT48684;
 AC
 DT 25-MAR-2003 (updated)
 DT 02-OCT-1997 (first entry)

XX Probe for detecting N-ras gene mutations in the codon at position 61.
 XX Mutated codon; single base mutation; human; acute myeloid leukaemia;
 KW tumour; activated ras gene; N-ras; H-ras; K-ras; ss.
 XX Synthetic.
 OS
 XX US5591582-A.
 PN
 XX 07-JAN-1997.
 PD
 XX 23-JUN-1994; 94US-0264425.
 PF
 XX 04-AUG-1987; 87US-0081490.
 PR 23-JUL-1985; 85US-0758104.
 PR 21-APR-1992; 92US-0873352.
 PR 23-JUN-1994; 94US-0264425.
 XX (UYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Bos JL, Van der Eb AJ;
 PI
 XX WPI; 1997-086629/08.
 DR
 XX Detection of activated ras gene - using oligo:nucleotide probes to
 PT detect mutated codon
 PT
 XX Claim 25; Column 29; 20pp; English.

CC A new method has been produced for the detection of an activated ras
 CC gene containing a mutated codon. The method involves: either cleaving a
 CC human subject's genomic DNA with a restriction enzyme to produce DNA
 CC fragments and treating the fragments to obtain single-stranded DNA
 CC molecules or isolating the subject's polyA+ mRNA; contacting the
 CC single-stranded DNA molecules or polyA+ mRNA under hybridising
 CC conditions with a labelled synthetic DNA molecule, optionally bound to
 CC a solid support, comprising 12-20 nucleotides, where the synthetic DNA
 CC molecule is 5'-B-Q-D-3' in the case of single-stranded DNA or is
 CC complementary to 5'-B-Q-D-3' in the case of polyA+ mRNA, B = 0-9
 CC nucleotides having a sequence complementary to a sequence in the
 CC activated ras gene 5' of the mutated codon, D = 0-12 nucleotides having
 CC a sequence complementary to a sequence in the activated ras gene 3' of
 CC the mutated codon, provided that B and D contain a total of at least 9
 CC nucleotides, and Q is complementary to the mutated codon; treating the
 CC resulting hybridised molecules under conditions permitting only fully
 CC complementary molecules to remain hybridised; and detecting the presence
 CC of the labelled synthetic DNA molecule in the hybridised molecules. The
 CC present sequence represents the synthetic DNA probe used for detecting
 CC the activated N-ras gene when the mutated codon is at position 61 and

CC has a single base substitution in the first or second nucleotide
 CC position so that it encodes an amino acid other than Glu. The method can
 CC be used for the diagnosis of acute myeloid leukaemia and other tumours.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 AGAAGTGGAGAGAGAGTGT 785
 Db 20 ACAGCTGGAGAGAGAGT 2

RESULT 943
 AAT77876
 ID AAT77876 standard; DNA; 20 BP.
 AC AAT77876;
 XX
 XX
 XX 25-MAR-2003 (updated)
 DT 02-OCT-1997 (first entry)
 XX
 XX Internal PCR primer MY48 for papillomavirus 88 generic probe.
 DE Papillomavirus 88; PAP88; generic probe; detection; primer;
 KW internal; polymerase chain reaction; PCR; amplification; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX US5639871-A.
 PN
 XX 17-JUN-1997.
 PD
 XX
 XX 01-JUN-1995; 95US-0457648.
 PF
 XX
 XX 14-NOV-1990; 90US-0613142.
 PR 24-SEP-1993; 93US-0126452.
 PR 09-SEP-1988; 88US-0243486.
 PR 10-MAR-1989; 89US-0322550.
 PR 29-AUG-1989; 89WO-US03747.
 PR 20-APR-1993; 93US-0050743.
 XX
 XX (HOFF) ROCHE MOLECULAR SYSTEMS INC.
 PA
 XX
 XX Bauer HM, Gravitt PE, Greer CE, Impraim CC, Manos MM;
 PI Resnick RM, Zhang TV;
 XX
 XX WPI; 1997-332084/30.
 DR
 XX

New oligo:nucleotide probes for human papilloma-virus - used for
 detecting and typing HPV and for detecting previously unknown HPV
 types and subtypes

Disclosure; Columns 63-64; 94pp; English.

The present sequence is an internal primer for the PCR
 amplification of a papillomavirus 88 (PAP88) specific generic
 probe.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX

SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 316 AAGACTGCAGAGAGCTGT 334
 Db 2 AGGTCTGCAGAGAGCTGT 20

RESULT 944
 AAT47349
 ID AAT47349 standard; DNA; 20 BP.
 XX
 AC AAT47349;
 XX
 XX 10-SEP-1997 (first entry)
 DT
 XX
 XX Variant #5 of universal primer sequence for M13mp18.
 DE
 XX
 XX PCR; primer; amplify; polymerase chain reaction; bacteriophage; M13mp18;
 KW cystic fibrosis transmembrane conductance regulator gene; multiplex PCR;
 KW chimeric primer; genetic screening; mutation detection; CFTR;
 KW Wilms Tumour gene; beta-thalassaemia gene; ss.
 XX
 OS Synthetic.
 XX
 XX WO9641012-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX
 XX 06-JUN-1996; 96WO-US09637.
 PF
 XX
 XX 07-JUN-1995; 95US-0474450.
 PR
 XX (GENZ) GENZYME CORP.
 PA
 XX
 XX Shuber AP;
 PI
 XX
 XX WPI; 1997-052372/05.
 DR
 XX

Universal primer used for multiplex DNA amplification - allows
 simultaneous amplification of multiple DNA target sequences for high
 throughput genetic screening

Claim 7; Page 10; 38pp; English.

AAT47345-T47374 represent variants of a universal primer sequence (see
 AAT47344) derived from the bacteriophage vector M13mp18. This sequence
 can be used as half of the DNA primer of the invention. The primers are
 used for amplification of a target DNA sequence, and can be used in a
 multiplex PCR amplification. The primers have the sequence 5'-X-3',
 where X is a sequence that does not hybridise to the target sequence
 (such as this sequence), and Y is a sequence contained within or
 flanking the target sequence. The melting temperature of a hybrid between
 X and its complement (in the absence of other sequences) is 60 degrees
 C. During early cycles of amplification, products are synthesised that
 contain the chimeric primers on either end. The primers then serve as
 high stringency recognition sequences for subsequent rounds of
 amplification. As a result, the annealing efficiency of different
 primers and their targets in a multiplex amplification reaction is
 normalised, thereby reducing preferential amplification of certain
 targets. The chimeric primer comprise a 5' universal domain and a 3'
 target-specific domain. They are used for the simultaneous PCR
 amplification of multiple DNA targets in a sample. The primer containing
 AAT47344 is particularly useful in high-throughput genetic screening for
 detecting the presence of multiple defined targets e.g. to detect
 mutations in genes like the cystic fibrosis transmembrane conductance
 regulator (CFTR), the Wilms Tumour, and the beta-thalassaemia genes.

Sequence 20 BP; 3 A; 8 C; 7 G; 2 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 606 GTGACCTGGCCATCTCAA 624
 Db 2 GCGGCCGGGCCATCTCAA 20


```

PR 26-MAR-1998; 98US-0048810.
XX (ISIS-) ISIS PHARM INC.
PA Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;
PI WPI; 1999-610754/52.
DR WPI; 1999-610754/52.
XX New antisense compounds used to treat eg. hyperproliferative conditions
PT -
PT Example 2; Page 38; 157pp; English.
PS
XX
CC AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention
CC describes novel nucleotide antisense compounds, targetted to the 5',
CC untranslated, translation termination codon, or 3' untranslated region
CC of a nucleic acid encoding human mdm2, that modulates expression of
CC human mdm2. The oligonucleotides mediate their effect by antisense
CC inhibition of hyperproliferative gene expression. The antisense compound
CC is used to treat an animal having a disease or condition associated
CC with mdm2, particularly a hyperproliferative condition, more
CC particularly cancer, especially of the blood, brain, breast, lung or soft
CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 465 GAGCTCCAGCACTTGGCA 483
DB 20 GATCTACAGCACTTGGTA 2

RESULT 948
AAZ37720
ID AAZ37720 standard; DNA; 20 BP.
XX
AC AAZ37720;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #250.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;
KW cancer; antisense; modulation; oligonucleotide; expression;
KW inhibition; hyperproliferation; blood cancer; brain cancer;
KW breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
KW atherosclerosis; restenosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949065-A1.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999; 99WO-US06702.
XX
PR 26-MAR-1998; 98US-0048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;
XX WPI; 1999-610754/52.
DR WPI; 1999-610754/52.
PT New antisense compounds used to treat eg. hyperproliferative conditions
XX

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PS Example 9; Page 54; 157pp; English.
XX
CC AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention
CC describes novel nucleotide antisense compounds, targetted to the 5',
CC untranslated, translation termination codon, or 3' untranslated region
CC of a nucleic acid encoding human mdm2, that modulates expression of
CC human mdm2. The oligonucleotides mediate their effect by antisense
CC inhibition of hyperproliferative gene expression. The antisense compound
CC is used to treat an animal having a disease or condition associated
CC with mdm2, particularly a hyperproliferative condition, more
CC particularly cancer, especially of the blood, brain, breast, lung or soft
CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
XX
SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAGGCTGAGGCTGGA 1009
DB 2 TTGGAGGCTGAGGCTGGA 20

RESULT 949
AAZ06049/C
ID AAZ06049 standard; DNA; 20 BP.
XX
AC AAZ06049;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB01939.
XX
PR 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 1820; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAZ36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,

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CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 XX
 SQ Sequence 20 BP; 7 A; 2 C; 8 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 86 TGGTTAGGACCTTCCTTC 104
 20 TAGTTACGACCTTCCTTC 2
 Db
 RESULT 950
 AAZ05954
 ID AAZ05954 standard; DNA; 20 BP.
 XX
 AC AAZ05954;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 OS
 PN WO9928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB01939.
 XX
 PR 04-NOV-1998; 98US-0107077.
 PR 28-NOV-1997; 97FR-0015041.
 PR 17-DEC-1997; 97FR-0016034.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-371125/31.
 XX
 PT Genome sequence of Chlamydia trachomatis
 PS Disclosure; Page 1813; 1755pp; English.
 XX
 CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 XX
 SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 795 CTGAGGACTGACTGAACC 813
 Db
 RESULT 952
 AAZ01622
 ID AAZ01622 standard; DNA; 20 BP.
 XX
 AC AAZ01622;
 XX
 DT 07-OCT-1999 (first entry)

Db 1 CTGAAGGACCGACTGAGCC 19
 RESULT 951
 AAZ04675/c
 ID AAZ04675 standard; DNA; 20 BP.
 XX
 AC AAZ04675;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 OS
 PN WO9928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB01939.
 XX
 PR 04-NOV-1998; 98US-0107077.
 PR 28-NOV-1997; 97FR-0015041.
 PR 17-DEC-1997; 97FR-0016034.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-371125/31.
 XX
 PT Genome sequence of Chlamydia trachomatis
 PS Disclosure; Page 1708; 1755pp; English.
 XX
 CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 XX
 SQ Sequence 20 BP; 6 A; 1 C; 10 G; 3 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 634 AGTCGCGCTCCCTGCAACC 652
 20 AGTCCTCTCCCTTTAACC 2
 Db
 RESULT 952
 AAZ01622
 ID AAZ01622 standard; DNA; 20 BP.
 XX
 AC AAZ01622;
 XX
 DT 07-OCT-1999 (first entry)

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XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX PD Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX PF paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
XX KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
XX KW Bartholinitis; pneumonia; pneumopathy; venereal lymphogranulomatosis; ss.
XX OS Synthetic.
XX OS Chlamydia trachomatis.
XX PN WO9928475-A2.
XX PD 10-JUN-1999.
XX PF 27-NOV-1998; 98WO-IB01939.
XX PR 04-NOV-1998; 98US-0107077.
XX PR 28-NOV-1997; 97FR-0015041.
XX PR 17-DEC-1997; 97FR-0016034.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-371125/31.
XX PT Genome sequence of Chlamydia trachomatis
XX PS Disclosure; Page 1458; 1755pp; English.
XX CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX CC encode polypeptides (see AAX36754-Y37949) which can be used as vaccines
XX CC against Chlamydia trachomatis. Antisense and ribozyme sequences
XX CC can also be used to control growth of the microorganism. Chlamydia
XX CC trachomatis is responsible for a large number of diseases, e.g. eye
XX CC diseases such as conventional trachoma, nonendemic trachoma,
XX CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
XX CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
XX CC perihepatitis, Bartholinitis; pneumopathy in breast feeding infants;
XX CC and venereal lymphogranulomatosis. The polypeptides of the
XX CC invention may be of use in treating these diseases.
XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;
      Query Match 1.3%; Score 14.2; DB 1; Length 20;
      Best Local Similarity 84.2%; Pred. No. 6.4e+02;
      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 807 CTGAACCTGTGCTACTGTGG 825
Db 1 CTGAACCTGTGCTACTGTGG 19
RESULT 953
AAX94936
ID AAX94936 standard; DNA; 20 BP.
XX AC AAX94936;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
XX KW vaccine; neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydia pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB01890.
XX PR 04-NOV-1998; 98US-0107078.
XX PR 21-NOV-1997; 97FR-0014673.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PN WO9927105-A2.

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XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB01890.
XX PR 04-NOV-1998; 98US-0107078.
XX PR 21-NOV-1997; 97FR-0014673.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PT Genome sequence of Chlamydia pneumoniae
XX PS Page 1708; Disclosure; 1912pp; English.
XX CC AAX91991-X97517 represent PCR primers used to amplify open reading
XX CC frames and other nucleic acid sequences from the genome of
XX CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
XX CC disease such as pneumonia and bronchitis and is thought to be a
XX CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
XX CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
XX CC by the open reading frames of the C. pneumoniae genome (see AAX94584-
XX CC AAV35879) can be used in immunogenic compositions as vaccines. Vectors
XX CC containing C. pneumoniae nucleotide sequences can also be used as
XX CC immunogenic compositions, especially where the vector directs the
XX CC expression of a neutralising epitope of C. pneumoniae.
XX SQ Sequence 20 BP; 2 A; 3 C; 7 G; 8 T; 0 other;
      Query Match 1.3%; Score 14.2; DB 1; Length 20;
      Best Local Similarity 84.2%; Pred. No. 6.4e+02;
      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 131 CATGCTCTCTTTGGGGGCT 149
Db 2 CATTTCTGCATTGGGGGTT 20
RESULT 954
AAX94007/c
ID AAX94007 standard; DNA; 20 BP.
XX AC AAX94007;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
XX KW vaccine; neutralising epitope; PCR primer; ss.
XX OS Synthetic.
XX OS Chlamydia pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB01890.
XX PR 04-NOV-1998; 98US-0107078.
XX PR 21-NOV-1997; 97FR-0014673.
XX PA (GEST ) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PN WO9927105-A2.

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PT Genome sequence of Chlamydia pneumoniae
 XX Page 1636; Disclosure; 1912pp; English.
 XX
 CC AAX91991-X97517 represent PCR primers used to amplify open reading
 CC frames and other nucleic acid sequences from the genome of
 CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
 CC disease such as pneumonia and bronchitis and is thought to be a
 CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 CC by the open reading frames of the C. pneumoniae genome (see AAX34584-
 CC AAX35879) can be used in immunogenic compositions as vaccines. Vectors
 CC containing C. pneumoniae nucleotide sequences can also be used as
 CC immunogenic compositions, especially where the vector directs the
 CC expression of a neutralising epitope of C. pneumoniae.
 XX
 XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 460 AGGAAGAGCTCGAGAACT 478
 Db 20 AGGAAGAGCTCGCTCTAACT 2
 RESULT 955
 AAX91991/C
 ID AAX91991 standard; DNA; 20 BP.
 XX AC AAX91991;
 XX AC
 XX 13-SEP-1999 (first entry)
 DT
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 KW vaccine; neutralising epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 XX WO9927105-A2.
 XX
 XX 03-JUN-1999.
 XX
 XX 20-NOV-1998; 98WO-IB01890.
 XX
 XX 04-NOV-1998; 98US-0107078.
 XX 21-NOV-1997; 97FR-0014673.
 XX
 XX (GEST) GENSET.
 XX
 XX Griffais R;
 XX
 XX WPI; 1999-357842/30.
 XX
 XX Genome sequence of Chlamydia pneumoniae
 XX
 XX Page 1476; Disclosure; 1912pp; English.
 XX
 CC AAX91991-X97517 represent PCR primers used to amplify open reading
 CC frames and other nucleic acid sequences from the genome of
 CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
 CC disease such as pneumonia and bronchitis and is thought to be a
 CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 CC by the open reading frames of the C. pneumoniae genome (see AAX34584-
 CC AAX35879) can be used in immunogenic compositions as vaccines. Vectors
 CC containing C. pneumoniae nucleotide sequences can also be used as
 CC immunogenic compositions, especially where the vector directs the

CC expression of a neutralising epitope of C. pneumoniae.
 XX
 SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 642 TCCCTGCAACCGAGTGTTC 660
 Db 20 TCCCTACCAACCAAGTGGTC 2
 RESULT 956
 AAX29926
 ID AAX29926 standard; DNA; 20 BP.
 XX AC AAX29926;
 XX AC
 XX 06-JUL-1999 (first entry)
 DT
 DE Primer 128 for PDZ domain-containing protein genes.
 XX
 KW PDZ domain; gene expression; human umbilical vascular endothelial cell;
 KW HUVEC; stimulation; tumour necrosis factor; TNF; protein binding; PCR;
 KW cell; proliferation disorder; cancer; primer; amplification; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9907846-A1.
 XX
 XX 18-FEB-1999.
 XX
 XX 12-AUG-1998; 98WO-JF03603.
 XX
 XX 19-JUN-1998; 98JP-0189944.
 XX 12-AUG-1997; 97JP-0230356.
 XX
 XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 XX Funahashi S, Miyata S;
 XX WPI; 1999-167423/14.
 XX
 XX Protein containing PDZ domain, whose expression is enhanced by TNF
 XX stimulation - plays an important role in protein/protein
 XX interactions and is used for screening for proteins for use in
 XX treatment of cell proliferation disorders such as cancer
 XX
 XX Example 2; Page 29; 240pp; Japanese.
 XX
 CC This sequence represents a primer use to amplify and isolate clones
 CC which encode new proteins containing PDZ domains whose expression in
 CC human umbilical vascular endothelial cells (HUVEC) are enhanced by
 CC stimulation with tumour necrosis factor (TNF) alpha. The new protein
 CC is used to identify proteins which bind to it (particularly to the PDZ
 CC domains) and the genes encoding them, for use in the treatment of cell
 CC proliferation disorders such as cancer.
 XX
 XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 other;
 SQ
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 473 GGAACCTGGCACTCTCTCAG 491
 Db 2 GGAATAGGCACTCTCTCAG 20
 RESULT 957
 AAV73038

ID AAV73038 standard; DNA; 20 BP.

XX AAV73038;

AC 09-FEB-1999 (first entry)

XX Human ras oncogene probe #13.

DT 09-FEB-1999 (first entry)

DE Ras oncogene; probe; point mutation; detection; cancer; ss.

XX Synthetic.

OS US5847095-A.

PN 08-DEC-1998.

XX 03-JAN-1997; 97US-0778543.

PF 04-AUG-1987; 87US-0081490.

XX 23-JUL-1985; 85US-0758104.

PR 21-APR-1992; 92US-0873352.

PR 23-JUN-1994; 94US-0264425.

PR 03-JAN-1997; 97US-0778543.

XX (UYLE-) RIJKSUNIV LEIDEN.

PA Bos JL, van der Eb AJ;

XX WPI; 1999-059149/05.

DR Probes for detecting ras oncogene point mutations - useful for the

PT diagnosis of cancer associated with single base mutations

XX Claim 6; Column 5; 18pp; English.

XX AAV73026-V73071 are probes used to detect a single-base mutation in a human ras oncogene. These probes comprise 12-43 nucleotides of formula 5'-B-Q-D-3', Q = 3 nucleotides complementary to the mutated codon, and B and D each = 0-20 nucleotides complementary to the ras sequences flanking the mutated codon. The probes are useful for detecting cancers associated with point mutations.

XX Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 AGAAGTGGAGAGAGAGTGT 785

DB 1 ACAGCTGGAGAGAGAGT 19

RESULT 958

AAV73141/C

ID AAV73141 standard; DNA; 20 BP.

XX AAV73141;

AC 09-FEB-1999 (first entry)

DT Human ras oncogene mutant detecting oligomer N-61a.

XX Ras oncogene; probe; point mutation; detection; cancer; ss.

XX Synthetic.

OS US5847095-A.

PN 08-DEC-1998.

XX 03-JAN-1997; 97US-0778543.

PF New antisense compound for inhibiting the expression of signal

XX transducer and activator of transcription 3 (STAT3) in cells or tissues and treating diseases or condition associated with STAT3, such as rheumatoid arthritis and cancer -

PR 04-AUG-1987; 87US-0081490.

PR 23-JUL-1985; 85US-0758104.

PR 21-APR-1992; 92US-0873352.

PR 23-JUN-1994; 94US-0264425.

PR 03-JAN-1997; 97US-0778543.

XX (UYLE-) RIJKSUNIV LEIDEN.

PA Bos JL, van der Eb AJ;

XX WPI; 1999-059149/05.

DR Probes for detecting ras oncogene point mutations - useful for the

PT diagnosis of cancer associated with single base mutations

XX Disclosure; Column 19-20; 18pp; English.

XX AAV73084-V73145 are oligomers used in a method to detect a single-base mutation in a human ras oncogene. These probes comprise 12-43 nucleotides of formula 5'-B-Q-D-3', Q = 3 nucleotides complementary to the mutated codon, and B and D each = 0-20 nucleotides complementary to the ras sequences flanking the mutated codon. The probes are useful for detecting cancers associated with point mutations.

XX Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 AGAAGTGGAGAGAGTGT 785

DB 20 ACAGCTGGAGAGAGT 2

RESULT 959

AAC93175

ID AAC93175 standard; DNA; 20 BP.

XX AAC93175;

AC 15-FEB-2001 (first entry)

DT Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:26.

XX Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;

XX modulation; signal transducer and activator of transcription;

XX DNA-binding protein; signal transduction; inhibition; apoptosis;

XX inflammatory disease; cancer; antinflammatory; antirheumatic;

XX cytosolic; immunostimulatory; rheumatoid arthritis; leukaemia;

XX myeloma; melanoma; lymphoma; diagnosis; ss.

XX Homo sapiens.

OS WO2000061602-A1.

PN 19-OCT-2000.

XX 06-APR-2000; 2000WO-US09054.

PF 08-APR-1999; 99US-0288461.

XX (ISIS-) ISIS PHARM INC.

PA Karas JG;

PI WPI; 2000-619223/59.

DR New antisense compound for inhibiting the expression of signal

XX transducer and activator of transcription 3 (STAT3) in cells or tissues and treating diseases or condition associated with STAT3, such as

XX rheumatoid arthritis and cancer -

PS Example 2; Page 46; 104pp; English.

XX The present invention describes an antisense compound (I), 8 to 30
CC nucleobases in length, that is targeted to a nucleic acid molecule
CC encoding STAT3 (Signal Transducer and Activator of Transcription) and
CC which inhibits the expression of it. (I) has antiinflammatory
CC antirheumatic, cytostatic and immunostimulatory activities. (I) is used
CC for inhibiting the expression of STAT3 in cells or tissues, treating
CC an animal having a disease or condition associated with STAT3 or a
CC human having a disease or condition characterised by a reduction in
CC apoptosis, and inducing apoptosis in a cell. Diseases or conditions
CC that are treated are rheumatoid arthritis, cancer of the breast,
CC prostate, brain, head and/or neck, leukaemia, myeloma or
CC lymphoma. (I) can also be used for diagnostic methods in detecting and
CC determining the role of STAT3 in various cell functions, physiological
CC processes and conditions and for diagnosing the conditions associated
CC with expression of STAT3. (I) can be used alone or with other drugs as
CC an immunostimulant. (I) is used in sandwich and colourimetric assays,
CC involving enzyme conjugation and radiolabeling and is used in
CC diagnostic kits. AAC93150 encodes human STAT3 and AAC93231 encodes mouse
CC STAT3 as given in the exemplification of the present invention. AAC93151
CC to AAC93230 and AAC93232 to AAC93299 represent STAT3 phosphorothioate
CC antisense oligonucleotides, and AAC93300 represents a mismatch control
CC oligonucleotide which are used in example from the present invention.

XX Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 876 TCCTTCGAGTCTTCGATG 894

DB 2 TCCTTCGAGTCTTCGATG 20

RESULT 960

AAA78302
ID AAA78302 standard; DNA; 20 BP.

XX AAA78302;

XX 16-NOV-2000 (first entry)

DE Human Ig H chain sequencing primer SHHR-12.

XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW immunosuppression; autoimmune disease; treatment; rheumatism;
KW anti-Fas antibody; primer; ss.

OS Homo sapiens.

XX JP2000154149-A.

XX 06-JUN-2000.

XX 17-SEP-1999; 99JP-0263984.

XX 18-SEP-1998; 98JP-0264598.

XX (SANY) SANKYO CO LTD.

XX WPI; 2000-454476/40.

XX Anti-human Fas humanizing antibody-containing antirheumatic agents -
PS Example 4; Page 21; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive

CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences
CC of the IgM light and heavy chains (see AAA78267-A78272) and the
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences
CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAA78277-A78318 and
CC AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention.

XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 445 AGCCAGATGCTTCACGGA 463

DB 2 ATCCGAGGCTTCACGGA 20

RESULT 961

AAA41064

ID AAA41064 standard; DNA; 20 BP.

XX AAA41064;

DT 16-AUG-2000 (first entry)

XX Human TNFalpha antisense oligonucleotide ISIS# 104703.

XX Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
KW pancreatitis; atopic dermatitis; allograft rejection;
KW autoimmune disease; inflammatory disease; ss.

XX Synthetic.

XX WO2000020645-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23205.

XX 05-OCT-1998; 98US-0166186.

XX 18-MAY-1999; 99US-0313932.

XX (ISIS-) ISIS PHARM INC.

XX Baker BF, Bennett CF, Butler MM, Shanahan WJ;

XX WPI; 2000-303808/26.

XX Oligonucleotide for treating diseases associated with human tumour
PT necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNFalpha -

XX Example 22; Page 101; 283pp; English.

XX This sequence represents an antisense oligonucleotide sequence which
CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
CC in host defence. It is produced mainly in macrophages and monocytes in
CC response to infection, invasion, injury or inflammation. Overexpression

CC of TNFalpha can result in disease states, particularly in infectious,
 CC inflammatory and autoimmune diseases. The invention relates to antisense
 CC oligonucleotides, such as that represented by the present sequence which
 CC are capable of modulating the TNFalpha gene expression. The
 CC oligonucleotides optionally have a phosphorothioate backbone, and may
 CC also optionally contain at least one 2'-O-methoxyethyl modification. The
 CC oligonucleotides are useful for modulating the expression of human
 CC TNFalpha in cells and tissues, reducing a human cell inflammatory
 CC response, reducing the blood glucose level in a human and treating a
 CC human having a disease or condition associated with TNFalpha. Examples of
 CC diseases associated with TNFalpha include diabetes, inflammatory bowel
 CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
 CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
 CC The antisense oligonucleotides are also useful for modulating the
 CC function of a selected nucleic acid sequence in adipose tissue.
 XX
 XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 743 AGCCTGGTGGCTTAAGGAG 761
 DB 2 AGCCTGGCTTGAAGAG 20

RESULT 962
 AAZ49574
 ID AAZ49574 standard; cDNA; 20 BP.
 AC AAZ49574;
 XX
 XX 07-APR-2000 (first entry)
 DE Reverse primer for PCR mapping studies of human MP-7 gene.

KW PCR primer; human myocardium protein-7; MP-7; congestive heart failure;
 KW cardiovascular disorder; cardiomyopathy; PCR mapping study; ss.

OS Homo sapiens.
 PN WO9967387-A2.
 XX
 XX 29-DEC-1999.

PF 24-JUN-1999; 99WO-US14307.
 XX
 XX 25-JUN-1998; 98US-0030579.
 PR 29-SEP-1998; 98US-0163284.
 PR 02-MAR-1999; 99US-0261759.

XX (MILL-) MILLENNIUM PHARM INC.

FA Khodadoust M;

PI WPI; 2000-136984/12.

XX Novel myocardium protein-7 polynucleotides, used to modulate a variety
 XX of cellular processes -

XX Example 2; Page 94; 116pp; English.

XX The present sequence is the reverse PCR primer designed from 3'UTR
 CC sequence of myocardium protein-7 (MP-7). This was used in PCR mapping
 CC studies to determine the chromosomal localisation of MP-7 gene. Specific
 CC amplification was carried on human and hamster cell line DNA. MP-7 is
 CC used to modulate a variety of cellular processes e.g. modulating the
 CC activity of proteins involved in cardiovascular disorders like
 CC congestive heart failure or cardiomyopathy.

XX Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 263 CAGGAGCACCTTCAGAAAG 281
 DB 1 CAGGAGCACCTTCAGAG 19

RESULT 963
 AAZ56049
 ID AAZ56049 standard; DNA; 20 BP.

XX AAZ56049;

XX 23-MAR-2000 (first entry)

XX PCR primer for beta-actin.

XX Nuclear factor of activated T cells; NFATp; bone fracture; osteoporosis;
 KW calcineurin interaction region; cartilage cell differentiation;
 KW endochondral ossification; chondrosarcoma; rheumatoid arthritis;
 KW osteoarthritis; osteosarcoma; fibrous sarcoma; chondroma; enchondroma;
 KW PCR primer; beta-actin; ss.

OS Mus sp.

XX WO9961908-A1.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11941.

XX 28-MAY-1998; 98US-0087139.

XX (HARD) HARVARD COLLEGE.

XX Glimcher LH, Ranger AM;

XX WPI; 2000-086734/07.

XX Modulating growth or differentiation of cartilage cells useful for
 XX treating chondrosarcoma, osteochondroma and arthritis in mammals -

XX Example 6; Page 57; 90pp; English.

XX PCR primers AAZ56049-Z56050 are used to amplify beta-actin from wild
 CC type and NFATp-/- cartilage cultures. The primers are used in the
 CC identification of the role that NFATp plays in cartilage cell growth and
 CC differentiation. The modulation of growth or differentiation of
 CC cartilage can be carried out through contacting cells deficient in the
 CC NFAT family genes, with a test compound. Modulating growth or
 CC differentiation of cartilage cells can be achieved by contacting the cells
 CC with a modulator of NFATp activity, where the modulator comprises a
 CC peptidic compound derived from the calcineurin interacting region of
 CC NFATp. The methods of the invention are useful for modulating the growth
 CC or differentiation of cartilage cells and endochondral ossification
 CC useful for repairing bone defects and fractures in mammals including
 CC humans, monkeys, dogs, cats, mice etc. The compound that modulates
 CC cartilage cell growth and differentiation is useful for diagnosing
 CC disorders such as chondrosarcoma, osteochondroma, chondromyxoid fibroma,
 CC chondroma, enchondroma, chondroblastoma, osteochondroma, fibrous
 CC dysplasia, ossifying fibroma, osteosarcoma or osteocartilaginous
 CC exostosis, which are associated with a change (elevated, reduced or
 CC mutated) in the expression of NFATp in cartilage cell. NFATp inhibitory
 CC compounds are useful for treating disorders such as rheumatoid arthritis,
 CC osteoarthritis and osteoporosis associated with cartilage degradation.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 771 CTGGAGAGAGCTGACC 789
D5 1 CTGGAGAGAGCTGAGC 19
RESULT 964
AAS29251/c
ID AAS29251 standard; DNA; 20 BP.
XX AAS29251;
AC AAS29251;
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 16515.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are
FT 2'-O-methoxyethyl bases, and bases 7-14 are
FT deoxynucleotides"
XX
PN US2001016575-A1.
XX
XX 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-0752983.
XX
XX 26-MAR-1999; 99US-0280805.
XX 26-MAR-1998; 98US-0048810.
XX
XX (MIRA/) MIRAGLIA L J.
XX (NERO/) NERO P.
XX (GRAH/) GRAHAM M J.
XX (MONT/) MONIA B P.
XX (COWS/) COWSERT L M.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX WPI; 2001-535565/59.
XX
XX An antisense compound, useful for treating e.g. cancer, comprises
XX nucleobases targeted a region (e.g. translation termination codon
XX region) of a nucleic acid encoding human mdm2 -
XX
XX Example 2; Page 11; 81pp; English.
XX
XX The present invention relates to antisense compounds, 8-30 nucleobases
XX in length targeted to the 5' untranslated region, translation
XX termination codon region, 3' untranslated region, coding region or
XX translation start site of a nucleic acid encoding human mdm2, where
XX the antisense compound modulates the expression of human mdm2. The
XX antisense oligonucleotides of the invention are useful for encoding
XX human mdm2 and for inhibiting the expression of human mdm2. They may be
XX used for treating an animal having a disease or condition associated
XX with amplification of mdm2 gene or overexpression of mdm2 e.g. a
XX hyperproliferative disorder such as cancer (blood, brain, breast, lung,
XX or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or
XX resenosis, tumours, colorectal carcinoma and chronic myelogenous
XX leukemia. The antisense compound may be administered with a
XX chemotherapeutic agent to overcome drug resistance. The antisense
XX compound reduces hyperproliferation of human cells. The method, which
XX involves the use of the antisense compound, is also useful for detecting
XX the role of mdm2 expression in various cell functions and physiological

CC processes and useful in both clinical research and diagnostic tools.
CC AAS29242-AAS29507 represent the human mdm2 antisense oligonucleotides
CC of the present invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 465 GAGCTCCAGCACTTGCCA 483
D5 20 GATCTACAGCACTTGCTA 2
RESULT 965
AAS29489
ID AAS29489 standard; DNA; 20 BP.
XX
AC AAS29489;
XX
DT 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31784.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are
FT 2'-O-methoxyethyl bases, and bases 7-14 are
FT deoxynucleotides"
XX
PN US2001016575-A1.
XX
XX 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-0752983.
XX
XX 26-MAR-1999; 99US-0280805.
XX 26-MAR-1998; 98US-0048810.
XX
XX (MIRA/) MIRAGLIA L J.
XX (NERO/) NERO P.
XX (GRAH/) GRAHAM M J.
XX (MONT/) MONIA B P.
XX (COWS/) COWSERT L M.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX WPI; 2001-535565/59.
XX
XX An antisense compound, useful for treating e.g. cancer, comprises
XX nucleobases targeted a region (e.g. translation termination codon
XX region) of a nucleic acid encoding human mdm2 -
XX
XX Example 9; Page 18; 81pp; English.
XX
XX The present invention relates to antisense compounds, 8-30 nucleobases
XX in length targeted to the 5' untranslated region, translation
XX termination codon region, 3' untranslated region, coding region or
XX translation start site of a nucleic acid encoding human mdm2, where
XX the antisense compound modulates the expression of human mdm2. The
XX antisense oligonucleotides of the invention are useful for encoding
XX human mdm2 and for inhibiting the expression of human mdm2. They may be
XX used for treating an animal having a disease or condition associated

CC with amplification of mdm2 gene or overexpression of mdm2 e.g. a
CC hyperproliferative disorder such as cancer (blood, brain, breast, lung,
CC or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or
CC restenosis, tumours, colorectal carcinoma and chronic myelogenous
CC leukemia. The antisense compound may be administered with a
CC chemotherapeutic agent to overcome drug resistance. The antisense
CC compound reduces hyperproliferation of human cells. The method, which
CC involves the use of the antisense compound, is also useful for detecting
CC the role of mdm2 expression in various cell functions and physiological
CC processes and useful in both clinical research and diagnostic tools.
CC AAS29242-AAS29507 represent the human mdm2 antisense oligonucleotides
CC of the present invention.

XX Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAGGCTGAGGCGGA 1009
DB 2 TTGGAGGCTGAGGCGGA 20

RESULT 966

AAD14791
ID AAD14791 standard; DNA; 20 BP.

AC AAD14791;

DT 01-NOV-2001 (first entry)

DE Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116632.

XX Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;
KW antisense therapy; diabetes; hyperproliferative disorder; inflammation;
KW neurological disorder; tumour; haematopoietic disorder; infection;
KW hyperproliferative disorder; developmental disorder; antisense;
KW phosphorothioate backbone; ss.

OS Homo sapiens.
OS Synthetic.

PH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"

FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"

FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"

FT modified_base 2
FT /tag= d
FT /mod_base= m5c

FT modified_base 9
FT /tag= e
FT /mod_base= m5c

FT modified_base 10
FT /tag= f
FT /mod_base= m5c

FT modified_base 11
FT /tag= g
FT /mod_base= m5c

FT modified_base 15
FT /tag= h
FT /mod_base= m5c

FT modified_base 18
FT /tag= i

FT /mod_base= m5c
FT modified_base 20
FT /tag= j
FT /mod_base= m5c

PN WO200152865-A1.

XX 26-JUL-2001.

PD 16-JAN-2001; 2001WO-US01411.

XX 21-JAN-2000; 2000US-048856.

PA (ISIS-) ISIS PHARM INC.

XX Monia BP, Mckay R, Butler MM, Wyatt JR;

DR WPI; 2001-442247/47.

XX Antisense compound 8 to 30 nucleobases in length comprising a compound
PT that is targeted to a nucleic acid molecule encoding glycogen synthase
PT kinase 3 alpha, useful for the treatment of e.g. diabetes and
PT hyperproliferative disorders -

XX Example 15; Page 83; 115pp; English.

XX The invention relates to an antisense compound 8 to 30 nucleobases in
CC length targeted to a nucleic acid encoding glycogen synthase kinase 3
CC alpha. The antisense compound specifically hybridises with and inhibits
CC the expression of glycogen synthase kinase 3 alpha. The antisense
CC compound is useful for the treatment of a disease associated with
CC glycogen synthase kinase 3 alpha such as diabetes, a neurological
CC disorder, a haematopoietic disorder, a hyperproliferative disorder or
CC a developmental disorder. The antisense compounds may also be used
CC prophylactically to prevent or delay infection, inflammation or tumour
CC formation. The present sequence is a phosphorothioate antisense
CC oligonucleotide targeted to human glycogen synthase kinase 3 alpha DNA.

XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 204 CTGGTTCCTCCAGCCCTCTC 222
DB 2 CTGGTTCCTCCAGCCCTCTC 20

RESULT 967
AAD09232/c

ID AAD09232 standard; DNA; 20 BP.

XX AAD09232;

DT 12-SEP-2001 (first entry)

DE Human c-ski oncoprotein encoding cDNA amplifying RT-PCR primer Nsk12.

XX Human; cytostatic; vaccine; gene therapy; immunogen; c-ski oncoprotein;
KW cytotoxic lymphocyte; CTL; tumour cell; human leukocyte antigen; HLA-A1;
KW HLA-A2; HLA-A3; cancer; melanoma; colorectal carcinoma; lung carcinoma;
KW ovarian carcinoma; prostate carcinoma; major histocompatibility complex;
KW MHC; cytokine; passive immunotherapy; RT-PCR primer; ss.

OS Homo sapiens.

XX WO200149310-A1.

PN 12-JUL-2001.

PD 03-JAN-2001; 2001WO-US00154.

XX

PR 03-JAN-2000; 2000US-0174296.
XX (ARGN-) ARGNOEX PHARM INC.
PA Hogan KT, Ross MW;
XX WPI; 2001-441786/47.
DR
XX New immunogenic peptides derived from c-ski oncoprotein, useful for
PT inducing cytotoxic T lymphocyte response in vivo and in vitro and for
PT diagnosing, preventing, treating melanoma, colorectal and lung
PT carcinomas
XX
XX Example 7; Page 47; 77pp; English.
XX
XX The present invention relates to peptide immunogens derived from c-ski
XX oncoprotein. The peptides are useful for inducing a cytotoxic lymphocyte
XX (CTL) response in vitro that is specific for a tumour cell expressing at
XX least one of human leukocyte antigens (HLA)-A1, HLA-A2 or HLA-A3. The
XX CTLs produced in vitro are useful for treating cancer such as melanoma,
XX colorectal carcinoma, ovarian carcinoma, lung carcinoma or prostate
XX carcinoma characterised by tumour cells expressing HLA-A1, -A2 or -A3 or
XX any class I major histocompatibility complex (MHC) molecule and the
XX c-ski oncogene by direct lysis or effecting destruction of tumour cells
XX indirectly through the elaboration of cytokines. The peptides can also
XX be used to screen a sample for the presence of CTL that specifically
XX recognise the corresponding epitopes. Peptides are used to prepare
XX class I MHC tetramers which can be used in conjunction with flow
XX cytometry to quantitate the frequency of peptide-specific CTL that are
XX present in a sample of lymphocytes from individuals. The immunogenic
XX peptides can also be used to stimulate the production of antibodies for
XX use in passive immunotherapy, as diagnostic reagents, as reagents such
XX as in affinity chromatography. The immunogenic peptides are used as
XX vaccine. c-ski gene is used in gene therapy.
XX The present sequence is human c-ski oncoprotein encoding cDNA amplifying
XX RT-PCR primer Nsk12.
XX
XX Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1000 TGAGGCTGGAGATGGCAA 1018
Db 20 TGAGGCTGGAGATGGCAA 2
RESULT 968
AAH42050/c
ID AAH42050 standard; DNA; 20 BP.
XX
XX AAH42050;
AC
XX
XX 05-SEP-2001 (first entry)
DT
XX Pollicular conjunctivitis related adenoviral DNA PCR primer #11.
DE
XX Pollicular conjunctivitis; antiserum; antiviral; vaccine; infection;
KW PCR primer; ss.
XX
XX Mastadenovirus.
OS
XX
XX JP2001095583-A.
PN
XX
XX 10-APR-2001.
PD
XX
XX 30-SEP-1999; 99JP-0278661.
PF
XX
XX 30-SEP-1999; 99JP-0278661.
PR
XX
XX (ITON/) ITO N.
PA
XX

DR WPI; 2001-341249/36.
XX
XX New adenovirus for the prevention and treatment of Ad infection -
PT
XX Example 1; Page 7; 45pp; Japanese.
PS
XX The present invention describes an adenovirus which is separated from the
XX conjunctiva of a follicular conjunctivitis patient and neutralised weakly
XX by an antiserum against the type 8 or type 9 prototype of adenovirus but
XX is not neutralised by the types 1-7 prototype or the type 10, 11, 14, 19,
XX 22, 34, 35, 37, 40 or 41 prototype. The adenovirus causes congestion in
XX the conjunctiva and follicular conjunctivitis, and the method of the
XX invention is used for their prevention.
XX
XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 other;
SQ
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 470 CCAGGAACTTGGCATTCCT 488
Db 20 CCAGGAACTTGGCATTCCT 2
RESULT 969
AAH45766
ID AAH45766 standard; DNA; 20 BP.
XX
XX AAH45766;
AC
XX
XX 07-SEP-2001 (first entry)
DT
XX Human E2F-2 gene PCR primer SEQ ID NO: 18.
DE
XX Nucleic acid amplification; adapter DNA; human; PCR primer; ss.
KW
XX Homo sapiens.
OS
XX
XX WO200138572-A1.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 16-NOV-2000; 2000WO-JP08073.
PF
XX
XX 19-NOV-1999; 99JP-0330726.
PR
XX
XX 25-JUL-2000; 2000JP-0224663.
PS
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX
XX Aoyagi K, Sasaki H, Terada M, Mineno J, Asada K, Kato I;
PI
XX
XX WPI; 2001-355947/37.
DR
XX
XX Amplifying nucleic acids with base sequences of mRNAs in sample while
PT sustaining the ratio among them used to monitor mRNA expression,
PT applicable in producing e.g. cRNA library and DNA microarrays -
XX
XX Example 1; Page 53; 67pp; Japanese.
XX
XX The present invention describes a method of amplifying nucleic acids,
XX involving forming a single-stranded DNA to an mRNA in a sample with a
XX primer, synthesising a DNA strand complementary to the single-stranded
XX DNA to form a double-stranded DNA, adding a single or double-stranded
XX adapter DNA to the double-stranded DNA, and amplifying the DNA strand
XX using a second primer with a nucleic acid sequence in the adapter DNA.
XX This can be used to amplify nucleic acids to monitor mRNA expression,
XX which is applicable in producing e.g. cRNA libraries, cDNA libraries, DNA
XX microarrays or membrane arrays in gene engineering and gene expression
XX analysis, and in drug development and health maintenance and
XX management. The present sequence is a PCR primer described in the
XX exemplification of the invention.
XX

SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 607 TGGACGTGGCCATCTCAAC 625
 ||||| ||||| |||||
 Db 1 TGGACTTGGCCACTTCAAC 19

RESULT 970
 AAD07541/c
 ID AAD07541 standard; DNA; 20 BP.
 AC AAD07541;
 DT 10-AUG-2001 (first entry)
 XX Human mdm2 antisense oligonucleotide (ISIS #16515).
 DE Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
 KW tumour; prophylaxis; antisense; ss.
 XX Homo sapiens.

Key Location/Qualifiers
 modified_base 1..20
 /tag= a
 /mod_base= OTHER
 /note= "Phosphorothioate backbone"
 modified_base 1..6
 /tag= b
 /mod_base= OTHER
 /note= "2'-methoxyethoxy residues"
 modified_base 1
 /tag= c
 /mod_base= m5c
 modified_base 4..5
 /tag= d
 /mod_base= m5c
 modified_base 15..20
 /tag= e
 /mod_base= OTHER
 /note= "2'-methoxyethoxy residues"
 modified_base 20
 /tag= f
 /mod_base= m5c

US6238921-B1.
 29-MAY-2001.
 26-MAR-1998; 98US-0048810.
 26-MAR-1998; 98US-0048810.
 (ISIS-) ISIS PHARM INC.
 Miraglia LJ, Nero P, Graham MJ, Monia BP;
 WPI; 2001-366477/38.
 New oligonucleotides 16506, 16507, 16518, 16520, 16521, 16522 and 16524, which inhibit human mdm2 expression, useful for inhibiting, diagnosing or treating abnormal proliferative conditions associated with mdm2 -
 Example 2; Column 16; 19pp; English.
 The present invention relates to compositions and methods for modulating the expression of human mdm2 gene, a naturally present cellular gene implicated in abnormal cell proliferation and tumour formation. The

CC invention also provides antisense oligonucleotides which are targeted to the mdm2 gene and are capable of inhibiting the expression of mdm2 gene. The oligonucleotides are useful in diagnostics, therapeutics, prophylaxis and as research reagents. They are especially useful for inhibiting, diagnosing and treating abnormal proliferative conditions associated with mdm2. The method is useful for detecting and determining the role of mdm2 expression in various cell functions and physiological processes and conditions, and for diagnosing conditions associated with mdm2 expression.
 CC The present sequence is human mdm2 antisense oligonucleotide (ISIS #16515) with a phosphorothioate backbone. This sequence is targeted to the coding region of the mdm-2 gene.
 CC Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;
 SQ Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 465 GAGCTCCAGGAACTGGCA 483
 ||||| ||||| |||||
 Db 20 GATCTACAGGAAGTTGGTA 2

RESULT 971
 AAF80636/c
 ID AAF80636 standard; DNA; 20 BP.
 XX AAF80636;
 DT 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #10.
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 KW Homo sapiens.
 OS US6184212-B1.
 PN 06-FEB-2001.
 PD 26-MAR-1999; 99US-0280805.
 PF 26-MAR-1998; 98US-0048810.
 PR (ISIS-) ISIS PHARM INC.
 DA Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowser LM;
 PI WPI; 2001-190948/19.
 XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic acid molecule encoding human mdm-2 useful for modulating the expression of human mdm-2 and reducing hyperproliferation of human cells -
 Example 2; Column 20; 77pp; English.
 CC The present invention relates to an antisense compound 8-30 nucleobases in length targeted to nucleobases 1-308 of the 5' untranslated region, 1776-1806 of the translation termination codon region or 1818-2370 of the 3' untranslated region of a nucleic acid molecule encoding human mdm-2. The invention is useful for reducing hyperproliferation of human cells, modulating the expression of mdm2 in human cells or tissues or in vitro. The hyperproliferative disorder includes cancer or psoriasis.
 CC Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;
 SQ Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 465 GAGCTCCAGGAACTTGGCA 483
 DB 20 GATCTACAGGAACTTGGTA 2

RESULT 972
 AAF80874
 ID AAF80874 standard; DNA; 20 BP.
 XX
 AC AAF80874;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Human mdm2 phosphorothioate oligonucleotide #248.
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX Homo sapiens.
 OS
 XX US6184212-B1.
 PN
 XX 06-FEB-2001.
 PD
 XX 26-MAR-1999; 99US-0280805.
 PF
 XX 26-MAR-1998; 98US-0048810.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowser LM;
 PI WPI; 2001-190948/19.
 DR
 XX Novel antisense compound 8-30 nucleobases in length targeted to a
 PT nucleic acid molecule encoding human mdm-2 useful for modulating the
 PT expression of human mdm-2 and reducing hyperproliferation of human
 PT cells -
 XX Example 9; Column 33; 77pp; English.
 PS
 XX The present invention relates to an antisense compound 8-30
 CC nucleobases in length targeted to nucleobases 1-308 of the
 CC 5' untranslated region, 1776-1806 of the translation termination
 CC codon region or 1818-2370 of the 3' untranslated region of a
 CC nucleic acid molecule encoding human mdm-2. The invention is
 CC useful for reducing hyperproliferation of human cells,
 CC modulating the expression of mdm2 in human cells or tissues
 CC or in vitro. The hyperproliferative disorder includes cancer or
 CC psoriasis.
 XX
 SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAAGTCTGAGGCTGGA 1009
 DB 2 TTGGGAGGCTGAGGCAGGA 20

RESULT 973
 AAL41518/c
 ID AAL41518 standard; DNA; 20 BP.
 XX
 AC AAL41518;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE Oligonucleotide initiator SEQ ID No 7.
 XX

XX Cytostatic; cancer; Slug gene; mesenchymal cancer cell; leukaemia;
 KW sarcoma; antitumour agent; antisense therapy; ds.
 XX Unidentified.
 OS
 XX WO200259361-A1.
 PN
 XX 01-AUG-2002.
 PD
 XX 23-JAN-2002; 2002WO-ES00026.
 PF
 XX 23-JAN-2001; 2001ES-0000151.
 PR
 XX (UYSA-) UNIV SALAMANCA OTRI.
 PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 XX Sanchez Garcia I, Orfao De Matos A, Perez Losada J;
 PI WPI; 2002-691533/74.
 DR
 XX Detecting cancerous cells, useful for diagnosis and prognosis,
 PT comprises measuring abnormally high expression of the Slug gene or its
 PT protein -
 XX Disclosure; Page 55; 61pp; Spanish.
 PS
 XX The invention relates to a method for detecting cancerous cells in a
 CC vertebrate sample. The method comprises determining aberrant expression
 CC of the Slug gene, relative to a normal control sample. The method is used
 CC to detect (for diagnosis, monitoring progression and detection of
 CC residual disease after treatment) mesenchymal cancer cells (leukaemia or
 CC sarcoma) in humans. Agents that inhibit Slug (at DNA, RNA or protein
 CC levels) are potential antitumour agents. The polynucleotides of the
 CC invention can be used in antisense therapy. This polynucleotide sequence
 CC represents an oligonucleotide relating to the Slug gene of the invention.
 XX
 SQ Sequence 20 BP; 9 A; 7 C; 2 G; 2 T; 0 other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 AGTTTGGCATTTGGGAGTC 531
 DB 19 AGTTTGGCTTTTGGAGGC 1

RESULT 974
 AAD42961
 ID AAD42961 standard; DNA; 20 BP.
 XX
 AC AAD42961;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human PLA2, group VI (Ca2+-independent) antisense oligo ISIS #129863.
 XX
 KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KW antisense therapy; PLA2; phosphorothioate backbone; ss.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX

Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20

```
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      2..3
FT      /*tag= d
FT      /mod_base= m5c
FT      6
FT      /*tag= e
FT      /mod_base= m5c
FT      8..9
FT      /*tag= f
FT      /mod_base= m5c
FT      11..12
FT      /*tag= g
FT      /mod_base= m5c
FT      18
FT      /*tag= h
FT      /mod_base= m5c
FT      20
FT      /*tag= i
FT      /mod_base= m5c
XX
XX      US6410325-B1.
XX
XX      25-JUN-2002.
XX
XX      09-MAY-2001; 2001US-0851896.
XX
XX      09-MAY-2001; 2001US-0851896.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett CF, Freier SM, Watt AT;
XX
XX      WPI; 2002-616513/66.
XX
XX      Novel antisense compounds useful for inhibiting gene expression of
XX      human phospholipase A2, group VI and for treating diseases associated
XX      with expression of phospholipase A2, group VI
XX
XX      Claim 1; Column 45; 72pp; English.
XX
XX      The present invention relates to novel antisense compounds which inhibit
XX      the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
XX      The invention is useful for inhibiting the expression of PLA2, group VI
XX      (Ca2+-independent) in human cells or tissues and for treating an animal,
XX      particularly a human suspected of having or being prone to a disease or
XX      condition associated with expression of human PLA2, group VI (Ca2+-
XX      independent). It is useful for diagnostics, therapeutics and as research
XX      reagent, e.g. prophylactically to prevent or delay infection, tumour
XX      formation or inflammation. The present DNA sequence is an antisense
XX      oligonucleotide targetted to human PLA2, group VI (Ca2+-independent) DNA.
XX
XX      Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 other;
XX
XX      Query Match      1.3%; Score 14.2; DB 1; Length 20;
XX      Best Local Similarity 84.2%; Pred. No. 6.4e+02;
XX      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX      QY      404 CCTGCTCCAGCGGCTCTC 422
XX      ||| ||||| ||||| |||||
XX      2 CCAGCTCCACCGAGCTC 20
XX
XX      RESULT 975
XX      AAD41747
XX      ID      AAD41747 standard; DNA; 20 BP.
XX
XX      AC      AAD41747;
XX
XX      DT      30-OCT-2002 (first entry)
XX
XX      DE      Human RECQL2 antisense oligonucleotide, ISIS #137527.
```

```
XX
XX      Antisense; RECQL2; Bloom's disorder; prophyllaxis; infection; tumour;
XX      inflammation; therapy; human; phosphorothioate; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..20
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "Phosphorothioate backbone"
XX      modified_base 1..5
XX      /*tag= b
XX      /mod_base= OTHER
XX      /note= "2'-methoxyethyl nucleotides"
XX      modified_base 16..20
XX      /*tag= c
XX      /mod_base= OTHER
XX      /note= "2'-methoxyethyl nucleotides"
XX      modified_base 4
XX      /*tag= d
XX      /mod_base= m5c
XX      modified_base 7
XX      /*tag= e
XX      /mod_base= m5c
XX      modified_base 11..12
XX      /*tag= f
XX      /mod_base= m5c
XX      modified_base 20
XX      /*tag= g
XX      /mod_base= m5c
XX
XX      US6399378-B1.
XX
XX      04-JUN-2002.
XX
XX      01-MAR-2001; 2001US-0798096.
XX
XX      01-MAR-2001; 2001US-0798096.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Ward DT, Watt AT;
XX
XX      WPI; 2002-535979/57.
XX
XX      Antisense compounds targetted to nucleic acids encoding RECQL2
XX      associated with Bloom's disorder, for modulating RECQL2 expression and
XX      treating diseases e.g. tumors associated with expression of the RECQL2
XX      in humans
XX
XX      Example 15; Column 44; 86pp; English.
XX
XX      The invention relates to antisense compounds targetted to nucleic acid
XX      encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the
XX      expression of RECQL2. Antisense compounds of the invention are useful
XX      for treating diseases associated with expression of RECQL2, in humans.
XX      They are useful for diagnostics, therapeutics and as research reagent,
XX      e.g. prophylactically to prevent or delay infection, inflammation or
XX      tumour formation. They are also useful in antisense therapy. The
XX      present sequence is an antisense oligonucleotide targetted to human
XX      RECQL2 DNA.
XX
XX      Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 other;
XX
XX      Query Match      1.3%; Score 14.2; DB 1; Length 20;
XX      Best Local Similarity 84.2%; Pred. No. 6.4e+02;
XX      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX      QY      952 AACAGCTGGCGAGGTGTC 970
XX      ||| ||||| ||||| |||||
XX      2 ATCAGCTGCCATGCTGTC 20
XX
XX      DB
```

```

RESULT 976
ABK99746
ID ABK99746 standard; DNA; 20 BP.
AC ABK99746;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human RAIDD antisense oligonucleotide #78.
XX
KW Antisense gene therapy; RAIDD; death domain; caspase recruitment domain;
KW CARD; hyperproliferative disorder; cancer; growth disorder; human;
KW metabolic disorder; infection; inflammation; tumour formation;
KW RIP associated ICH-1/CED-3-homologous protein with death domain;
KW receptor interacting protein; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200248314-A2.
XX
PD 20-JUN-2002.
XX
PF 29-OCT-2001; 2001WO-US50914.
XX
PR 01-NOV-2000; 2000US-0705267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Zhang H, Freier SM, Watt AT;
XX
DR WPI; 2002-583496/62.
XX
PT Novel antisense compound that hybridizes and inhibits nucleic acid
PT encoding RAIDD which is an adaptor molecule containing both death
PT domain and caspase recruitment domains, for treating hyperproliferative
PT disorder -
XX
PS Claim 3; Page 93; 144pp; English.
XX
CC The invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule (II) encoding RAIDD which is an
CC adaptor molecule containing both death domain (DD) and caspase
CC recruitment domains (CARD), where (I) specifically hybridises with and
CC inhibits expression of RAIDD, or specifically hybridises with at least
CC an 8-nucleobase portion of an active site on (II). (I) is useful for
CC inhibiting the expression of RAIDD (Receptor interacting protein (RIP)
CC associated ICH-1/CED-3-homologous protein with death domain) in cells or
CC tissues, and for treating an animal having a disease or condition
CC associated with RAIDD, where the disease or condition is a
CC hyperproliferative disorder such as cancer, or a growth or metabolic
CC disorder. (I) is also useful for diagnostics, therapeutics, prophylaxis,
CC as research reagents and kits, for distinguishing functions of various
CC members of a biological pathway, and in antisense gene therapy. (I) is
CC also useful prophylactically, e.g. to prevent or delay infection,
CC inflammation or tumour formation. This sequence represents a human RAIDD
CC antisense oligonucleotide used to control expression of the RAIDD
CC protein.
XX
SQ Sequence 20 BP; 6 A; 3 C; 8 G; 3 T; 0 other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 955 AGCTGGCGAGGGTGGCACA 973
DB 1 AGCAGGGCATGTGGGCAA 19
RESULT 977
ABQ62490/c
ID ABQ62490 standard; DNA; 20 BP.
AC ABQ62490;
XX
DT 16-AUG-2002 (first entry)
XX
DE Mouse syntaxin 4 interacting protein antisense oligonucleotide 77.
XX
KW Mouse; antisense gene therapy; Syntaxin 4 interacting protein; ss;
KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
KW inflammation; tumour formation; phosphorothioate backbone;
KW 2'-O-methoxyethyl wing.
XX
OS Mus musculus.
XX
PN WO200224864-A2.
XX
PD 28-MAR-2002.
XX
PF 19-SEP-2001; 2001WO-US29251.
XX
PR 22-SEP-2000; 2000US-0668313.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Wyatt JR;
XX
DR WPI; 2002-401986/43.
XX
PT Novel antisense compound that hybridizes and inhibits nucleic acid
PT molecule encoding Syntaxin 4 interacting protein, useful for treating
PT diabetes, obesity and skeletal muscle disorder -
XX
PS Claim 3; Page 89; 154pp; English.
XX
CC The invention comprises antisense oligonucleotides designed to inhibit
CC expression of Syntaxin 4 interacting protein. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents a
CC mouse Syntaxin 4 interacting protein antisense oligonucleotide.
CC NOTE: The present sequence contains a phosphorothioate backbone and
CC 2'-O-methoxyethyl wings.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1030 GCGTGGCTTCATAGTGAG 1048
DB 20 GCGTGGCTTCATAGTGAG 2
RESULT 978
AAD36641/c
ID AAD36641 standard; DNA; 20 BP.
XX
AC AAD36641;
XX
DT 09-AUG-2002 (first entry)
XX
DE Human Her-1 antisense oligonucleotide ISIS #128515.
XX
KW Human; epidermal growth factor receptor; hyperproliferative disease;
KW Her1; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
KW tumour; cancer; ss.
XX

```


CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hyperproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC Stat3 antisense oligonucleotide.

XX SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 876 TCATTGAGTCTCGCATG 894
 Db 2 TCATTGAGTCTCGCATG 20

RESULT 980
 AAD34671
 ID AAD34671 standard; DNA; 20 BP.
 XX AC AAD34671;
 XX DT 16-JUL-2002 (first entry)
 XX DE DST CHS1_23 cDNA specific forward PCR primer.
 XX KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
 XX KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
 XX KW DST; digital sequence analysis; PCR; primer; ss.
 XX OS Unidentified.
 XX PN WO20022783-A2.
 XX PD 21-MAR-2002.
 XX PF 17-SEP-2001; 2001WO-US29123.
 XX PR 15-SEP-2000; 2000US-233176P.
 XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;
 XX WPI; 2002-339865/37.
 XX PT Preventing and treating hepatitis viral infection in a mammal,
 XX PT comprises administering nucleic acid molecules that up- or
 XX PT down-regulate in hepatitis B virus infection or polypeptides encoded by
 XX PT the nucleic acid molecules -
 XX PS Disclosure; Page 78; 125pp; English.

CC The present invention relates to a method for preventing, treating,
 CC modulating or ameliorating a medical condition. The method involves
 CC administering one or more nucleic acid molecules up- or down-regulated
 CC in hepatitis B virus (HBV) infection or polypeptides encoded by the
 CC nucleic acid molecules or antibodies that bind to the polypeptide. The
 CC method is useful for preventing, treating, modulating or ameliorating
 CC a medical condition. It is also useful for determining the presence or
 CC absence of a mutation in the nucleic acid molecules or detecting an
 CC alteration in expression of the polypeptide which is useful for the
 CC diagnosis of hepatitis viral infection. The method is useful for
 CC assessing the stage of hepatitis viral infection (e.g., acute hepatitis
 CC versus chronic hepatitis) or assessing the efficacy or toxicity of
 CC therapeutic treatment for hepatitis viral infection and a gene expression
 CC profile is useful for identifying polypeptides and polynucleotides which
 CC are associated with hepatitis viral infection. Sequences of the invention
 CC are used in gene therapy and as vaccines. Nucleic acid sequences are
 CC useful as a diagnostic markers for HBV infection and for treating
 CC infectious diseases. The present DNA sequence is a PCR primer which
 CC is specific for DST (digital sequence analysis) CHS1_23 cDNA.

XX SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 other;
 Query Match 1.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1024 AGCTGGCCTGGCTTTCAT 1042
 Db 1 AGCAGGGCCTGGCTATCTT 19

RESULT 981
 AAS97928
 ID AAS97928 standard; DNA; 20 BP.
 XX AC AAS97928;
 XX DT 12-MAR-2002 (first entry)
 XX DE Murine SAC1 gene-specific oligonucleotide PCR primer #481.
 XX KW Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
 XX KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
 XX KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
 XX KW protein replacement therapy.
 XX OS Mus sp.
 XX PN WO200183749-A2.
 XX PD 08-NOV-2001.
 XX PF 25-APR-2001; 2001WO-US13387.
 XX PR 28-APR-2000; 2000US-200794P.
 XX PR 28-JUL-2000; 2000US-221419P.
 XX PR 10-NOV-2000; 2000US-247443P.
 XX PA (WARN) WARNER LAMBERT CO.
 XX PA (NONE-) MONELL CHEM SENSES CENT.
 XX PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong FJ, Li S, Li X;
 XX PI Ohmen JD, Reed DR, Ross D, Tordoff MG;
 XX WPI; 2002-075162/10.
 XX PT Novel isolated polypeptide comprising variant form of mouse or human
 XX PT SAC1 polypeptide, and is associated with altered preference for
 XX PT carbohydrates or other sweeteners, useful for preventing obesity,
 XX PT diabetes, alcoholism -
 XX PS Claim 14; Page 93; 239pp; English.

CC The invention relates to an isolated polypeptide, comprising a variant
 CC form of mouse or human SAC1 polypeptide. The variant form is associated
 CC with altered preference for carbohydrates, other sweeteners or ethanol.
 CC The polypeptide and its associated DNA sequence can be produced by
 CC recombinant techniques and is useful for preventing obesity, diabetes or
 CC alcoholism associated with SAC1 expression. The sequences are useful in
 CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
 CC embryos may be used in screening for and identifying agents that induce
 CC or repress function of SAC1. Predisposition to diabetes, obesity or
 CC alcoholism can be ascertained by testing any fluid or tissue of a human
 CC (such as blood, pancreas or tongue) for sequence variations of the SAC1
 CC gene. A sequence variation of the SAC1 locus may indicate a
 CC predisposition to diabetes, obesity and/or alcoholism and may provide a
 CC diagnostic mark. The polynucleotide can be detected in a biological
 CC sample by contacting the DNA with a probe to form a hybridisation complex
 CC which is then detected. The sequences represent cDNA encoding human and
 CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes.
 XX SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 other;

QY 876 TCCATTGAGGTCTGCATG 894

Db 2 TCCATTGAGATCTTGGCATG 20

RESULT 984
ABL44478
ID ABL44478 standard; DNA; 20 BP.
XX ABL44478;
AC ABL44478;
XX 11-APR-2002 (first entry)
DT Human chromosome 1p36-35 PCR primer SEQ ID NO:1522.
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
KW genome; PCR primer; ss.
XX Homo sapiens.
OS JP2001321190-A.
XX 20-NOV-2001.
PD 12-MAR-2001; 2001JP-0068285.
PF 10-MAR-2000; 2000JP-0066716.
PR (RIKA) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
PA WPI; 2002-144136/19.
DR Arraying genome clones -
XX Claim 4; Page 34; 528pp; Japanese.
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention.
XX Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 other;
SQ Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 994 GAAGTCTGAGGCTGGAGAA 1012
DB 2 GAAGGCTAAGCAGAGAA 20

RESULT 985
ABV77208
ID ABV77208 standard; DNA; 20 BP.
XX ABV77208;
AC ABV77208;

XX 28-MAR-2003 (first entry)
PCR primer used to amplify consensus region B of hMOR cDNA.
XX Mu-opioid receptor; hMOR; G-protein coupled receptor; GPCR; GPCR array;
KW ion-related disease; asthma; diabetes; AIDS; allergy; dermatitis;
KW psoriasis; Alzheimer's disease; Parkinson's disease; arthritis;
KW depression; narcolepsy; infection; transplant rejection; lupus;
KW hepatitis; autism; cancer; renal disorders; PCR; primer; ss.
XX Homo sapiens.
OS WO200295065-A2.
XX 28-NOV-2002.
PD 21-MAY-2002; 2002WO-DK00337.
PF 18-MAY-2001; 2001DK-0000802.
PR (AZIG-) AZION BIOSCIENCE AS.
XX Thirstrup K, Madsen LS, Jensen JB, Hummel R, Jensen BS;
PI WPI; 2003-129439/12.
DR New G-protein coupled receptor array comprising individual
XX polynucleotide spots stably associated with a surface and a solid
PT support useful for determining the pathogenesis of different
PT ion-related conditions or diseases in humans -
XX Example 2; Page 30; 43pp; English.
XX PCR primers ABV77208-09 were used to amplify a consensus region of the
CC human mu-opioid receptor (hMOR). This opiod receptor belongs to the
CC G-protein coupled receptor (GPCR) family. The amplified fragment was
CC used to produce a GPCR array of the invention. The specification
CC describes a GPCR array comprising a multiplicity of individual
CC polynucleotide spots stably associated with a surface and a solid
CC support. The individual GPCR polynucleotide spot comprises a GPCR
CC polynucleotide composition consisting of a non-conserved region of a GPCR
CC polynucleotide family member, where the spots represent at least two
CC different regions of a GPCR polynucleotide family member. The GPCR array
CC is useful for determining the pathogenesis of different ion-related
CC conditions or diseases in humans, e.g. asthma, diabetes, AIDS, allergies,
CC dermatitis, psoriasis, Alzheimer's disease, Parkinson's disease,
CC arthritis, depression, narcolepsy, viral or parasitic infections,
CC transplant rejection, lupus, hepatitis, autism, cancer, renal disorders,
CC etc..
XX Sequence 20 BP; 1 A; 8 C; 5 G; 6 T; 0 other;
SQ Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 411 CAGCAGGCTCTCGGCTGC 429
DB 2 CCGCAGCTCTCTCGGCTGC 20

RESULT 986
AAQ33508
ID AAQ33508 standard; DNA; 14 BP.
XX AAQ33508;
AC AAQ33508;
XX 25-MAR-2003 (updated)
DT 02-FEB-1993 (first entry)
XX Sequence of microsatellite from clone AGLA206.
XX

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX Bos taurus.
 XX WO9213102-A1.
 PN 06-AUG-1992.
 XX 15-JAN-1992; 92WO-US00340.
 XX 15-JAN-1991; 91US-0642342.
 XX (GENM-) GENMARK.
 PA Georges M, Massey JM;
 PI WPI; 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification,
 PT gene mapping, and selective breeding
 XX Table 7; Page 131; 517pp; English.
 XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a genomic library of bovine MboI DNA fragments of between
 CC 250 and 500 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe.
 CC One out of 50 clones cross-hybridised. Assuming independent
 CC distribution of microsatellites and MboI sites, the frequency of
 CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
 CC 000. The sequence information for ca. 230 such bovine microsatellites
 CC is summarised in the specification and indexed herein (see below).
 CC The sequences upstream and downstream of the microsatellite sequence
 CC were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRIM). The microsatellites may be used to identify individuals,
 CC for parentage testing, and in the genetic mapping of economic trait
 CC loci, or genes involved the determination of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AAQ3501-34437.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 DB 1 AAAAAAAAAAAAAA 14

RESULT 987
 AA09230/C
 ID AA09230 standard; DNA; 14 BP.
 XX AA09230;
 XX 07-JUL-1998 (first entry)
 XX 3' poly(T) primer 6.
 XX 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
 KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
 XX Synthetic.
 XX WO9749832-A2.
 XX 31-DEC-1997.
 XX 23-JUN-1997; 97WO-CA00488.

XX 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX Petkovich PM;
 XX WPI; 1998-077193/07.
 XX Identifying DNA encoding inducible or suppressible cytochrome P450 -
 PT by screening for drugs which reduce the catabolism of retinoic acid,
 PT useful in cancer chemotherapy and the treatment of acne and
 PT psoriasis
 XX Example 1; Page 50; 113pp; English.
 XX This is a 3' poly(T) PCR primer used in the amplification of the
 CC inducible cytochrome P450RAI gene which specifically metabolises a
 CC derivative of the retinoic acid (RA). The cytochrome P450 gene in
 CC general produces enzymes involved in the oxidative metabolism of
 CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
 CC sequence can be used to induce or suppress the expression of its
 CC protein. P450RAI is highly induced by RA in cell lines and tissues.
 CC This allows for the development of a drug screen using promoters and
 CC nucleotide sequences to identify drugs which are useful for reducing
 CC the catabolism of RA.
 XX Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAA 1095
 DB 14 TTAATAAAAAAAAA 1

RESULT 988
 AA012222/C
 ID AA012222 standard; DNA; 14 BP.
 XX AA012222;
 XX 22-JUN-1998 (first entry)
 XX Poly(T) oligonucleotide used in differential display PCR.
 XX Retinoid metabolising protein; P450RAI; retinoid oxidase;
 KW retinoic acid; zebrafish; inhibitor; antisense; cancer;
 KW actinic keratosis; oral leukoplakia; head tumour; neck tumour;
 KW non-small cell lung carcinoma; basal cell carcinoma;
 KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
 KW ichthyosis; therapy; diagnosis; screening; differential display;
 KW PCR; primer; ss.
 XX Synthetic.
 XX WO9749815-A1.
 XX 31-DEC-1997.
 XX 23-JUN-1997; 97WO-CA00440.
 XX 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX Beckett BR, Jones G, Petkovich PM, White JA;
 XX WPI; 1998-077178/07.

XX Retinoid metabolising protein - useful to develop products to treat,
PT e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
PT ichthyosis
XX
PS Disclosure; Page 14; 110pp; English.
XX
CC PolyT oligonucleotides (see AAV12217-28) were used in reverse
CC transcription reactions on polyA+ RNA isolated from the fins of
CC control or retinoic acid-treated zebrafish (Danio rerio). Several
CC combinations of the polyT primers were used with degenerate
CC upstream primers (see AAV12229-33) for differential display PCR.
CC Bands demonstrating reproducible differential amplifications were
CC found using the primers given in AAV12221 and AAV12231. This PCR
CC product was reamplified (see AAV12234-35). A differential display
CC product (see AAV12213) which exhibited a dependence on the presence
CC of retinoic acid for its expression was isolated, and was used to
CC isolate a full-length clone (see AAV12203) coding for a novel
CC retinoid metabolising protein (see AAW44159), designated zP450RAI.
XX
SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
Db 14 TTAATAAAAAAAAAA 1

RESULT 989
AA57019/C
ID AAX57019 standard; DNA; 14 BP.
XX
AC AAX57019;
XX
DT 19-JUL-1999 (first entry)
XX
DE WO9923258 oligonucleotide primer 1.
XX
KW Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW agglutination; bridging molecule; ss.
XX
OS Synthetic.
XX
PN WO9923258-AL.
XX
PD 14-MAY-1999.
XX
PF 30-OCT-1998; 98WO-US23267.
XX
PR 31-OCT-1997; 97US-0063969.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Reshatoff MR, Stull PD, Weisburg WG;
XX
DR WPI; 1999-326994/27.
XX
PT Optical detection of hybridization complexes for specific target
PT nucleic acid sequences
XX
PS Example 1; Page 40; 46pp; English.
XX
CC This invention describes a novel method for the visual detection of
CC target nucleic acid presence in a sample. A preferred target is a
CC Mycobacterium complex nucleic acid sequence. The detection method uses
CC visual detection of a change in the hybridization without aid of
CC instrumentation. Multiple copies of a target nucleic acid sequence are
CC mixed with first and second detectable probes under hybridizing
CC conditions favouring particle agglutination via a bridging molecule
CC allowing for visual detection of the target nucleic acid sequence. The

CC bridging molecule enhances or inhibits formation of a hybridization
CC complex.
XX
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
Db 14 AAAAAAAAAAAAAA 1

RESULT 990
AAX19465/C
ID AAX19465 standard; DNA; 14 BP.
XX
AC AAX19465;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:7.
XX
KW Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9907893-AL.
XX
PD 18-FEB-1999.
XX
PF 05-AUG-1998; 98WO-US16343.
XX
PR 08-AUG-1997; 97US-0908873.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Hosier S, Kubbies M, Swisshelm K;
XX
DR WPI; 1999-167454/14.
XX
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT polypeptide - useful for inducing a senescence phenotype in a cell
XX
PS Example 1; Page 18; 44pp; English.
XX
CC The present invention describes human senescence factor p23. An
CC expression vector for p23 is useful for inducing a senescent phenotype
CC in a cell (preferably eukaryotic). This may help in regulating diseases,
CC including cancer, persistent inflammation, and various proliferative and
CC degenerative disorders. These transgenic cells are useful in gene
CC therapy for treating cancer, particularly where antisense
CC oligonucleotides are useful for blocking normal or mutant p23 expression
CC in cancer cells or other proliferating cells. Transgenic cells are also
CC useful for producing the p23 polypeptide in large quantities. The
CC antibodies are useful for raising antiserum against p23, and for
CC identifying senescent cells in culture and tissue biopsies. The p23
CC polynucleotides are useful for modulating or altering p23 activity in a
CC cell, and for identifying and isolating the whole gene encoding p23,
CC and variants of p23. Assays based on p23 elements, which detect p23
CC levels and activity are useful as diagnostic markers for staging tumours,
CC determining prognosis, and/or predicting therapeutic success. These
CC elements also provide an assay for detecting chromosomal rearrangements
CC in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
CC permits the manipulation of malignant growth in cancer. The present
CC sequence represents a primer used in an example from the present
XX invention.
SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 other;

```
Query Match      1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1097
DB 14 TTAATAAAAAAAAAA 1

RESULT 991
AAX14688
ID AAX14688 standard; DNA; 14 BP.
XX
AC AAX14688;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 962-975 of Esterase D gene.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Homo sapiens.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-0173489.
XX
PR 22-DEC-1993; 93US-0173489.
PR 29-OCT-1992; 92US-0968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PF Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria
XX
PS Disclosure; Columns 15-16; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX
SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 U; 0 other;

Query Match      1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
DB 1 AAAAAAAAAAAAAA 14

RESULT 992
AAX14689
ID AAX14689 standard; DNA; 14 BP.
XX
AC AAX14689;
XX
DT 06-NOV-2000 (first entry)
XX
DE Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW Conformationally-locked oligonucleotide; antisense inhibitor;
```

```
XX
AC AAX14689;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix third strand of Esterase D gene nucleotides 962-975.
XX
KW Triplex formation; DNA detection; triple helix; identification;
KW bacteria; oncogene; virus; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-0173489.
XX
PR 22-DEC-1993; 93US-0173489.
PR 29-OCT-1992; 92US-0968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PF Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria
XX
PS Disclosure; Columns 15-16; 168pp; English.
XX
CC The present sequence represents a polynucleotide that is able to
CC form a triple helix with a double stranded sequence. Cytosine bases
CC in the present can be replaced with 5-methylcytosine for increased
CC triplex stability. The present sequence is used in the assay of the
CC invention, where it can be part of the anchor DNA or reporter DNA
CC sequence. The assay comprises adding a sample containing double-stranded
CC DNA test sequences to an aqueous medium containing at least one complex
CC of anchor DNA, attached to a solid support, and reporter DNA, where
CC either a part of the anchor DNA or reporter DNA is designed to form
CC a triple-strand structure with part of the test sequence. Triplex
CC formation results in displacement of the reporter DNA which is
CC detected as an indication of the presence of the DNA test sequence.
CC The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 other;

Query Match      1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
DB 14 AAAAAAAAAAAAAA 1

RESULT 993
AAX62349/C
ID AAX62349 standard; DNA; 14 BP.
XX
AC AAX62349;
XX
DT 06-NOV-2000 (first entry)
XX
DE Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW Conformationally-locked oligonucleotide; antisense inhibitor;
```

KW bicyclic sugar nucleoside analogue; gene probe; ds.
 XX Synthetic.
 OS

Key Location/Qualifiers
 modified_base 1 /tag= a
 /mod_base= OTHER
 modified_base 3 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
 /tag= b
 /mod_base= OTHER
 modified_base 5 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
 /tag= c
 /mod_base= OTHER
 modified_base 7 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
 /tag= d
 /mod_base= OTHER
 modified_base 9 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
 /tag= e
 /mod_base= OTHER
 modified_base 10 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
 /tag= f
 /mod_base= OTHER
 modified_base 12 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
 /tag= g
 /mod_base= OTHER
 /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"

US6083482-A.

04-JUL-2000.

11-MAY-1999; 99US-0309742.

11-MAY-1999; 99US-0309742.

(ICNC) ICN PHARM INC.

Wang G;

WPI; 2000-451496/39.

New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific diagnostics -

Example 20; Column 16; 10pp; English.

The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesizer. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropically advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics.

Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
 DB 14 AAAAAAAAAAAAAA 1

RESULT 994

AAF84160/c

ID AAF84160 standard; DNA; 14 BP.

AC AAF84160;

DT 08-JUN-2001 (first entry)

DE Oligonucleotide #2.

Light responsive oligonucleotide; light irradiation; gene therapy; ss.

Unidentified.

WO200121637-A1.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000WO-JP06415.

PR 20-SEP-1999; 99JP-0304479.

PA (KOMI/) KOMIYAMA M.

PI Komiyama M, Asanuma H, Yoshida T;

WPI; 2001-266061/27.

Light-responsive oligonucleotides, useful in controlling DNA synthesis and gene expression, have structural isomerization on irradiation, and reversible change in melting temperature of the formed double or triple strands -

Example 3; Page 20; 43pp; Japanese.

The present invention relates to light responsive oligonucleotide, which contain one or more organic groups which can undergo structural isomerisation upon irradiation at a specific wavelength. The melting temperature of a double-strand formed by the light-responsive oligonucleotide, and another oligonucleotide complementary to the light-responsive oligonucleotide, reversibly changes depending on light irradiation. The oligonucleotides are useful in biotechnology, e.g. in controlling DNA elongation, gene expression, amplification and transcription, and for efficient gene diagnosis and gene therapy. The present sequence is an oligonucleotide used in the present invention.

Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 other;

Query Match 1.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097

DB 14 AAAAAAAAAAAAAA 1

RESULT 995

AAC83821

ID AAC83821 standard; RNA; 14 BP.

AC AAC83821;

DT 28-FEB-2001 (first entry)

DE RNA oligonucleotide #1 used in a binding assay.

L-ribo-configured Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.

XX OS Unidentified.
 XX PN WO200066604-A2.
 XX PD 09-NOV-2000.
 XX PF 04-MAY-2000; 2000WO-DK00225.
 XX PR 04-MAY-1999; 99DK-0000603.
 XX PR 01-SEP-1999; 99DK-0001225.
 XX PR 11-JAN-2000; 2000DK-0000032.
 XX PA (EXIQ-) EXIQON AS.
 XX PI Wengel J;
 XX DR WPI; 2001-060972/07.
 XX PT Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides,
 XX PT useful for therapeutic purposes e.g. in the construction of
 XX PT oligonucleotides, as substrates for nucleic acids polymerases and in
 XX PT RNA mediated catalytic processes -
 XX PS Example 11; Page 56; 79pp; English.
 XX CC The present invention relates to an oligomer comprising
 XX CC L-ribo-configured Locked Nucleoside Analogues (L-ribo-LNA analogues).
 XX CC The present sequence is an RNA oligonucleotide. Binding studies of the
 XX CC L-ribo-LNA analogues towards the present sequence were carried out, to
 XX CC determine the thermostability of the L-ribo-LNA analogues. The analogs of
 XX CC the present invention have a variety of uses e.g. in the preparation of
 XX CC conjugates of the L-ribo-LNA modified oligonucleotides (oligonucleotides).
 XX SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 DB 1 AAAAAAAAAAAAAA 14
 RESULT 996
 ABQ83269
 ID ABQ83269 standard; DNA; 14 BP.
 AC ABQ83269;
 DT 18-JAN-2003 (first entry)
 DE EGI cDNA tag related oligonucleotide SEQ ID NO:42.
 XX cDNA tag; identification; gene expression analysis; linker;
 XX expressed gene identification; EGI; ss.
 XX Synthetic.
 XX WO200274951-A1.
 XX 26-SEP-2002.
 XX 13-MAR-2002; 2002WO-JP02338.
 XX 15-MAR-2001; 2001JP-0073959.
 XX (KURE) KUREHA CHEM IND CO LTD.
 XX PA (YAMA/) YAMAMOTO M.
 XX PA (YAMA/) YAMAMOTO N.
 XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
 WPI; 2002-759896/82.
 Construction of cDNA tags for identifying expressed genes with specific
 linkers and recognition sequences, applicable in gene expression
 analysis, disease diagnosis and identifying target for gene therapy -
 Example 1; Page 24; 59pp; Japanese.

XX WPI; 2002-759896/82.
 XX Construction of cDNA tags for identifying expressed genes with specific
 XX linkers and recognition sequences, applicable in gene expression
 XX analysis, disease diagnosis and identifying target for gene therapy -
 XX Example 1; Page 24; 59pp; Japanese.
 XX The present invention describes a method for constructing a cDNA tag for
 XX identifying an expressed gene. The method comprises: (a) preparation of
 XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
 XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
 XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
 XX linker Y ligated material; and (e) cleaving the amplification product.
 XX The method can be used for the construction of cDNA tags for identifying
 XX expressed genes, which is applicable in gene expression analysis, disease
 XX diagnosis and identifying target for gene therapy, including the
 XX clarification of difference in function or morphology of cells under
 XX physiological or pathological conditions. The cDNA or cells for assay can
 XX be specifically expressed, with reproducibility and accuracy in the
 XX detection of genes. The present sequence represents an expressed gene
 XX identification (EGI) cDNA tag related oligonucleotide which is used in
 XX an example from the present invention.
 XX SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 DB 1 AAAAAAAAAAAAAA 14
 RESULT 997
 ABQ83275/c
 ID ABQ83275 standard; DNA; 14 BP.
 AC ABQ83275;
 DT 18-JAN-2003 (first entry)
 DE EGI cDNA tag related oligonucleotide SEQ ID NO:48.
 XX cDNA tag; identification; gene expression analysis; linker;
 XX expressed gene identification; EGI; ss.
 XX Synthetic.
 XX WO200274951-A1.
 XX 26-SEP-2002.
 XX 13-MAR-2002; 2002WO-JP02338.
 XX 15-MAR-2001; 2001JP-0073959.
 XX (KURE) KUREHA CHEM IND CO LTD.
 XX PA (YAMA/) YAMAMOTO M.
 XX PA (YAMA/) YAMAMOTO N.
 XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
 WPI; 2002-759896/82.
 Construction of cDNA tags for identifying expressed genes with specific
 linkers and recognition sequences, applicable in gene expression
 analysis, disease diagnosis and identifying target for gene therapy -
 Example 1; Page 24; 59pp; Japanese.

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 812 CCTGGTACTGTGGGT 827
||| ||||| |||||
Db 17 CCCAGGTACTGTGGGT 2

RESULT 1447

ABZ65434/c

ID ABZ65434 standard; RNA; 17 BP.

XX AC ABZ65434;
XX XX
XX 21-MAR-2003 (first entry)
XX DE Human HER2 DNzyme substrate #891.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.

XX XX

XX WO200297114-A2.

XX XX

XX 05-DEC-2002.

XX XX

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX XX

XX (RIBO-) RIBOZYME PHARM INC.

XX XX

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

XX treating cancer, modulates the expression of a nucleic acid encoding

XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 4; Page 150; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

XX acid molecule or an enzymatic nucleic acid molecule, that modulates

XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic

XX acid molecule of the invention has cytosstatic, anti-HIV, and

XX anti-rheumatic activity. The nucleic acid molecules are useful for

XX acids are also useful for treating breast, ovarian, colorectal, lung,

XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.

XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,

XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

XX sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 U; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 811 ACCCTGGTACTGTGGG 826
||| ||||| |||||
Db 16 ACCCAGGTACTGTGGG 1

RESULT 1448

ABZ65434/c

ID ABZ65434 standard; RNA; 17 BP.

XX AC ABZ65434;
XX XX
XX 21-MAR-2003 (first entry)
XX DE Human HER2 DNzyme substrate #891.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.

XX XX

XX WO200297114-A2.

XX XX

XX 05-DEC-2002.

XX XX

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX XX

XX (RIBO-) RIBOZYME PHARM INC.

XX XX

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

XX treating cancer, modulates the expression of a nucleic acid encoding

XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 4; Page 150; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

XX acid molecule or an enzymatic nucleic acid molecule, that modulates

XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic

XX acid molecule of the invention has cytosstatic, anti-HIV, and

XX anti-rheumatic activity. The nucleic acid molecules are useful for

XX acids are also useful for treating breast, ovarian, colorectal, lung,

XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.

XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,

XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

XX sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 U; 0 other;

ABZ65527/c
ID ABZ65527 standard; RNA; 17 BP.

XX AC ABZ65527;
XX XX

XX 21-MAR-2003 (first entry)
XX XX

XX Human HER2 DNzyme substrate #984.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;

XX anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US16840.

XX 29-MAY-2001; 2001US-294140P.

XX 06-JUN-2001; 2001US-296249P.

XX 10-SEP-2001; 2001US-318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

XX treating cancer, modulates the expression of a nucleic acid encoding

XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

XX Claim 4; Page 152; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

XX acid molecule or an enzymatic nucleic acid molecule, that modulates

XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic

XX acid molecule of the invention has cytosstatic, anti-HIV, and

XX anti-rheumatic activity. The nucleic acid molecules are useful for

XX acids are also useful for treating breast, ovarian, colorectal, lung,

XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.

XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,

XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

XX sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 0 A; 1 C; 2 G; 14 U; 0 other;

SQ Query Match 1.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099

||| ||||| |||||

Db 17 AAACAAACAAAAAA 2

RESULT 1449

AAQ20007/c

ID AAQ20007 standard; DNA; 18 BP.

XX AC AAQ20007;

XX 01-APR-1992 (first entry)

XX Oligonucleotide #3 able to covalently cross-link to target DNA.

XX deoxyribonucleic acid; major groove; ethanoino group;

XX aziridinylcytosine; cross-linking group; ss.

```

XX OS Synthetic.
XX FH Key
XX FT modified_base 1 Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT modified_base 9 /note= "N4N4-ethanocytosine"
XX FT /*tag= b
XX FT /mod_base= m5c
XX FT modified_base 15
XX FT /*tag= c
XX FT /mod_base= m5c
XX FT modified_base 18
XX FT /*tag= da
XX FT /mod_base= OTHER
XX FT /note= "N4N4-ethanocytosine"
XX PN W09118997-A.
XX XX
XX PD 12-DEC-1991.
XX XX
XX PF 24-MAY-1991; 91WO-1003680.
XX XX
XX PR 14-JAN-1991; 91US-0640654.
XX PR 25-MAY-1990; 90US-0529346.
XX XX
XX PA (GILE-) GILEAD SCIE INC.
XX PI Matteucci MD, Krawczyk S;
XX PI WPI; 1992-007480/01.
XX DR
XX PT New sequence-specific non-photo-activated crosslinking agents -
XX PT bind to the major groove of duplex DNA and are esp. useful for
XX PT treating latent infections e.g. HIV
XX PS Example 2; Page 21; 42pp; English.
XX CC The 3' end of this oligonucleotide carries 1,3-propanediol. The
XX CC oligo is one of four oligonucleotides which were designed to
XX CC specifically bind and cross-link to the duplex target sequence
XX CC AAQ20004. Oligo #3 has a covalent cross-linking group, i.e.
XX CC N4N4-ethanocytosine, at its 5'- and 3'-ends. An assay for
XX CC crosslinked triple helix showed the most complete reaction with
XX CC Oligo #3. A control oligo with no cross-linking group showed no
XX CC reaction while Oligos #1 (see AAQ20005) and #2 (AAQ20006) with the
XX CC crosslinking group at the 5' and 3' ends, respectively, showed
XX CC considerable reaction. An oligonucleotide with N4N4-ethanocytosine
XX CC within its sequence (see AAQ20008) showed less effective binding.
XX SQ Sequence 18 BP; 0 A; 4 C; 0 G; 14 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1099
DB 17 AAGAAAAAGAAAAAAAAA 2

RESULT 1450
AAQ26202
ID AAQ26202 standard; DNA; 18 BP.
XX AC AAQ26202;
XX XX
XX DT 25-MAR-2003 (updated)
XX DT 04-JAN-1993 (first entry)
XX XX
XX DE HLA-DR beta sub-type tailed probe DRB98 hybridising region.

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```

XX KW Tissue typing; identity determination; disease susceptible; ss.
XX OS Synthetic.
XX PN W09210589-A1.
XX PD 25-JUN-1992.
XX PF 06-DEC-1991; 91WO-US09294.
XX PR 06-DEC-1990; 90US-0623098.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Apple RJ, Begovich AB, Bugawan T, Erlich HA, Griffith RL,
XX PI Scharf SJ;
XX DR WPI; 1992-234644/28.
XX PT Method for determining HLA-DR beta sub-type in DNA sample -
XX PT comprises amplification and hybridisation with probes and
XX PT primers, useful in tissue typing
XX PS Example; Page 39; 90pp; English.
XX CC The sequence is that of the hybridising region of tailed probe DRB98 for
XX CC use in a method for determining HLA-DR beta sub-type in a nucleic acid
XX CC sample. The method allows specific nucleic acid sequences of the second
XX CC exon of HLA-DR beta genes to be amplified then probed for identification
XX CC of polymorphic sequences. The amplified DNA is useful for typing
XX CC homozygous or heterozygous samples from a variety of sources and for
XX CC detecting allelic variants not distinguishable by serological methods.
XX CC The typing system can be used in a reverse dot blot format which is
XX CC simple and rapid to perform, produces detectable signals in minutes and
XX CC can be utilised in tissue typing, determination of individual identity
XX CC and identifying disease susceptible individuals.
XX CC See also AAQ26092-Q26367.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 90 TAGGACCTTCTCTTCG 105
DB 3 TAGGACCTTCTGTCCG 18

RESULT 1451
AAQ41404
ID AAQ41404 standard; DNA; 18 BP.
XX AC AAQ41404;
XX XX
XX DT 25-MAR-2003 (updated)
XX DT 13-SEP-1993 (first entry)
XX XX
XX DE Monomer DRB3705 for typing of HLA DR beta.
XX KW Reverse dot blot hybridisation; tandem; head to tail monomers;
XX KW probe; staggered complementary primers; HLA molecular typing; ds.
XX OS Synthetic.
XX PN W09309245-A1.
XX PD 13-MAY-1993.
XX PF 22-OCT-1992; 92WO-US09113.

```


XX WPI; 1996-371338/37.
XX New substd. quinoline and quinoxaline cpds. - are monomers for
PT triple helix-forming oligonucleotide analogues useful e.g. for
PT treating tumours or viral infection
XX
XX Disclosure; Fig 1; 102pp; English.
XX
XX The present sequence represents a triple helix forming oligonucleotide
CC that form a triple helix with the double-stranded DNA sequence described
CC in AAX15195. The specification describes novel monomeric compositions
CC which are substituted quinoline or quinoxaline-based structures capable
CC of hydrogen bonding specifically with interstrand purine-pyrimidine
CC pairs in a double stranded Watson-Crick DNA molecule to form a
CC triple-helix.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 18 BP; 0 A; 3 C; 0 G; 15 T; 0 other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. NO. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1099
|||||
Db 16 AAAAAAAAAAGAAA 1
RESULT 1454
AAX15198/c
ID AAX15198 standard; DNA; 18 BP.
XX
AC AAX15198;
XX
DT 25-MAR-2003 (updated)
DT 28-APR-1999 (first entry)
XX
DE Triple helix forming oligonucleotide.
XX
KW Double-stranded DNA; triple helix; quinoline;
KW quinoxaline-based structure; hydrogen bonding; ss.
XX
OS Synthetic.
XX
PN WO9623777-A1.
XX
XX 08-AUG-1996.
XX
PF 29-JAN-1996; 96WO-US01473.
XX
PR 01-FEB-1995; 95US-0384324.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold BI;
XX
XX WPI; 1996-371338/37.
XX
XX New substd. quinoline and quinoxaline cpds. - are monomers for
PT triple helix-forming oligonucleotide analogues useful e.g. for
PT treating tumours or viral infection
XX
XX Disclosure; Fig 2; 102pp; English.
XX
XX The present sequence represents a triple helix forming oligonucleotide
CC that form a triple helix with the double-stranded DNA sequence described
CC in AAX15197. The specification describes novel monomeric compositions
CC which are substituted quinoline or quinoxaline-based structures capable
CC of hydrogen bonding specifically with interstrand purine-pyrimidine
CC pairs in a double stranded Watson-Crick DNA molecule to form a
CC triple-helix.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC

XX
SQ Sequence 18 BP; 0 A; 3 C; 0 G; 15 T; 0 other;
XX
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. NO. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1099
|||||
Db 18 AAAAAAAAAAGAAA 3
RESULT 1455
AAT32141
ID AAT32141 standard; DNA; 18 BP.
XX
AC AAT32141;
XX
DT 16-SEP-1996 (first entry)
XX
DE DNA sequencing "primer" (primer/linker) complementary sense strand.
XX
KW Sense strand; DNA sequencing; oligonucleotide; primer;
KW primer; linker; priming site; labelling region; cohesive end;
KW complementary strand; ds.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT misc_feature 1..18
FT /*tag= a
FT /note= "forms doubled stranded segment when
FT bound to nucleotides 5-22 of the
FT sequence given in AAT12342"
XX
PN WO9602673-A1.
XX
XX 01-FEB-1996.
XX
XX 14-JUL-1995; 95WO-US08894.
XX
XX 14-JUL-1994; 94US-0275169.
PR 25-FEB-1994; 94US-0202400.
XX
XX (AMIC-) AMICON INC.
PA (GRAC) GRACE & CO-CONN W R.
XX
XX Leonard JT;
XX
XX WPI; 1996-105934/11.
XX
XX New oligo:nucleotide(s) for DNA sequencing - having a priming site,
PT a labelling region and a cohesive end complementary to a restriction
PT fragment sequence
XX
XX Disclosure; Page 5; 23pp; English.
XX
XX The present sequence is an example of a complementary sense strand
CC from a novel DNA sequencing oligonucleotide called a "primer"
CC (primer/linker), which comprises a priming site, labelling region,
CC cohesive end and complementary strand. The priming site is the
CC optimal target for annealing prior to treatment with polymerase.
CC The labelling region is a template sequence which directs DNA
CC polymerase to incorporate multiple labelled, e.g. radioactive
CC nucleotides. The cohesive end provides compatible ends
CC for ligation of primers to restriction fragments. The
CC complementary strand provides a region of double stranded DNA which
CC is required by DNA ligases for the attachment of the primer to a
CC restriction fragment.
CC A prefd. sequencing procedure comprises the generation of
CC restriction fragments from the DNA mol. to be sequenced, ligation
CC of primers to the fragments, sepn. and purificn. of primer
CC attached restriction fragments, conc. and buffer exchange,
CC

CC generation and sepn. of sequencing prods., exposure of X-ray film
CC to sequencing prods. and detection of the signal on the film.

XX
SQ Sequence 18 BP; 14 A; 2 C; 1 G; 1 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
||| ||||| |||||
Db 1 AAAAAAAAAAAAAA 16

RESULT 1456
AAT16419/C
ID AAT16419 standard; DNA; 18 BP.
XX
AC AAT16419;
XX
DT 13-SEP-1996 (first entry)
XX
DE Primer #2 for SWSS1392 human obesity gene.

XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; Immunoassay; PCR;
KW primer; amplify; polymerase chain reaction; ss.
XX

OS Synthetic.

XX GB2292382-A.

PN 21-FEB-1996.

XX 17-AUG-1995; 95GB-0016947.

XX 07-JUN-1995; 95US-0483211.

PR 17-AUG-1994; 94US-0292345.

PR 30-NOV-1994; 94US-0347563.

PR 10-MAY-1995; 95US-0438431.

XX (UYRQ) UNIV ROCKEFELLER.

XX Burley SK, Friedhan JM, Gajiwala K, Halaas JL, Maffei M;

XX Proenca R, Zhang Y;

XX WPI; 1996-099009/11.

XX Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
XX reducing wt. in treatment of diabetes, high blood pressure and high
XX cholesterol and for cosmetic reasons

XX Example 10; Page 142; 304pp; English.

XX AAT16392-T16429 represent amplification primers for the human obesity
XX polypeptide (OBP) gene sequence (see AAT16373). These sequences were
XX used to amplify the OBP gene sequence from the YAC contig containing the
XX human OBP gene, in a series of sequence tagged-site (STS)-specific PCR
XX assays. There were 19 STS found within the YAC contig human OBP gene
XX sequence. This sequence was used in conjunction with AAT16418 to amplify
XX the STS SWSS1392. OBP has effects on both food intake and energy
XX expenditure. OBP and its analogues are useful for modifying body weight
XX (optionally combined with known medicaments), for treating diabetes, high
XX blood pressure or high cholesterol. The OBP coding sequence (and
XX sequences complementary to it) can be used in gene therapy for modifying
XX body weight. The protein can be used for reducing weight for health or
XX cosmetic reasons in obese humans, or to produce leaner food animals.
XX Antagonists of OBP (including antibodies) are useful for increasing body
XX weight, e.g. for treating weight loss associated with cancer, or for
XX cosmetic reasons in humans, or for production of Kobe beef or Foie gras
XX in domestic animals. OBP antibodies (Ab) can also be used in diagnostic
XX immunoassays for the presence of OBP. The formation of Ab-OBP complexes

CC enables in vitro evaluation of levels of OBP in a sample, especially to
CC detect diseases associated with elevated or decreased levels, and to
CC monitor treatment of these diseases.

XX
SQ Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 313 GGAAGAGACTGCAGAGA 328
||| ||||| |||||
Db 18 GAAAGAGATGCAGAGA 3

RESULT 1457
AAT18697
ID AAT18697 standard; DNA; 18 BP.

XX
AC AAT18697;

XX 05-JUL-1996 (first entry)

XX cDNA3 sense primer 8.

XX RAP-1; radiation protecting checkpoint protein; apoptosis;
KW cell death; cancer; diagnosis; therapy; radiotherapy;
KW antisense RNA; gene therapy; polymerase chain reaction; PCR;
KW primer; ss.

XX OS Synthetic.

XX WO9611562-A2.

PN 25-APR-1996.

XX 11-OCT-1995; 95WO-US12445.

XX 11-OCT-1994; 94IL-0111238.

XX (SHOS/) SHOSHAN H Z.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Canaani D;

XX WPI; 1996-221643/22.

XX New gene encoding a radiation protecting checkpoint protein - useful
XX for diagnosis and treatment of cancer and other diseases involving
XX abnormal apoptosis

XX Disclosure; Page 9; 29pp; English.

XX The presence of a naturally-occurring antisense RNA to the 4.0 kb
XX mRNA in xeroderma-pigmentosum-C cells was verified using PCR
XX primers (AAT18697) specific to the cDNA3 region of novel human RAP-1
XX radiation protecting checkpoint gene (see AAT18696). Reverse
XX transcription reactions preceding the PCR were performed using
XX cDNA3 sense primer 8 (AAT18697) and cDNA3 antisense primer 10
XX (AAT18698). PCR was then performed using cDNA3 sense primer 62
XX (AAT18699), which is nested to primer 8, and cDNA3 antisense primer
XX 10. The antisense RNA can be used as a general effector of gene
XX therapy by modulating activity of genes fused to the RAP-1 3' UTR
XX tag.

XX Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 471 CAGGAAGCTGGCATTTC 486
||| ||||| |||||

Db 3 CAGGAAGTACGATGC 18

RESULT 1458

AAAX71751/c
ID AAX71751 standard; RNA; 18 BP.

XX AC AAX71751;

XX DT 28-JUL-1999 (first entry)

XX DE Human KDR VEGF receptor hairpin ribozyme substrate #49.

XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

XX OS Homo sapiens.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US17480.

XX PR 11-JAN-1996; 96US-0584040.

XX PR 26-OCT-1995; 95US-0005974.

XX PA (CHIR) CHIRON CORP.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX DR WPI; 1997-259017/23.

XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient

XX PS Claim 4; Page 120; 218pp; English.

XX SQ The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.

XX SQ Sequence 18 BP; 3 A; 7 C; 4 G; 4 U; 0 other;

Query Match

Best Local Similarity 1.2%; Score 12.8; DB 1; Length 18;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 997 GTCTGAGGCTGGAGAA 1012

Db 16 GTGTGAGGCTGGAGAA 1

RESULT 1459

AAV13327/c
ID AAV13327 standard; DNA; 18 BP.

XX AC AAV13327;

XX DT 14-MAY-1998 (first entry)

DE Sense primer Exon 9 for human 5-lipoxygenase gene.

XX Inflammatory disease; polymorphism; 5-lipoxygenase;
KW asthma; ulcerative colitis; bronchitis; sinusitis; psoriasis;
KW rhinitis; arthritis; diagnosis; treatment; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9742347-A2.

XX PD 13-NOV-1997.

XX PF 29-APR-1997; 97WO-US07137.

XX PR 25-APR-1997; 97US-0846020.

XX PR 06-MAY-1996; 96US-0016890.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI Asano K, Beier D, Drazen JM, Grobholz J, In K;

XX DR WPI; 1997-558997/51.

XX PT Classifying patients with inflammatory disease, specifically asthma
PT - according to polymorphisms in 5-lipoxygenase gene regulatory
PT region, e.g. to identify candidates for lipoxygenase inhibitor
PT treatment

XX PS Example 1; Page 19; 56pp; English.

XX SQ The present sequence was used in the development of a novel method
CC for classifying patients suffering from an inflammatory disease.
CC The method comprises identifying in DNA from at least 1 patient a
CC sequence polymorphism, as compared with the normal 5-lipoxygenase
CC (5-LOX) gene (AA78431), in a 5-LOX regulatory gene sequence.
CC The method can be applied to subjects with asthma, ulcerative
CC colitis, bronchitis, sinusitis, psoriasis, allergic and
CC non-allergic rhinitis, lupus or rheumatoid arthritis. Specifically
CC it can be used to diagnose asthma or susceptibility to disease.
CC Identify treatments suitable for individual patients or assess the
CC likely success of treatment.

XX SQ Sequence 18 BP; 1 A; 9 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 1.2%; Score 12.8; DB 1; Length 18;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 951 CAACAGCTGGGCGAGGG 966

Db 16 CAGCAGCTGGGCGAGGG 1

RESULT 1460

AAV40031

ID AAV40031 standard; DNA; 18 BP.

XX AC AAV40031;

XX DT 12-OCT-1998 (first entry)

XX DE Mouse Pax4 PCR sense primer SEQ ID NO:15.

XX KW Mouse; Pax4; Pax6; pancreatic cell; differentiation status; tumour;
KW developmental status; transgenic mammal; diabetes; neuronal disorder;
KW PCR primer; ss.

XX OS Synthetic.

XX OS Mus sp.

XX PN WO9829566-A2.

PD 09-JUL-1998.
 XX
 PF 30-DEC-1997; 97WO-EP07321.
 XX
 PR 31-DEC-1996; 96US-0778423.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Gruss P, Sosa-Pineda B;
 XX
 DR WPI; 1998-388144/33.
 XX
 PT Use of Pax4 nucleic acids and proteins - useful for, e.g. developing
 PT products for diagnosis, prevention and treatment of diabetes,
 PT neuronal disorders and tumours
 XX
 PS Example 2; Page 28-29; 70pp; English.
 XX
 CC A method has been developed for testing the developmental status in
 CC pancreatic cells (PC's) of a mammal comprising: (a) determining the
 CC level or status of Pax4 mRNA in PC's of the mammal; and/or (b)
 CC determining the level or status of Pax4 protein in PC's of the mammal;
 CC and (c) comparing the level or status of Pax4 mRNA and/or Pax4 protein
 CC with the corresponding level in normal PC's. The present invention also
 CC describes a nucleic acid sequence encoding a functional and expressible
 CC Pax4 protein and optionally a second nucleic acid sequence encoding a
 CC functional and expressible Pax6 protein, for the preparation of a
 CC therapeutic composition for treating, preventing and/or delaying
 CC diabetes and/or a neuronal disorder in a mammal. The present sequence
 CC represents a PCR primer used in an example of the present invention for
 CC the expression of Pax4. The method can be used for determining the
 CC development of PC's as indicative of diabetes, neuronal disorders or
 CC tumours. The products can be used for developing agents for treating
 CC these disorders.
 XX
 SQ Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 455 CTTCCAGAGGAGCTC 470
 DB 1 CTTCCAGAGGAGCTC 16
 RESULT 1461
 AA15663/c
 ID AA15663 standard; DNA; 18 BP.
 AC AA15663;
 XX
 XX 22-MAY-1998 (first entry)
 DT
 DE LDR oligonucleotide sequence.
 XX
 XX Detection; single-base change; insertion; deletion; translocation;
 KW ligase detection reaction; LDR; PCR; ss.
 XX
 OS Synthetic.
 XX
 FN WO9745559-A1.
 XX
 XX 04-DEC-1997.
 PD
 XX 27-MAY-1997; 97WO-US09012.
 PF
 XX 29-MAY-1996; 96US-0018532.
 PR
 XX (CORR) CORNELL RES FOUND INC.
 PA
 XX Barany F, Belgrader P, Lubin M;
 PI
 XX

DR WPI; 1998-032663/03.
 XX
 XX Multiplex detection of nucleic acid sequence differences - using
 PT ligase detection reaction coupled to PCR, useful for determining
 PT gene dosage, for detecting genetic disorders, etc.
 XX
 XX Example 8; Page 84; 158pp; English.
 XX
 CC The present sequence was used in the development of three novel
 CC methods for the detection nucleic acid sequence differences, i.e.
 CC single-base changes, insertions, deletions or translocations. The
 CC 1st uses the ligase detection reaction (LDR) coupled to PCR, the
 CC 2nd a 1st PCR coupled to a 2nd PCR coupled to a LDR and the 3rd a
 CC 1st PCR coupled to a 2nd PCR.
 XX
 SQ Sequence 18 BP; 4 A; 9 C; 4 G; 1 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 297 GTCGGGGCCCTGCATG 312
 DB 18 GTCGGGGCCCTGCATG 3
 RESULT 1462
 AA241189
 ID AA241189 standard; DNA; 18 BP.
 XX
 AC AA241189;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE Human AKT-1 phosphorothioate antisense oligonucleotide SEQ ID NO:341.
 XX
 KW Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO9953101-A1.
 XX
 XX 21-OCT-1999.
 PD
 XX 13-APR-1999; 99WO-US08268.
 PF
 XX 13-APR-1999; 98US-0081483.
 PR
 XX 28-APR-1998; 98US-0067638.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Cowser LM, Baker BF, McNeil J, Freier SM, Sasnor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX
 DR WPI; 1999-620446/53.
 XX
 XX Identifying compounds which modulate expression of nucleic acids, used
 PT to provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity -
 XX
 XX Example 30; Page 113; 264pp; English.
 PS
 CC A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of
 CC the compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria,
 CC and evaluating in silico the binding of the virtual compounds with the
 CC tNA according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONS) that modulate the expression of

a tNA sequence via binding of the ONs with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONs with the tNA according to defined criteria; and (2) a method of defining a set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences that are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAZ52701 to AAZ52706, represent sequences used in the exemplification of the present invention.

Sequence 18 BP; 6 A; 2 C; 6 G; 4 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CAGAGAAGCTGTGGAG 338
|||||
Db 3 CAGAGAAGTTGTGAG 18

RESULT 1463
AAZ22205
ID AAZ22205 standard; DNA; 18 BP.
AC AAZ22205;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human Akt-1 mRNA inhibiting antisense oligo ISIS #28888.
KW Human; Akt-1; antisense; diagnostic; therapeutic; prophylaxis;
KW infection; inflammation; tumor formation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
EN US958773-A.
XX
PD 28-SEP-1999.
XX
PF 17-DEC-1998; 98US-0212771.
XX
PR 17-DEC-1998; 98US-0212771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowser LM;
XX
DR WPI; 1999-561048/47.
XX
PT Antisense compounds complementary to Akt-1 useful for, e.g.
PT diagnostics, therapeutics and as research reagents -
XX
PS Claim 3; Column 39; 32pp; English.

The invention provides antisense compounds of 8-30 nucleotides that inhibit the expression of human Akt-1. The antisense compounds may be used for diagnostics, therapeutics (for modulating the expression of Akt-1), prophylaxis (e.g. to prevent or delay infection, inflammation, or tumor formation), as research reagents (e.g. to distinguish between members of a biological pathway) and in kits. Sequences AAZ22197-236 represent phosphorothioate oligonucleotides used for antisense inhibition of Akt-1 mRNA.

Sequence 18 BP; 6 A; 2 C; 6 G; 4 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 323 CAGAGAAGCTGTGGAG 338
|||||
Db 3 CAGAGAAGTTGTGAG 18

RESULT 1464
AAZ10941
ID AAZ10941 standard; DNA; 18 BP.
XX
AC AAZ10941;
XX

DT 27-OCT-1999 (first entry)
XX
DE PCR primer for Pax4 coding sequence.
XX
KW Pax4; Pax6; developmental status determination; pancreatic cell;
KW diagnosis; diabetes; juvenile diabetes; diabetes mellitus;
KW hormone secreting tumour; PCR primer; ss.

OS Synthetic.
OS Mus sp.
XX
EN US5948623-A.
XX
PD 07-SEP-1999.
XX
PF 27-OCT-1997; 97US-0958642.
XX
PR 31-DEC-1996; 96US-0787423.
PR 27-OCT-1997; 97US-0958642.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Gruss P, Sosa-Pineda B;
XX
DR WPI; 1999-517948/43.
XX
PT Testing the developmental status of pancreatic cells useful for the
PT diagnosis and detection of diseases such as diabetes
XX
PS Example 2; Column 14; 57pp; English.

This sequence represents a PCR primer for DNA encoding the Pax4 protein. The invention relates to a method for testing the developmental status of the pancreatic cells of a mammal comprising: (a) determining the level or status of Pax4 mRNA and/or protein in the pancreatic cells; and (b) comparing the level to the corresponding level in normal pancreatic cells. The method can further comprise detecting the level or status of Pax4 mRNA and/or protein in the pancreatic cells. The method is useful for the diagnosis and detection of diseases which arise from certain pancreatic cells, especially diabetes, e.g. juvenile diabetes, diabetes mellitus, and hormone secreting tumours.

Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 455 CTTCAGAGAGAGCTC 470
|||||
Db 1 CTTCAGAGAGAGCTC 16

RESULT 1465
AAZ18138
ID AAZ18138 standard; DNA; 18 BP.
XX
AC AAZ18138;
XX

DT 11-OCT-1999 (first entry)

XX DE STK 8 gene specific primer.
 XX KW Genetic proximity; gene expression; cell characterisation; homeobox gene;
 KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
 KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
 KW primer; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9934016-A2.
 XX PD 08-JUL-1999.
 XX PF 28-DEC-1998; 98WO-IL00625.
 XX PR 16-OCT-1998; 98IL-0126627.
 XX PR 29-DEC-1997; 97IL-0122793.
 XX PA (GENE-) GENENA LTD.
 XX PI Vidar B;
 XX DR WPI; 1999-419113/35.
 XX DR P-PSDB; AAY14673.
 XX PT Identifying and characterizing cells by comparing the pattern of
 PT gene expression in a selected gene family
 XX PS Claim 4; Page 44; 102pp; English.
 XX CC The invention provides a new method for identifying and characterising
 CC cells. The method for determining the genetic proximity of a first cell
 CC and a second cell comprises: (a) obtaining the first cell and the second
 CC cell; (b) determining in the first cell and the second cell the pattern
 CC of expression of genes in a selected gene family; and (c) calculating a
 CC proximity index using a specified formula. The methods can be used for
 CC characterising cells, e.g. for determining the origin of a cell, its
 CC genetic status, whether it carries a genetic defect, or whether it is
 CC transformed. They can be used for detecting a selected genetic defect in
 CC an individual, e.g. a fetus. They can also be used for determining the
 CC effect of a selected treatment on a test cell. They can also be used for
 CC obtaining cells capable of expressing an homeobox related desired
 CC property. The method uses reverse transcriptase polymerase chain
 CC reaction (RT-PCR) for determining the pattern of gene expression in a
 CC selected gene family. Sequences AAZ17803-Z18342 represent primers that
 CC can be used in the RT-PCR reactions to determine the pattern of gene
 CC expression. The gene family can be selected from a set of homeobox genes,
 CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid
 CC receptor superfamily genes or cadherin superfamily genes.
 XX SQ Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 349 CCAGCGCCCAACCTGTC 364
 Db 3 CCAGCGCCCAACCTGTC 18
 RESULT 1466
 AAZ18140
 ID AAZ18140 standard; DNA; 18 BP.
 XX AC AAZ18140;
 XX AC AAZ18140;
 XX DT 11-OCT-1999 (first entry)
 XX DE STK 9 gene specific primer.
 XX KW Genetic proximity; gene expression; cell characterisation; homeobox gene;
 KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
 KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
 KW primer; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9934016-A2.
 XX PD 08-JUL-1999.
 XX PF 28-DEC-1998; 98WO-IL00625.
 XX PR 16-OCT-1998; 98IL-0126627.
 XX PR 29-DEC-1997; 97IL-0122793.
 XX PA (GENE-) GENENA LTD.
 XX PI Vidar B;
 XX DR WPI; 1999-419113/35.
 XX DR P-PSDB; AAY14673.
 XX PT Identifying and characterizing cells by comparing the pattern of
 PT gene expression in a selected gene family
 XX PS Claim 4; Page 44; 102pp; English.
 XX CC The invention provides a new method for identifying and characterising
 CC cells. The method for determining the genetic proximity of a first cell
 CC and a second cell comprises: (a) obtaining the first cell and the second
 CC cell; (b) determining in the first cell and the second cell the pattern
 CC of expression of genes in a selected gene family; and (c) calculating a
 CC proximity index using a specified formula. The methods can be used for
 CC characterising cells, e.g. for determining the origin of a cell, its
 CC genetic status, whether it carries a genetic defect, or whether it is
 CC transformed. They can be used for detecting a selected genetic defect in
 CC an individual, e.g. a fetus. They can also be used for determining the
 CC effect of a selected treatment on a test cell. They can also be used for
 CC obtaining cells capable of expressing an homeobox related desired
 CC property. The method uses reverse transcriptase polymerase chain
 CC reaction (RT-PCR) for determining the pattern of gene expression in a
 CC selected gene family. Sequences AAZ17803-Z18342 represent primers that
 CC can be used in the RT-PCR reactions to determine the pattern of gene
 CC expression. The gene family can be selected from a set of homeobox genes,
 CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid
 CC receptor superfamily genes or cadherin superfamily genes.
 XX SQ Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 349 CCAGCGCCCAACCTGTC 364
 Db 3 CCAGCGCCCAACCTGTC 18
 RESULT 1466
 AAZ18140
 ID AAZ18140 standard; DNA; 18 BP.
 XX AC AAZ18140;
 XX AC AAZ18140;
 XX DT 11-OCT-1999 (first entry)
 XX DE STK 9 gene specific primer.

XX KW Genetic proximity; gene expression; cell characterisation; homeobox gene;
 KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
 KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
 KW primer; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9934016-A2.
 XX PD 08-JUL-1999.
 XX PF 28-DEC-1998; 98WO-IL00625.
 XX PR 16-OCT-1998; 98IL-0126627.
 XX PR 29-DEC-1997; 97IL-0122793.
 XX PA (GENE-) GENENA LTD.
 XX PI Vidar B;
 XX DR WPI; 1999-419113/35.
 XX DR P-PSDB; AAY14675.
 XX PT Identifying and characterizing cells by comparing the pattern of
 PT gene expression in a selected gene family
 XX PS Claim 4; Page 44; 102pp; English.
 XX CC The invention provides a new method for identifying and characterising
 CC cells. The method for determining the genetic proximity of a first cell
 CC and a second cell comprises: (a) obtaining the first cell and the second
 CC cell; (b) determining in the first cell and the second cell the pattern
 CC of expression of genes in a selected gene family; and (c) calculating a
 CC proximity index using a specified formula. The methods can be used for
 CC characterising cells, e.g. for determining the origin of a cell, its
 CC genetic status, whether it carries a genetic defect, or whether it is
 CC transformed. They can be used for detecting a selected genetic defect in
 CC an individual, e.g. a fetus. They can also be used for determining the
 CC effect of a selected treatment on a test cell. They can also be used for
 CC obtaining cells capable of expressing an homeobox related desired
 CC property. The method uses reverse transcriptase polymerase chain
 CC reaction (RT-PCR) for determining the pattern of gene expression in a
 CC selected gene family. Sequences AAZ17803-Z18342 represent primers that
 CC can be used in the RT-PCR reactions to determine the pattern of gene
 CC expression. The gene family can be selected from a set of homeobox genes,
 CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid
 CC receptor superfamily genes or cadherin superfamily genes.
 XX SQ Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 349 CCAGCGCCCAACCTGTC 364
 Db 3 CCAGCGCCCAACCTGTC 18
 RESULT 1467
 AAZ18142
 ID AAZ18142 standard; DNA; 18 BP.
 XX AC AAZ18142;
 XX AC AAZ18142;
 XX DT 11-OCT-1999 (first entry)
 XX DE STK 10 gene specific primer.
 XX KW Genetic proximity; gene expression; cell characterisation; homeobox gene;
 KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
 KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
 KW primer; ss.

```

KW primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9934016-A2.
XX
XX PD 08-JUL-1999.
XX
XX PF 28-DEC-1998; 98WO-IL00625.
XX
XX PR 16-OCT-1998; 98IL-0126627.
XX
XX PR 29-DEC-1997; 97IL-0122793.
XX
XX PA (GENE-) GENENA LTD.
XX
XX PI Vidar B;
XX
XX DR WPI; 1999-419113/35.
XX
XX DR P-PSDB; AAY14677.
XX
XX PT Identifying and characterizing cells by comparing the pattern of
XX PT gene expression in a selected gene family
XX
XX PS Claim 4; Page 44; 102pp; English.
XX
XX CC The invention provides a new method for identifying and characterising
XX CC cells. The method for determining the genetic proximity of a first cell
XX CC and a second cell comprises: (a) obtaining the first cell and the second
XX CC cell; (b) determining in the first cell and the second cell the pattern
XX CC of expression of genes in a selected gene family; and (c) calculating a
XX CC proximity index using a specified formula. The methods can be used for
XX CC characterising cells, e.g. for determining the origin of a cell, its
XX CC genetic status, whether it carries a genetic defect, or whether it is
XX CC transformed. They can be used for detecting a selected genetic defect in
XX CC an individual, e.g. a fetus. They can also be used for determining the
XX CC effect of a selected treatment on a test cell. They can also be used for
XX CC obtaining cells capable of expressing an homeobox related desired
XX CC property. The method uses reverse transcriptase polymerase chain
XX CC reaction (RT-PCR) for determining the pattern of gene expression in a
XX CC selected gene family. Sequences AA217803-218342 represent primers that
XX CC can be used in the RT-PCR reactions to determine the pattern of gene
XX CC expression. The gene family can be selected from a set of homeobox genes,
XX CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid
XX CC receptor superfamily genes or cadherin superfamily genes.
XX
XX SQ Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 349 CCAGCGCCACCTGTC 364
Db 3 CCAGCGCCACATGTC 18

RESULT 1468
AAZ18144
ID AAZ18144 standard; DNA; 18 BP.
XX
XX AC AAZ18144;
XX
XX AC AAZ18144;
XX
XX DT 11-OCT-1999 (first entry)
XX
XX DE STK 11 gene specific primer.
XX
XX KW Genetic proximity; gene expression; cell characterisation; homeobox gene;
XX KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
XX KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
XX KW primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO9934016-A2.

```

XX PD 08-JUL-1999.

XX XX 28-DEC-1998; 98WO-IL00625.

XX PF 16-OCT-1998; 98IL-0126627.

XX PR 29-DEC-1997; 97IL-0122793.

XX XX (GENE-) GENENA LTD.

XX PA Vidar B;

XX PI WPI; 1999-419113/35.

XX DR P-PSDB; AAY14681.

XX XX Identifying and characterizing cells by comparing the pattern of

PT gene expression in a selected gene family

XX Claim 4; Page 44; 102pp; English.

XX The invention provides a new method for identifying and characterising

CC cells. The method for determining the genetic proximity of a first cell

CC and a second cell comprises: (a) obtaining the first cell and the second

CC cell; (b) determining in the first cell and the second cell the pattern

CC of expression of genes in a selected gene family; and (c) calculating a

CC proximity index using a specified formula. The methods can be used for

CC characterising cells, e.g. for determining the origin of a cell, its

CC genetic status, whether it carries a genetic defect, or whether it is

CC transformed. They can be used for detecting a selected genetic defect in

CC an individual, e.g. a fetus. They can also be used for determining the

CC effect of a selected treatment on a test cell. They can also be used for

CC obtaining cells capable of expressing an homeobox related desired

CC property. The method uses reverse transcriptase polymerase chain

CC reaction (RT-PCR) for determining the pattern of gene expression in a

CC selected gene family. Sequences AA217803-218342 represent primers that

CC can be used in the RT-PCR reactions to determine the pattern of gene

CC expression. The gene family can be selected from a set of homeobox genes,

CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid

CC receptor superfamily genes or cadherin superfamily genes.

XX Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 other;

SQ

Query Match 1.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 349 CCAGCGCCCACTGTC 364

Db 3 CCAGCGCCCACTGTC 18

RESULT 1470

AA218148

ID AA218148 standard; DNA; 18 BP.

AC AA218148;

XX 11-OCT-1999 (first entry)

DE STK 13 gene specific primer.

XX Genetic proximity; gene expression; cell characterisation; homeobox gene;

KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;

KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;

KW primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9934016-A2.

PN 08-JUL-1999.

XX PD 08-JUL-1999.

XX PF 28-DEC-1998; 98WO-IL00625.

XX XX 16-OCT-1998; 98IL-0126627.

PF 28-DEC-1998; 98WO-IL00625.

XX 16-OCT-1998; 98IL-0126627.

PR 29-DEC-1997; 97IL-0122793.

XX (GENE-) GENENA LTD.

XX PA Vidar B;

XX PI WPI; 1999-419113/35.

XX DR P-PSDB; AAY14683.

XX XX Identifying and characterizing cells by comparing the pattern of

PT gene expression in a selected gene family

XX Claim 4; Page 44; 102pp; English.

XX The invention provides a new method for identifying and characterising

CC cells. The method for determining the genetic proximity of a first cell

CC and a second cell comprises: (a) obtaining the first cell and the second

CC cell; (b) determining in the first cell and the second cell the pattern

CC of expression of genes in a selected gene family; and (c) calculating a

CC proximity index using a specified formula. The methods can be used for

CC characterising cells, e.g. for determining the origin of a cell, its

CC genetic status, whether it carries a genetic defect, or whether it is

CC transformed. They can be used for detecting a selected genetic defect in

CC an individual, e.g. a fetus. They can also be used for determining the

CC effect of a selected treatment on a test cell. They can also be used for

CC obtaining cells capable of expressing an homeobox related desired

CC property. The method uses reverse transcriptase polymerase chain

CC reaction (RT-PCR) for determining the pattern of gene expression in a

CC selected gene family. Sequences AA217803-218342 represent primers that

CC can be used in the RT-PCR reactions to determine the pattern of gene

CC expression. The gene family can be selected from a set of homeobox genes,

CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid

CC receptor superfamily genes or cadherin superfamily genes.

XX Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 other;

SQ

Query Match 1.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 349 CCAGCGCCCACTGTC 364

Db 3 CCAGCGCCCACTGTC 18

RESULT 1471

AA218150

ID AA218150 standard; DNA; 18 BP.

AC AA218150;

XX 11-OCT-1999 (first entry)

DE STK 14 gene specific primer.

XX Genetic proximity; gene expression; cell characterisation; homeobox gene;

KW genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;

KW kinase gene; protein phosphatase; P450; steroid receptor; cadherin;

KW primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9934016-A2.

PN 08-JUL-1999.

XX PD 28-DEC-1998; 98WO-IL00625.

XX XX 16-OCT-1998; 98IL-0126627.

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

CC Sequence 18 BP; 5 A; 3 C; 5 G; 5 T; 0 other;
SQ

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 73 TGTATGCAACTGTGG 88
DB 3 TGGATGCAACTTGG 18
|||||

RESULT 1474

AAZ72978
ID AAZ72978 standard; DNA; 18 BP.

XX AC AAZ72978;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker upstream amplification primer SEQ ID NO:7334.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB00822.

XX 21-APR-1998; 98US-0082614.

XX 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -

XX Claim 9; Page 1794; 2745pp; English.

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of

CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

XX Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 324 AGAGAAGCTGTGGAC 339
DB 2 AGAGAAGCTGTGTAAC 17
|||||

RESULT 1475

AAZ74871/C

ID AAZ74871 standard; DNA; 18 BP.

XX AC AAZ74871;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker downstream amplification primer SEQ ID NO:9227.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB00822.

XX 21-APR-1998; 98US-0082614.

XX 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -

XX Claim 8; Page 2198; 2745pp; English.

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

XX SQ Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 404 CTGCTCCAGCGGCT 419
 DB 18 CTGCTCCAGTATGCT 3
 RESULT 1476
 AAZ76819
 ID AAZ76819 standard; DNA; 18 BP.
 XX AC AAZ76819;
 XX DT 10-SEP-2001 (first entry)
 XX DE Human biallelic marker downstream amplification primer SEQ ID NO:11175.
 XX KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX OS Homo sapiens.
 XX PN WO9954500-A2.
 XX PD 28-OCT-1999.
 XX PF 21-APR-1999; 99WO-IB00822.
 XX PR 21-APR-1998; 98US-0082614.
 XX PR 23-NOV-1998; 98US-0109732.
 XX PA (GEST) GENSET.
 XX PI Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX PT Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome -
 XX Claim 9; Page 2613; 2745pp; English.
 XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses; they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2952, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.
 XX SQ Sequence 18 BP; 8 A; 5 C; 4 G; 1 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 792 AAACCTGCAGGACTGAC 807
 DB 3 ACACAGCAGGACTGAC 18
 RESULT 1477
 AAC62614/c
 ID AAC62614 standard; DNA; 18 BP.
 XX AC AAC62614;
 XX DT 01-FEB-2001 (first entry)
 XX DE Human OB gene sequence tagged-site-specific PCR primer #28.
 XX KW Human; mouse; OB gene; obesity; adiposity; body weight; PCR primer; ss.
 XX OS Homo sapiens.
 XX PN US6124448-A.
 XX PD 26-SEP-2000.
 XX PF 07-JUN-1995; 95US-0488208.
 XX PR 17-AUG-1994; 94US-0292345.
 XX PR 30-NOV-1994; 94US-0347563.
 XX PR 10-MAY-1995; 95US-0438431.
 XX PA (UYRQ) UNIV ROCKEFELLER.
 XX PI Maffei M, Proenca R, Zhang Y, Friedman JM;
 XX WPI; 2000-601556/57.
 XX DR Nucleic acid primers and probes useful for detecting mutations in
 PT mammalian OB gene associated with regulation of body weight and
 PT adiposity -
 XX Example 10; Column 80; 153pp; English.
 XX CC The present sequence is a PCR primer which was used in an invention
 CC relating to the control of body weight of animals including
 CC humans. Nucleic acids of at least 10 nucleotides which are hybridisable
 CC to a non-coding region of an OB nucleic acid have been created. The OB
 CC gene plays a critical role in the regulation of body weight and
 CC adiposity. The nucleic acids may be used as probes or as primers for PCR.
 CC They are useful for evaluating the presence of mutations in the human OB
 CC gene or for evaluating the level of expression of OB mRNA. Defects
 CC associated with OB gene expression result in obese phenotypes.
 XX SQ Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 313 GGAAAGACTGCAGAGA 328
 DB 18 GAAAGAAATGCAGAGA 3
 RESULT 1478
 AAC62694/c
 ID AAC62694 standard; DNA; 18 BP.
 XX AC AAC62694;
 XX DT 01-FEB-2001 (first entry)
 XX DE Human OB gene sequence tagged-site-specific PCR primer #28.
 XX KW Human; mouse; anabolic; cytostatic; immunostimulant;

KW OB polypeptide inhibitor; body weight; obesity; OB gene; cancer; AIDS;
 KW anorexia nervosa; hypertension; heart disease; Type II diabetes;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS US6124439-A.
 FN
 XX 26-SEP-2000.
 XX
 XX 07-JUN-1995; 95US-0488214.
 XX
 XX 17-AUG-1994; 94US-0292345.
 XX 30-NOV-1994; 94US-0347563.
 XX 10-MAY-1995; 95US-0438431.
 XX
 FA (UTRQ) UNIV ROCKEFELLER.
 XX
 XX Proenca R, Zhang Y, Friedman JM;
 XX WPI; 2000-611018/58.
 XX
 XX Novel antibody to mammalian obesity polypeptide useful for diagnosis
 PT and treatment of weight loss associated with disorders such as cancer,
 PT AIDS and anorexia nervosa -
 XX
 XX Example 10; Column 80; 150pp; English.
 XX
 CC The present sequence is a PCR primer which was used in an invention
 CC relating to the control of body weight of animals including humans.
 CC Antibodies against the mammalian obesity (OB) polypeptide have been
 CC identified. The antibodies are useful for modulating the activity of OB
 CC to control body weight and fat content and/or to treat certain
 CC pathological conditions in which there is abnormal depression or
 CC elevation of body weight. The antibodies are used to treat weight loss
 CC associated with cancer, AIDS and anorexia nervosa. They are useful for
 CC the diagnosis of nutritional disorders such as obesity and diseases
 CC associated with obesity, such as hypertension, heart disease and Type II
 CC diabetes. The kits are used to determine the presence or amount of OB in
 CC the blood or plasma of an individual.
 XX
 XX Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 313 GGAAAGACTGCAGAGA 328
 DB 18 GAAAGAAGTGCAGAGA 3
 RESULT 1479
 AAA09486/C
 ID AAA09486 standard; DNA; 18 BP.
 XX
 AC AAA09486;
 XX
 XX 29-AUG-2000 (first entry)
 DT
 XX Antisense primer for human Zsig24 gene mapping.
 DE
 XX Zsig24; membrane-associated; glucose metabolism; chromosome 11q23-24;
 KW obesity; diabetes; antigenic peptide; antibody; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200024767-A2.
 FN
 XX 04-MAY-2000.
 PD
 XX 20-OCT-1999; 99WO-US24662.
 PF
 XX

PR 23-OCT-1998; 98US-0178009.
 PR 23-JUN-1999; 99US-0339395.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Jelinek LJ, Whitmore TE;
 PI
 XX WPI; 2000-350689/30.
 DR
 XX
 XX Zsig24 nucleic acids and peptides useful for detecting chromosome 11
 PT abnormalities associated with glucose metabolism such as diabetes and
 PT obesity
 PT
 XX Example 2; Page 70; 81pp; English.
 PS
 XX The human Zsig24 gene encodes a membrane associated protein, and is
 CC linked to defects in glucose metabolism. The gene has been mapped to
 CC chromosome 11q23-24. The nucleic acids and the proteins they encode
 CC may be used to screen for defects in chromosome 11 that are associated
 CC with glucose metabolism and therefore may be involved in the development
 CC of obesity and diabetes. For example the peptides may be used to produce
 CC antibodies that may be used in immunoassays and the nucleic acids may
 CC be used as probes/primers for polymerase chain reaction analysis.
 XX
 XX Sequence 18 BP; 2 A; 8 C; 3 G; 5 T; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 36 TCCAGGTGCAGAGGC 51
 DB 17 TCCAGGTGCAGAGGC 2
 RESULT 1480
 AAA12336/C
 ID AAA12336 standard; DNA; 18 BP.
 XX
 AC AAA12336;
 XX
 XX 18-AUG-2000 (first entry)
 DT
 XX Human OB DNA PCR primer SWS1392 #2.
 DE
 XX OB gene; body weight; obesity; anorectic; adipose tissue; brain;
 KW human; PCR primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX US6048837-A.
 FN
 XX 11-APR-2000.
 PD
 XX 07-JUN-1995; 95US-0485942.
 XX
 XX 17-AUG-1994; 94US-0292345.
 PR 30-NOV-1994; 94US-0347563.
 PR 10-MAY-1995; 95US-0438431.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Proenca R, Zhang Y, Friedman JM;
 PI
 XX WPI; 2000-302788/26.
 DR
 XX Modifying body weight of an animal comprises administering mammalian
 PT obesity polypeptide obtained from humans and murine -
 PT
 XX Example 10; Column 147-148; 153pp; English.
 PS
 XX This invention describes a novel method for modifying body weight of
 CC an animal which comprises administering mammalian obesity (OB)
 CC

CC polypeptide. The products of the invention have anorectic activity.
CC The OB polypeptide at a dose of 5 mg/g/day in 300 micro litres of PBS
CC was injected intraperitoneally into mice. Control mice were injected
CC with PBS dialysate of the recombinant protein. The body weight of the
CC mice was noted. The results shows that recombinant the OB polypeptide
CC is capable of reducing a body weight and is found to be effective when
CC it is administered daily. The OB polypeptide acts as a part of the
CC signalling pathway by which adipose tissue communicates with the brain
CC and other organs. (i) is useful for modulating body weight of an animal
CC especially humans. This sequence represents a PCR primer used in the
CC amplification of a human OB protein described in the method of the
CC invention.
XX
SQ Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. NO. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 313 GGAAGACTGCAGAGA 328
DB 18 GAAAGAATGCAGAGA 3
RESULT 1481
AAA40933/c
ID AAA40933 standard; DNA; 18 BP.
XX
AC AAA40933;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human TNFalpha antisense oligonucleotide ISIS# 100280.
XX
KW Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
KW pancreatitis; atopic dermatitis; allograft rejection;
KW autoimmune disease; inflammatory disease; ss.
XX
OS Synthetic.
XX
PN WO200020645-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23205.
XX
PR 05-OCT-1998; 98US-0166186.
PR 18-MAY-1999; 99US-0313932.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Bennett CF, Butler MM, Shanahan WJ;
XX
DR WPI; 2000-303808/26.
XX
PT Oligonucleotide for treating diseases associated with human tumour
PT necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNFalpha -
XX
PS Example 19; Page 92; 283pp; English.
XX
CC This sequence represents an antisense oligonucleotide sequence which
CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
CC in host defence. It is produced mainly in macrophages and monocytes in
CC response to infection, invasion, injury or inflammation. Overexpression
CC of TNFalpha can result in disease states, particularly in infectious,
CC inflammatory and autoimmune diseases. The invention relates to antisense
CC oligonucleotides, such as that represented by the present sequence which
CC are capable of modulating the TNFalpha gene expression. The

CC oligonucleotides optionally have a phosphorothioate backbone, and may
CC also optionally contain at least one 2'-O-methoxyethyl modification. The
CC oligonucleotides are useful for modulating the expression of human
CC TNFalpha in cells and tissues, reducing a human cell inflammatory
CC response, reducing the blood glucose level in a human and treating a
CC human having a disease or condition associated with TNFalpha. Examples of
CC diseases associated with TNFalpha include diabetes, inflammatory bowel
CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
CC The antisense oligonucleotides are also useful for modulating the
CC function of a selected nucleic acid sequence in adipose tissue.
XX
SQ Sequence 18 BP; 4 A; 8 C; 2 G; 4 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. NO. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 123 GAAGAAGCTGCTCTG 138
DB 18 GAAGATAGGCTCTG 3
RESULT 1482
AAA40934/c
ID AAA40934 standard; DNA; 18 BP.
XX
AC AAA40934;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human TNFalpha antisense oligonucleotide ISIS# 100281.
XX
KW Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
KW pancreatitis; atopic dermatitis; allograft rejection;
KW autoimmune disease; inflammatory disease; ss.
XX
OS Synthetic.
XX
PN WO200020645-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23205.
XX
PR 05-OCT-1998; 98US-0166186.
PR 18-MAY-1999; 99US-0313932.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Bennett CF, Butler MM, Shanahan WJ;
XX
DR WPI; 2000-303808/26.
XX
PT Oligonucleotide for treating diseases associated with human tumour
PT necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid
PT arthritis, comprises nucleotide sequence complementary to intron of
PT nucleic acid encoding TNFalpha -
XX
PS Example 19; Page 92; 283pp; English.
XX
CC This sequence represents an antisense oligonucleotide sequence which
CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
CC in host defence. It is produced mainly in macrophages and monocytes in
CC response to infection, invasion, injury or inflammation. Overexpression
CC of TNFalpha can result in disease states, particularly in infectious,
CC inflammatory and autoimmune diseases. The invention relates to antisense
CC oligonucleotides, such as that represented by the present sequence which
CC are capable of modulating the TNFalpha gene expression. The
CC oligonucleotides optionally have a phosphorothioate backbone, and may

CC also optionally contain at least one 2'-O-methoxyethyl modification. The
 CC oligonucleotides are useful for modulating the expression of human
 CC TNFalpha in cells and tissues, reducing a human cell inflammatory
 CC response, reducing the blood glucose level in a human and treating a
 CC human having a disease or condition associated with TNFalpha. Examples of
 CC diseases associated with TNFalpha include diabetes, inflammatory bowel
 CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
 CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
 CC The antisense oligonucleotides are also useful for modulating the
 CC function of a selected nucleic acid sequence in adipose tissue.
 XX
 SQ Sequence 18 BP; 4 A; 8 C; 1 G; 5 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 123 GAAGAAGGATGCTG 138
 |||||
 Db 17 GAAGATAGGCTGCTG 2

RESULT 1483

AAA40935/c

ID AAA40935 standard; DNA; 18 BP.

XX

AC AAA40935;

XX

DT 16-AUG-2000 (first entry)

XX

DE Human TNFalpha antisense oligonucleotide ISIS# 100282.

XX

XX Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
 KW tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
 KW rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;
 KW pancreatitis; atopic dermatitis; allograft rejection;
 KW autoimmune disease; inflammatory disease; ss.

XX

OS Synthetic.

XX

PN WO200020645-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US23205.

XX

PR 05-OCT-1998; 98US-0166186.

XX

PR 18-MAY-1999; 99US-0313932.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Baker BF, Bennett CF, Butler MM, Shanahan WJ;

XX

DR WPI; 2000-303808/26.

XX

PT Oligonucleotide for treating diseases associated with human tumour
 PT necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid
 PT arthritis, comprises nucleotide sequence complementary to intron of
 PT nucleic acid encoding TNFalpha -

XX

PS Example 19; Page 92; 283pp; English.

XX

CC This sequence represents an antisense oligonucleotide sequence which
 CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
 CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
 CC in host defence. It is produced mainly in macrophages and monocytes in
 CC response to infection, invasion, injury or inflammation. Overexpression
 CC of TNFalpha can result in disease states, particularly in infectious,
 CC inflammatory and autoimmune diseases. The invention relates to antisense
 CC oligonucleotides, such as that represented by the present sequence which
 CC are capable of modulating the TNFalpha gene expression. The
 CC oligonucleotides optionally have a phosphorothioate backbone, and may
 CC also optionally contain at least one 2'-O-methoxyethyl modification. The

CC oligonucleotides are useful for modulating the expression of human
 CC TNFalpha in cells and tissues, reducing a human cell inflammatory
 CC response, reducing the blood glucose level in a human and treating a
 CC human having a disease or condition associated with TNFalpha. Examples of
 CC diseases associated with TNFalpha include diabetes, inflammatory bowel
 CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
 CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
 CC The antisense oligonucleotides are also useful for modulating the
 CC function of a selected nucleic acid sequence in adipose tissue.
 XX
 SQ Sequence 18 BP; 4 A; 7 C; 1 G; 6 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 123 GAAGAAGGATGCTG 138
 |||||
 Db 16 GAAGATAGGCTGCTG 1

RESULT 1484

AAZ56420

ID AAZ56420 standard; DNA; 18 BP.

XX

AC AAZ56420;

XX

DT 17-MAR-2000 (first entry)

XX

DE Escherichia coli H25 flagellin PCR primer #2653.

XX

KW Flagellin; fliC; antigen; detection; PCR primer; ss.

XX

OS Escherichia coli.

XX

PN WO9961458-A1.

XX

PD 02-DEC-1999.

XX

PF 21-MAY-1999; 99WO-AU00385.

XX

PR 21-MAY-1998; 98AU-0003634.

XX

PA (UNSY) UNIV SYDNEY.

XX

PI Reeves PR, Wang L;

XX

DR WPI; 2000-072598/06.

XX

PT Novel nucleic acid molecule useful for the detection of flagellated

PT bacterial strains in food, faeces, etc. -

XX

PS Disclosure; Page 48; 245pp; English.

XX

CC AAZ56331 to AAZ56398 represent nucleic acid molecules (I) encoding all
 CC or part of an Escherichia coli flagellin protein except a protein
 CC expressed by E. coli H1, H7, H12 or H48 type strains. The present
 CC invention also describes a method of detecting the presence of E. coli
 CC of a particular H serotype in a sample, comprising specifically
 CC hybridising a nucleic acid, preferably at least a pair, derived from a
 CC flagellating gene, specific for a particular flagellin gene associated
 CC with the H serotype, to any E. coli in the sample which contain the gene,
 CC and detecting any hybridised molecules, identifying the presence of that
 CC serotype in the sample. (I) are useful for: (1) detecting the presence
 CC of E. coli of H serotype in a sample by hybridising at least one or a
 CC pair of (I) to any E. coli in the sample and detecting the hybridised
 CC nucleic acid molecules; and (2) for detecting the presence of both O
 CC and H-serotypes of E. coli by hybridising at least one or a pair of (I)
 CC to any E. coli present in the sample and detecting the hybridised
 CC nucleic acid molecules. (I) is particularly useful for detecting the
 CC combination of O and H antigen. Hybridised (I) when using at least one
 CC (I) is detected by southern blot analysis and, when using a pair of (I),
 CC is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420

CC represent primers used in the exemplification of the present invention.
 XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 357 AACCTGTCAGAGAGC 372
 DB 1 AACCTGTCAGAGGC 16

RESULT 1485
 ID AAH26010 standard; DNA; 18 BP.
 XX AC AAH26010;

XX DT 05-SEP-2001 (first entry)

DE PCR primer Syk-M for human Syk cDNA.

XX SYK; tyrosine kinase; human; antisense; asthma; gene therapy;
 KW antiasthmatic; inflammation; antiinflammatory; phagocytosis;
 KW PCR primer; ss.

XX OS Homo sapiens.

XX FN US6242427-B1.

XX PD 05-JUN-2001.

XX DP 14-SEP-1998; 98US-0158980.

XX PR 07-JUN-1996; 96US-0657884.

XX PR 30-SEP-1993; 93US-0129381.

XX PR 30-SEP-1994; 94US-0316425.

XX PR 07-JUN-1995; 95US-0483530.

XX PA (UTPE-) UNIV PENNSYLVANIA.

XX PI Schreiber AD, Park J;

XX DR WPI; 2001-380484/40.

XX PT Inhibiting the release of a mediator from a Syk-producing cell, useful
 PT in gene therapy for treating inflammatory conditions or asthma, by
 PT introducing into the cell Syk antisense oligonucleotides -

XX PS Example 5; Column 19; 35pp; English.

XX CC The present sequence is that of PCR primer Syk-M, which
 CC corresponds to nucleotides 550-564 of human Syk mRNA. Syk-M was
 CC used with primer Syk-H (see AAH26090) in the PCR amplification
 CC of human Syk cDNA derived from monocyte mRNA. Experiments were
 CC performed to compare the efficacy of linear and stem-loop antisense
 CC oligonucleotides (see AAH26001), targeted to Syk mRNA, for
 CC reducing the level of phagocytosis from cultured monocytes; Syk
 CC tyrosine kinase is a major signal transducer for Fc-gamma-RIIA
 CC mediated phagocytosis in monocytes. The invention provides a
 CC claimed method of inhibiting the release of a mediator from a
 CC Syk-producing cell. This involves introducing into the cell an
 CC antisense construct that targets an Syk encoding sequence such that
 CC inhibition is effected. The cell is preferably present in the lung
 CC of an asthma patient. Also claimed is a method of treating an
 CC inflammatory condition in a patient by administering an antisense
 CC construct that targets Syk encoding sequences and inhibits Syk
 CC kinase production.

SQ Sequence 18 BP; 0 A; 7 C; 7 G; 4 T; 0 other;

Query Match

1.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 GCTGGGGGACACAC 401
 DB 17 GCCGGGGGACACAC 2

RESULT 1486
 AAH63028/c
 ID AAH63028 standard; DNA; 18 BP.

XX AC AAH63028;

XX DT 11-SEP-2001 (first entry)

XX DE Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 189.

XX KW Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
 KW antiviral agent; gene expression; antisense construct; probe; primer;
 KW transgenic viral resistant shrimp; ss.

XX OS White spot syndrome virus.

XX PN WO200138351-A2.

XX PD 31-MAY-2001.

XX PF 08-NOV-2000; 2000WO-US28888.

XX PR 24-NOV-1999; 99CN-0124717.

XX PA (PENY-) PE CORP NY.

XX PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.

XX PI (SINO-) SINOGENOMAX CO LTD.

XX PI Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;

XX DR WPI; 2001-355877/37.

XX PT Primary nucleotide sequence of the shrimp white spot Bacilliform virus
 PT (WSBV), useful for producing viral polypeptides that can be used to
 PT screen for agents that are useful for treating WSBV infection -

XX PS Disclosure; Figure 3; 626pp; English.

XX CC The invention provides the primary nucleotide sequence of the WSBV genome
 CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
 CC encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
 CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
 CC molecules and proteins of the invention are useful for diagnosis and
 CC monitoring viral infection, in screens for antiviral agents and for
 CC monitoring viral gene expression or activity during a treatment regimen.
 CC The nucleic acid molecules are also useful as antisense constructs to
 CC control viral gene expression in infected cells and tissues and to create
 CC transgenic viral resistant shrimp.

SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 other;

Query Match

1.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 216 CCCTCTCCAGAGTGA 231

DB 17 CCACTCCAGAGTGA 2

RESULT 1487

AAC85987/c

ID AAC85987 standard; DNA; 18 BP.

XX AC AAC85987;

```
XX 22-AUG-2001 (first entry)
XX Primer PC2 to amplify DoPEV genomic fragment.
XX
XX Domestic pig; retrovirus; DoPEV; detection; retroviral genome; PCR;
XX hybridization; amplification; antibody; xenotransplantation; primer;
XX zoonotic infectious disease; graft; human; tissue; organ; probe;
XX polymerase chain reaction; gag; pol; ss.
XX
XX Synthetic.
XX
XX BP1106703-A1.
XX
XX 13-JUN-2001.
XX
XX 09-DEC-1999; 99EP-0204219.
XX
XX 09-DEC-1999; 99EP-0204219.
XX
XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Mang R, Van Der Kuyl AC;
XX
XX WPI; 2001-383572/41.
XX
XX Testing xenotransplantation, cells, tissue or organ for retroviral
XX genomes comprises isolating recombinant nucleic acid comprising a
XX consensus retroviral sequence partly derived from a domestic pig
XX retrovirus sequence -
XX
XX Example; Page 7; 35pp; English.
XX
XX The sequences given in AAC85986-AAC86001 are primers which were used
XX to amplify fragments of the domestic pig retrovirus sequence (DoPEV).
XX Detection of DoPEV sequences in the method of the invention allows
XX identification of different types of RT sequences from DoPEV. DoPEV
XX contains consensus retroviral sequences allowing detection of a
XX retroviral genome by nucleic acid hybridization and/or amplification.
XX Fragments of the DoPEV nucleic acid and antibodies directed against it,
XX are used to test a mammalian xenotransplantation source (i.e. pig cells,
XX tissue or organ), recipient or contact of the recipient, for the presence
XX of a retroviral genome or fragment in order to reduce the risk of
XX zoonotic infectious diseases. This will allow pigs to become a major
XX graft and transplant source for human tissues and organs.
XX
XX Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 18;
XX Best Local Similarity 87.5%; Pred. No. 9.7e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 206 GGGTTCACAGCCCTCT 221
XX Db ||||| ||||| |||||
XX 18 GGGTTCACAGCCCACT 3
XX
XX RESULT 1488
XX AAH40933/c
XX ID AAH40933 standard; DNA; 18 BP.
XX
XX AC AAH40933;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific upper PCR primer SEQ ID 3729.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
```

```
XX OS Homo sapiens.
XX XX WO200129262-A2.
XX XX 26-APR-2001.
XX XX 13-OCT-2000; 2000WO-US28436.
XX XX 15-OCT-1999; 99US-0160096.
XX XX (ORCH-) ORCHID BIOSCIENCES INC.
XX XX Picoult-Newburg L, Pohl M;
XX XX WPI; 2001-290930/30.
XX XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample -
XX
XX Claim 1; Page 69; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a PCR primer specific
XX for a human SNP containing DNA sequence.
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
XX
XX Query Match 1.2%; Score 12.8; DB 1; Length 18;
XX Best Local Similarity 87.5%; Pred. No. 9.7e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 820 CTGTGGGTGCTGAAGC 835
XX Db ||||| ||||| |||||
XX 17 CTGTGGGGGAGAGC 2
XX
XX RESULT 1489
XX AAS01839/c
XX ID AAS01839 standard; DNA; 18 BP.
XX
XX AC AAS01839;
XX
XX 04-JUL-2001 (first entry)
XX
XX Cytochrome P-450 (CYP)3A4 gene sequencing primer 3A410R.
XX
XX CYP3A4; CYP3A7; human; exon/intron boundary; cytochrome P-450; cancer;
XX abnormal drug response; environmental carcinogen; genotype; polymorphism;
XX drug candidate; protein malfunction; inhibitor; hypersensitivity; ss;
XX hypersensitivity; sequencing primer.
XX
```

OS Homo sapiens.
XX WO200120025-A2.
XX 22-MAR-2001.
XX 01-SEP-2000; 2000WO-EP08570.
XX 10-SEP-1999; 99EP-0118120.
XX (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
XX Wojnowski L, Eisele R;
XX WPI; 2001-244818/25.
XX Novel variant of CYP3A4 and CYP3A7 genes, associated with insufficient
PT metabolism and/or sensitivity to drugs, useful for diagnosing and
PT treating diseases with drugs that are modulators of their gene product
PT -
XX Claim 37; Page 39; 106pp; English.
XX The sequence represents a primer used to determine the exon/intron
CC boundaries of the cytochrome P-450 (CYP)3A4 gene. Polymorphic
CC polynucleotides of the CYP3A4 or CYP3A7 genes are associated with
CC abnormal drug response or individual predisposition to several common
CC cancers caused by environmental carcinogens. The primer sequences can be
CC used in the production of variant CYP3A4 and CYP3A7 proteins in order to
CC study the malfunction of the proteins, and in diagnostic tests designed
CC for the specific detection and genotyping of CYP3A4 and CYP3A7 alleles in
CC humans. The invention provides methods for identifying and obtaining drug
CC candidates and inhibitors of the genes for therapy of disorders related
CC to acquired drug hypo- or hypersensitivity.
XX
SQ Sequence 18 BP; 2 A; 8 C; 2 G; 6 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 994 GAAGTCTGAGGCTGGA 1009
DB 18 GAAATCTGAGGCGGGA 3
RESULT 1490
AAS01840
ID AAS01840 standard; DNA; 18 BP.
XX AAS01840;
XX 04-JUL-2001 (first entry)
XX Cytochrome P-450 (CYP)3A4 gene sequencing primer 3A411F.
XX CYP3A4; CYP3A7; human; exon/intron boundary; cytochrome P-450; cancer;
KW abnormal drug response; environmental carcinogen; genotype; polymorphism;
KW drug candidate; protein malfunction; inhibitor; hypersensitivity; ss;
KW hypersensitivity; sequencing primer.
XX Homo sapiens.
OS
XX WO200120025-A2.
XX 22-MAR-2001.
XX 01-SEP-2000; 2000WO-EP08570.
XX 10-SEP-1999; 99EP-0118120.
XX (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
XX

PI Wojnowski L, Eisele R;
XX WPI; 2001-244818/25.
XX Novel variant of CYP3A4 and CYP3A7 genes, associated with insufficient
PT metabolism and/or sensitivity to drugs, useful for diagnosing and
PT treating diseases with drugs that are modulators of their gene product
PT -
XX Claim 37; Page 39; 106pp; English.
XX The sequence represents a primer used to determine the exon/intron
CC boundaries of the cytochrome P-450 (CYP)3A4 gene. Polymorphic
CC polynucleotides of the CYP3A4 or CYP3A7 genes are associated with
CC abnormal drug response or individual predisposition to several common
CC cancers caused by environmental carcinogens. The primer sequences can be
CC used in the production of variant CYP3A4 and CYP3A7 proteins in order to
CC study the malfunction of the proteins, and in diagnostic tests designed
CC for the specific detection and genotyping of CYP3A4 and CYP3A7 alleles in
CC humans. The invention provides methods for identifying and obtaining drug
CC candidates and inhibitors of the genes for therapy of disorders related
CC to acquired drug hypo- or hypersensitivity.
XX
SQ Sequence 18 BP; 6 A; 2 C; 8 G; 2 T; 0 other;
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 994 GAAGTCTGAGGCTGGA 1009
DB 1 GAAATCTGAGGCGGGA 16
RESULT 1491
AAF77404
ID AAF77404 standard; DNA; 18 BP.
XX AAF77404;
XX 12-JUN-2001 (first entry)
XX Human phospholipase A2 (PLA2) cDNA specific PCR primer SEQ ID 33.
XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;
KW antiinflammatory; tranquilizer; antiasthmatic; antiallergic; trauma;
KW antirheumatic; antiarthritic; septic shock; pancreatitis; PCR primer;
KW adult respiratory distress syndrome; ARDS; bronchial asthma; human;
KW allergic rhinitis; rheumatoid arthritis; ss.
XX Homo sapiens.
OS
XX WO200121775-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-JP06344.
XX 21-SEP-1999; 99JP-0266616.
XX (SHIO) SHIONOGI & CO LTD.
XX Ishizaki J, Suzuki N, Hanasaki K;
XX WPI; 2001-290432/30.
XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis
PT of and screening drug candidates for treating associated diseases e.g.
PT septic shock, adult respiratory distress syndrome and rheumatoid
PT arthritis -
XX Example 5; Page 47; 50pp; Japanese.
XX

CC This invention relates to human secretory phospholipase A2 (PLA2) protein
 CC and the gene encoding it. Inhibitors of phospholipase A2 have
 CC antibacterial; immunosuppressive; anti-inflammatory; tranquiliser;
 CC vulnary; antischmatic; antiallergic; antineumatic; and antiarthritic
 CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
 CC allergic rhinitis and rheumatoid arthritis. The present sequence
 CC represents a PCR primer specific for human cDNA encoding PLA2.
 CC
 CC Sequence 18 BP; 2 A; 3 C; 11 G; 2 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 954 CAGCTGGCGGAGGGTGG 969
 ||||| ||||| |||||
 Db 2 CAGCGAGGCGGGGTGG 17

RESULT 1492
 ABX89568/c
 ID ABX89568 standard; DNA; 18 BP.

AC ABX89568;

DT 08-MAY-2003 (first entry)

DE Human sequence tagged specific PCR primer sWes1392 #2.

XX ss; human; obese polypeptide; body weight; PCR; ob polypeptide; leptin;
 XX adipocyte; appetite reduction; cosmetic; primer; fat deposit reduction;
 XX improved body appearance; heart disease; obesity; agriculture;
 KW nutritional disorder; cancer associated weight loss; type II diabetes;
 KW obesity associated disease; AIDS associated weight loss; hypertension;
 KW gene therapy.

XX Homo sapiens.

XX US2002107211-A1.

PD 08-AUG-2002.

PF 13-DEC-2000; 2000US-0736084.

PR 07-JUN-1995; 95US-0485943.

XX (UYRQ) UNIV ROCKEFELLER.

XX Friedman JM, Halaas JL, Gajiwala K, Burley SK, Zhang Y, Proenca R;
 PI Maffei M;

XX WPI; 2002-722695/78.

XX New obese polypeptide useful for inducing reduction of body weight in
 PT an animal, for preparing a composition for treating obesity, disease
 PT associated with obesity such as hypertension, heart disease or type II
 PT diabetes -

XX Example 10; Page 44; 144pp; English.

XX The invention relates to an obese (ob) polypeptide, also known as leptin,
 CC expressed predominantly by adipocytes and capable of inducing reduction
 CC of body weight in an animal. The polypeptide is useful for monitoring
 CC therapeutic treatment of a disease associated with elevated or decreased
 CC levels of ob polypeptide in a mammalian subject; for use in
 CC radioimmunoassays for measuring fat and/or plasma levels of ob protein or
 CC as detecting the presence and level of receptor for ob on tissues, such
 CC as hypothalamus; for screening expression libraries to isolate active
 CC receptors; for use in cosmetics by improving body appearance by reducing
 CC fat deposits or appetite or both and is used independently or in
 CC conjugation with other cosmetic strategies e.g. surgery for its cosmetic

CC effect; for identifying agonists or antagonists that affect its activity
 CC and has potential agricultural uses e.g. increasing the body weight of
 CC animals. Nucleic acid encoding the polypeptide is useful for identifying
 CC mutation in ob nucleotide, in gene therapy for obesity and in the
 CC measurement of its encoded RNA and protein in nutritional disorders. A
 CC host cell transfected with a vector expressing the polypeptide is useful
 CC in the preparation of modulators of the polypeptide and its nucleic acid.
 CC An immunogenic fragment of the polypeptide is useful for preparing an
 CC antibody. The antibody is useful for measuring the presence of the
 CC polypeptide in a sample; for evaluating the level of ob polypeptide in a
 CC biological sample to detect or diagnose the presence of a disease
 CC associated with elevated or decreased levels of ob polypeptide in a
 CC mammalian subject; for imaging ob polypeptide in situ. A composition
 CC comprising the polypeptide is useful for reducing body weight of an
 CC animal, in particular humans. A composition comprising an antagonist of
 CC the polypeptide is useful for increasing body weight of an animal.
 CC Compositions containing the polypeptide and the antagonist are useful for
 CC treating obesity, weight loss associated with cancer or AIDS, disease
 CC associated with obesity such as hypertension, heart disease or type II
 CC diabetes. The present sequence represents a human sequence tagged
 CC specific PCR primer.
 XX

SQ Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 313 GGAAAGACTGCAGAGA 328

Db 18 GAAAGAGATGCAGAGA 3

RESULT 1493
 ABL61442/c
 ID ABL61442 standard; DNA; 18 BP.

XX ABL61442;

XX 16-OCT-2002 (first entry)

XX Human Ob gene STS sWSS1392 AFM206xc1 PCR primer #2.

XX Ob; human; obese; adiposity; body weight; anorectic; anabolic;
 KW PCR; primer; chromosome 7; STS; sequence tagged site; 7q31.3;
 KW microsatellite marker; ss.

XX Homo sapiens.

XX US6350730-B1.

XX 26-FEB-2002.

XX 07-JUN-1995; 95US-0488223.

XX 17-AUG-1994; 94US-0292345.

XX 30-NOV-1994; 94US-0347563.

XX 10-MAY-1995; 95US-0438431.

XX (UYRQ) UNIV ROCKEFELLER.

XX Friedman JM, Zhang Y, Proenca R;

XX WPI; 2002-412914/44.

XX Modifying the body weight of an animal comprises administering an obese
 PT gene (OB) polypeptide analog -

XX Example 10; Column 79-80; 152pp; English.

XX This invention describes a novel method of modifying the body weight of
 CC an animal comprising administering an obese gene (OB) polypeptide
 CC analogue, capable of modulating body weight and adiposity. The invention

CC has anorectic and anabolic activity. ABL61415-ABL61468 represent PCR
 CC primers used in the detection of sequence tagged sites (STS's) and
 CC microsatellite markers used in the mapping of the human Ob gene onto
 CC chromosome 7. These genetic markers represent an important tool for
 CC studying the possible role of the Ob gene in inherited forms of human
 CC obesity.

XX SQ Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 313 GGAAAGACTGCAGAGA 328
 | ||||| |||||
 Db 18 GAAAGAAGTGCAGAGA 3

RESULT 1494

ABK98126/c
 ID ABK98126 standard; DNA; 18 BP.

XX AC ABK98126;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #15.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 gene expression; regulatory sequence; pathogenic double-stranded DNA;
 pathogenic bacteria; virus; replication; virulence; cancer;
 oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-0168920.

XX PR 17-SEP-1992; 92US-0946976.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX PS WPI; 2002-536030/57.

XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
 oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targetting sequences on alternate strands of DHNA to
 PT control gene expression -

XX PS Example 7; Column 41; 108pp; English.

XX CC The present invention relates to methods and oligonucleotides for
 forming a triple-helix comprising a double helical nucleic acid
 CC comprising first and second substantially complementary strands, and
 CC an oligonucleotide bound to a purine-rich target sequence within the
 CC double helical nucleic acid, where the oligonucleotide binds in a
 CC parallel and antiparallel orientation, respectively, to target
 CC sequences on alternate strands of the double helical nucleic acid.
 CC The method has therapeutic applications, where gene expression is
 CC controlled by selective triple-helix formation within expression
 CC regulatory sequences of a target gene. The oligonucleotides can be
 CC used to form triple-helices, and are useful to detect the presence or
 CC absence of specific sequences within genomic DNA for diagnostic and
 CC therapeutic purposes. The oligonucleotides can be selected to
 CC specifically bind to pathogenic double-stranded DNA including specific
 CC sequences required by pathogenic bacteria or viruses for replication or
 CC virulence, reducing their pathogenicity. Alternatively, the
 CC oligonucleotide can be chosen to target a unique sequence of the

CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or
 CC viral origin. Such therapeutic oligonucleotides are capable of forming
 CC triple-helices with such sequences in cancerous cells containing the
 CC activated oncogene, so preferentially killing or repressing the cancer
 CC causing cell. the present sequence represents an oligonucleotide
 CC used in the methods of the present invention.

XX SQ Sequence 18 BP; 0 A; 2 C; 0 G; 14 T; 2 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 81.2%; Pred. No. 9.7e+02;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
 |||||:|||||
 Db 16 AAAAAHAGAAAHAAA 1

RESULT 1495

ABL59012/c

ID ABL59012 standard; DNA; 18 BP.

XX AC ABL59012;

XX DT 20-AUG-2002 (first entry)

XX DE Nucleotide sequence of PCR primer P4.

XX KW Antibacterial protein; microbe resistance; plant; PCR; primer; ss.

XX OS Synthetic.

XX PN JP2002095477-A.

XX PD 02-APR-2002.

XX PF 20-SEP-2000; 2000JP-0285905.

XX PR 20-SEP-2000; 2000JP-0285905.

XX PA (MTU) MITSUBISHI CHEM CORP.

XX PA (BADA-) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.

XX PA (FANR-) FT FAKRIE BROS.

XX PA (BIOI-) BIOINDUSTRY KYOKAI SH.

XX PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.

XX DR WPI; 2002-439987/47.

XX PT New protein and its gene, useful for creating plants with high
 PT resistance to pathogenic microbes -

XX PS Example; Page 7; 13pp; Japanese.

XX CC The specification describes a polypeptide which has antibacterial
 CC activity. The antibacterial protein and its polynucleotide can be used
 CC for the creation of a plant with resistance against pathogenic
 CC microbes. PCR primers ABL59011-12 were used in the course of the
 CC invention.

XX SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 73 TGTAAATGCAACTCTGG 88

||| ||||| |||||

Db 17 TGAATGCAACAGTGG 2

RESULT 1496

ABK30214/c
ID ABK30214 standard; DNA; 18 BP.
AC ABK30214;
XX
XX
XX 23-APR-2002 (first entry)
XX
XX CYP2D6 gene polymorphism detection primer #53.
XX
XX Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
XX ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200196604-A2.
XX
XX 20-DEC-2001.
XX
XX 11-JUN-2001; 2001WO-US18912.
XX
XX 12-JUN-2000; 2000US-210988P.
XX
XX (GENI-) GENICON SCI CORP.
XX
XX Bee G, Kohne DE, Korb L, Peterson T, Yguerabide J;
XX WPI; 2002-130745/17.
XX
XX Determining the presence of a CYP2D6 target sequence in a DNA sample
XX containing CYP2D6 nucleic acid, for detecting mutations or
XX polymorphisms, comprises detecting the scattered light from a particle
XX bound to the target sequence -
XX
XX Example 2; Figure 6; 66pp; English.
XX
XX The invention relates to a method of determining the presence or absence
XX of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
XX acid. Determining the presence or absence of a CYP2D6 target sequence in
XX a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
XX nucleic acid with a probe under stringent binding conditions, and
XX detecting the presence or absence of the target sequence bound with the
XX probe with a scattered light detectable particle, by observing light
XX scattered from the particle which indicates the presence of the target
XX sequence. The method is useful for determining the presence or
XX absence of particular single nucleotide polymorphisms or alleles in
XX genomic nucleic acid, especially in a pharmacogenetically relevant gene
XX or genes in a DNA sample, and to detect and measure one or more target
XX sequences in a sample. The method may also be used to detect specific
XX mutations to identify the phenotypic classification of an individual.
XX ABK30162-ABK30230 represent CYP2D6 target sequence-specific primers
XX of the invention.
XX
XX Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 399 CACACCTGCTCCAGC 414
DB 16 CACCCACTGCTCCAGC 1
RESULT 1497
ABL43118/c
ID ABL43118 standard; DNA; 18 BP.
XX
XX ABL43118;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:162.

XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
KW genome; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-0068285.
XX
XX 10-MAR-2000; 2000JP-0066716.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones -
XX
XX Claim 4; Page 8; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45123 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention.
XX
XX Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 818 TACTGTGGTGTCTGAA 833
DB 16 TACTGTGGTGTCTCAA 1
RESULT 1498
ABL44184
ID ABL44184 standard; DNA; 18 BP.
XX
XX ABL44184;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1228.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX genome; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX

us09904568-1.rng

Thu Jan 8 16:51:41 2004

PR 10-MAY-1995; 95US-0438431.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Friedman JM, Zhang Y, Proenca R;
 XX WPI; 2003-298093/29.
 XX
 XX New human or mouse OB polypeptide, also referred to as leptin
 XX polypeptide, which is capable of modulating body weight, useful for
 XX treating obesity -
 XX
 XX Example 10; Column 79-80; 153pp; English.
 XX
 XX The invention describes an OB (obese) polypeptide (also referred as
 XX leptin) (1), capable of modulating body weight, comprising amino acids
 XX 22 - 167 of a human or mouse OB polypeptide sequence of 167 amino acids
 XX (S1), given in the specification, or amino acids 22 - 166 a human or
 XX mouse OB polypeptide sequence of 166 amino acids (S2), given in the
 XX specification. The OB polypeptide is useful for reducing body weight in
 XX conditions of obesity, and as a target for neutralising antibodies
 XX which results in weight gain (protein therapy), for treating weight loss
 XX associated with cancer, acquired immunodeficiency syndrome (AIDS) or
 XX anorexia nervosa. This sequence represents a primer associated with the
 XX isolation of the human obese (ob) or leptin gene.
 XX
 XX Sequence 18 BP; 1 A; 5 C; 2 G; 10 T; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. NO. 9.7e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2;
 QY 313 GGAAAGACTGCAGAGA 328
 Db 18 GAAAGAAATGCAGAGA 3
 RESULT 1500
 ABX10913/c
 ID ABX10913 standard; DNA; 18 BP.
 XX
 XX AC ABX10913;
 XX
 XX DT 28-APR-2003 (first entry)
 XX
 XX DE Novel human membrane associated protein Zsig24, antisense primer.
 XX
 XX KW Human; membrane associated protein; Zsig24; metabolic disease; obesity;
 KW diabetes; type II diabetes; Pima Indian; polymorphism identification;
 KW chromosome 11q23-q24; PCR; primer; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US2002164701-A1.
 XX
 XX PD 07-NOV-2002.
 XX
 XX PF 25-OCT-2001; 2001US-0001631.
 XX
 XX PR 23-OCT-1998; 98US-105450P.
 PR 23-JUN-1999; 99US-141519P.
 PR 20-OCT-1999; 99US-0422052.
 XX
 XX (SHEP/) SHEPPARD P O.
 PA (JELI/) JELINEK L J.
 PA (WHIT/) WHITMORE T E.
 XX
 XX Sheppard PO, Jelinek LJ, Whitmore TE;
 XX WPI; 2003-247256/24.
 DR
 XX New isolated Zsig24 polypeptide and polynucleotides encoding the
 PT polypeptide, useful for diagnosing chromosome 11 abnormalities, or for

PD 20-NOV-2001.
 XX
 XX PF 12-MAR-2001; 2001JP-0068285.
 XX
 XX PR 10-MAR-2000; 2000JP-0066716.
 XX
 XX (RIKA) RIKAGAKU KENKYUSHO.
 XX (GENO-) GENOTEX YG.
 XX
 XX WPI; 2002-144136/19.
 XX
 XX Arraying genome clones -
 XX
 XX Claim 4; Page 29; 528pp; Japanese.
 XX
 XX The present invention describes a method of arraying genome clones. The
 XX method comprises: (a) clones of the genomic libraries contained in
 XX multiwell plates numbered for discrimination are mixed in each of the
 XX multiwell plates; (b) a primer designed based on the chromosome marker
 XX sequence is added to the mixture to carry out an amplification reaction;
 XX (c) a signal corresponding to the marker is detected from the resultant
 XX amplified product to specify the discrimination Nos. of the multiwell
 XX plates containing the clones having said marker sequence; (d) the order
 XX of the markers is changed so that the same discrimination Nos. succeed to
 XX the maximum in the specified discrimination Nos. to array the multiwell
 XX plates; (e) the clones in the multiwell plates of the specified
 XX discrimination Nos. are mixed respectively in each wells of longitudinal
 XX and lateral directions; (f) the mixed clones are cultured and the
 XX resultant cultures are amplified by using the above primer; (g) signals
 XX are detected from the amplified products; (h) the clones in the multiwell
 XX plates are specified from the detected result; and (i) the clones are
 XX reconstituted as the positions on the chromosome and arrayed. The
 XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 XX represent PCR primers for human chromosome 21q22.1, which are
 XX specifically claimed for use in the present invention.
 XX
 XX Sequence 18 BP; 0 A; 6 C; 4 G; 8 T; 0 other;
 SQ
 Query Match 1.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. NO. 9.7e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2;
 QY 1025 GCTGGGCTGCTTC 1040
 Db 3 GCTGTGCTGGCTTC 18
 RESULT 1499
 ABX96428/c
 ID ABX96428 standard; DNA; 18 BP.
 XX
 XX AC ABX96428;
 XX
 XX DT 13-MAY-2003 (first entry)
 XX
 XX DE Human obese (ob) gene associated PCR primer #28.
 XX
 XX KW OB polypeptide; obese polypeptide; leptin; body weight; obesity;
 KW weight gain; protein therapy; weight loss; cancer; AIDS; human;
 KW acquired immunodeficiency syndrome; anorexia nervosa; PCR; primer;
 KW ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US6471956-B1.
 XX
 XX PD 29-OCT-2002.
 XX
 XX PF 07-JUN-1995; 95US-0488225.
 PR 17-AUG-1994; 94US-0292345.
 PR 30-NOV-1994; 94US-0347563.
 PR

PT diagnosing obesity or type II diabetes in an individual e.g., Pima
XX Indian
PS Example 2; Page 29; 34pp; English.
XX
CC The invention describes an isolated polypeptide (I) comprising an amino
CC acid sequence which shares at least 70% or greater than 95% percent
CC identity with a fully defined human Zsig24 polypeptide sequence (S1).
CC the polynucleotide encoding Zsig24 is useful as a diagnostic reagent for
CC detecting a chromosome 11 abnormality in a subject, involving amplifying
CC nucleic acid molecules that encode Zsig24 from RNA isolated from a
CC biological sample of the subject, and detecting a mutation in the
CC amplified nucleic acid molecules, where the presence of a mutation
CC indicates a chromosome 11 abnormality. The polynucleotide is also useful
CC for diagnosing a metabolic disease (e.g., obesity or diabetes, preferably
CC type II diabetes) or susceptibility to a metabolic disease in an
CC individual (e.g., Pima Indian), where the disease is related to the
CC expression or activity of Zsig24 polypeptide comprising sequence of (S1)
CC in that individual. The method optionally involves amplifying nucleic
CC acid molecules that encode Zsig24 from RNA isolated from a biological
CC sample of the individual, and detecting a mutation in the amplified
CC nucleic acid molecules, where the presence of a mutation indicates
CC a metabolic disease or susceptibility to a metabolic disease or amplifying
CC nucleic acid molecules that encode Zsig24 from RNA isolated from a
CC biological sample of the subject, and transcribing the amplified nucleic
CC acid molecules to produce Zsig24 mRNA, translating Zsig24 mRNA to produce
CC (I), and detecting a mutation (I). The methods are for identifying
CC polymorphisms in a new human gene that resides on chromosome 11q23-q24, a
CC locus linked with a heritable form of diabetes. This sequence represents
CC a primer used to locate the novel human membrane associated protein
CC Zsig24 gene to chromosome 11.

SQ Sequence 18 BP; 2 A; 8 C; 3 G; 5 T; 0 other;

Query Match 1.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 36 TCACAGTGCAGAGGGC 51
DB 17 TCACAGTGCAGAGGGC 2

RESULT 1501

ABX15434/c

ID ABX15434 standard; DNA; 18 BP.

AC ABX15434;

XX

DT 08-APR-2003 (first entry)

XX

DE Human Syk cDNA specific PCR primer Syk H.

XX

Human; ss; Syk; kinase; immunosuppressive; dermatological;

KW antiinflammatory; antiarthritic; antiheumatic; antiasthmatic;

KW phagocytosis; immune complex; kinase inhibitor; autoimmune disease;

KW immune mediated disease; aschma; systemic lupus erythematosus;

KW rheumatoid arthritis; PCR; primer; Syk H.

XX

OS Homo sapiens.

XX

PN US2002068703-A1.

XX

PD 06-JUN-2002.

XX

PF 20-MAR-2001; 2001US-0811492.

XX

PR 14-SEP-1998; 98US-0158980.

PR 30-SEP-1993; 93US-0129381.

PR 30-SEP-1994; 94US-0316425.

PR 07-JUN-1995; 95US-0483530.

PR 07-JUN-1996; 96US-0657884.

XX

PA (UYPE-) UNIV PENNSYLVANIA.

XX

PI Schreiber AD, Park J;

XX WPI; 2003-165571/16.

DR

XX

XX

PT Preventing phagocytosis of immune complexes used for treating e.g.

PT autoimmune diseases comprises introducing inhibitor of kinase

PT endogenous to phagocytic cells associated with Fc receptor at membrane

XX of cells -

XX

PS Example 5; Page 11; 26pp; English.

XX

XX

CC This invention relates to a novel method for preventing phagocytosis of

CC immune complexes comprising introducing an inhibitor of a kinase

CC endogenous to phagocytic cells associated with an Fc receptor at the

CC membrane of the cells under conditions so that the phagocytic potential

CC of the cells is inhibited. The method of the invention may have

CC immunosuppressive, dermatological, antiinflammatory, antiarthritic,

CC antiheumatic and antiasthmatic activities and may be used as a kinase

CC inhibitor. The method and compositions of the invention may be used for

CC modulating the clearance of antibody coated cells, viruses and soluble

CC antigens by inhibiting phagocytosis and modulating the interaction of

CC immune complexes with cellular to tissue Fc receptors. The method is

CC used for treating autoimmune diseases, immune mediated diseases e.g.

CC asthma and immune complex diseases e.g. lupus erythematosus and

CC rheumatoid arthritis, and for preventing immune complexes deposition in

CC tissues e.g. the kidneys and in the joints. The present sequence

CC represents a human Syk kinase PCR primer used to amplify the Syk

CC mRNA for use as a template in the method of the invention.

XX

SQ Sequence 18 BP; 0 A; 7 C; 7 G; 4 T; 0 other;

QY 386 GCTGGGGGCACAC 401

DB 17 GCCGGAGGCACAC 2

RESULT 1502

AAL54275/c

ID AAL54275 standard; DNA; 18 BP.

XX

AC AAL54275;

XX

DT 27-MAR-2003 (first entry)

XX

DE Mouse BSP PCR primer #2.

XX

XX

KW Antinflammatory; rat periodontium; cell strain; bioactivity;

KW tooth disease; periodontitis; periodontosis; mouse; murine; PCR; primer;

XX ss.

XX

OS Mus sp.

XX

PN JP2002262862-A.

XX

PD 17-SEP-2002.

XX

PF 12-MAR-2001; 2001JP-0069249.

XX

PR 12-MAR-2001; 2001JP-0069249.

XX

PA (TOHO-) TOHOKU TECHNARCH KK.

XX

XX

DR WPI; 2003-132121/13.

XX

PT A new cell strain derived from rat periodontium useful for treating or

PT preventing tooth diseases such as periodontitis

XX

PS Example 1; Page 9; 28pp; Japanese.

CC The invention relates to a cell strain which is derived from rat
CC periodontium and can be maintained in passage. The methods of the
CC invention are useful for acquiring a cell strain, establishing a cell
CC strain, and measuring the bioactivity against the cell of a rat-derived
CC periodontium. The cell strain can be used for treating and preventing
CC tooth diseases such as periodontitis and periodontosis. This
CC polynucleotide sequence represents a PCR primer used in the
CC exemplification of the invention.

XX SQ Sequence 18 BP; 3 A; 3 C; 8 G; 4 T; 0 other;

Query Match 1.2%; Score 12.9; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 9.7e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 217 CCTCTCCAGAGTGAC 232

DB 18 CCTCTCCAGAGTGAC 3

RESULT 1503

AAC91374

ID AAC91374 standard; DNA; 21 BP.

XX AC AAC91374;

DT 16-MAR-2001 (first entry)

XX Oligo JT-296 for construction of annexin expression vector pJ117.

DE Human; annexin; chelation site; nuclear imaging; apoptosis;

KW transplant rejection; pJ117; ss.

XX OS Homo sapiens.

XX PN WO200073332-A1.

XX PD 07-DEC-2000.

XX PF 25-MAY-2000; 2000WO-US14324.

XX PR 01-JUN-1999; 99US-0324096.

XX PA (UNIV) UNIV WASHINGTON.

XX PI Tait JF, Brown DS;

XX WPI; 2001-080465/09.

XX Novel modified annexin useful for imaging vascular thrombi and
PT apoptosis, has N-terminal chelation site comprising amino acid
PT extension which comprises a glycine and a cysteine residue -

PS Example 1; Page 12; 39pp; English.

XX The present sequence was used in the construction of an expression
CC vector encoding a modified annexin having an N-terminal
CC chelation site, which comprises an amino acid extension including a
CC glycine and a cysteine residue. The modified annexin is useful for
CC imaging vascular thrombi or apoptosis which is associated with response
CC to a chemotherapeutic agent or with rejection as a result of
CC transplantation. The modified annexin can effectively chelate a
CC radionuclide and retain annexin bioactivity. It can be readily prepared
CC in high radiochemical yield and with high radiochemical purity. In
CC contrast to conventional conjugation chemistries that provide a
CC distribution of conjugation products, the modified annexin has a single
CC chelation site remote from the site of biological activity.

XX SQ Sequence 21 BP; 5 A; 9 C; 4 G; 3 T; 0 other;

Query Match

1.2%; Score 12.8; DB 1; Length 21;

Best Local Similarity 87.5%; Pred. No. 1.1e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCCACAGCCAGCTACC 22

DB 5 GCCACAGCCAGCTGCC 20

RESULT 1504

ABCI3098/c

ID ABCI3098 standard; DNA; 13 BP.

XX AC ABCI3098;

XX DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 13105 for detecting SNP TSC0003045.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-1019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

PS Claim 1; SEQ ID 13105; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI99989 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 13 BP; 0 A; 0 C; 0 G; 12 T; 1 other;

Query Match

1.1%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 7.9e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAA 1096

DB 13 RAAAAAAAAAAAA 1

RESULT 1505

ABCI3099

ID ABCI3099 standard; DNA; 13 BP.

XX AC ABCI3099;

designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1; SEQ ID 97320; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 8 A; 3 C; 0 G; 1 T; 1 other;

Query Match 1.1%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.9e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 934 GGTTTTCGTTTAT 946
|||||
Db 13 GGTTTTCGTTTAY 1

RESULT 1508
ABF14878/c

ID ABF14878 standard; DNA; 13 BP.

AC ABF14878;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 114875 for detecting SNP TSC0028771.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX

WO200177384-A2.

XX

18-OCT-2001.

XX

06-APR-2001; 2001WO-IB00713.

XX

07-APR-2000; 2000DE-1019173.

XX

(EPIG-) EPIGENOMICS AG.

PA

Olek A, Piepenbrock C, Berlin K;

PI

WPI; 2001-657177/75.

DR

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

PT

XX

Claim 1; SEQ ID 114875; 29pp + Sequence Listing; German.

PS

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

CC

AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC

ABT00010-ABT99989 represent the oligomers described in the invention.

CC

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

CC

ftp.wipo.int/pub/published_pct_sequences.

XX

Sequence 13 BP; 8 A; 3 C; 0 G; 1 T; 1 other;

SQ

Db 1 RTTAAAAA 13

RESULT 1510
ABF49492/c
ID ABF49492 standard; DNA; 13 BP.
AC ABF49492;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 149489 for detecting SNP TSC0037734.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX Oligonucleotide SEQ ID NO 149489 for detecting SNP TSC0037734.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 149489; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 3 A; 0 C; 1 G; 8 T; 1 other;
XX
XX Query Match 1.1%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.9e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1077 RACTATTAAAAA 1089
Db 13 RACTATTAAAAA 1
XX
XX RESULT 1511
ABF49493
ID ABF49493 standard; DNA; 13 BP.
XX
XX AC ABF49493;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 149490 for detecting SNP TSC0037734.
XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX Claim 1; SEQ ID 149490; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 8 A; 1 C; 0 G; 3 T; 1 other;
XX
XX Query Match 1.1%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.9e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1077 RACTATTAAAAA 1089
Db 1 RACTATTAAAAA 13
XX
XX RESULT 1512
ABF77924
ID ABF77924 standard; DNA; 13 BP.
XX
XX AC ABF77924;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 177921 for detecting SNP TSC0044096.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.

XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 177921; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 2 A; 0 C; 5 G; 5 T; 1 other;
 Query Match 1.1%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 7.9e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 499 TTGAGATTGGC 511
 Db 1 TTGAGATTGGY 13
 RESULT 1513
 ABF77925/c
 ID ABF77925 standard; DNA; 13 BP.
 XX AC ABF77925;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 177922 for detecting SNP TSC0044096.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 177922; 29pp + Sequence Listing; German.
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 5 A; 5 C; 0 G; 2 T; 1 other;
 Query Match 1.1%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 7.9e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 499 TTGAGATTGGC 511
 Db 13 TTGAGATTGGY 1
 RESULT 1514
 ABF99038
 ID ABF99038 standard; DNA; 13 BP.
 XX AC ABF99038;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 199035 for detecting SNP TSC0044987.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 199035; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

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SQ Sequence 13 BP; 3 A; 0 C; 3 G; 6 T; 1 other;
  Query Match 1.1%; Score 12.6; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 7.9e+02;
  Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 68 GTATTGTAATGC 80
Db 1 GTATTGTAATGY 13

RESULT 1515
ABF99039/c
ID ABF99039 standard; DNA; 13 BP.
XX
AC ABF99039;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 199036 for detecting SNP TSC0048987.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIC-) EPGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 199036; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 6 A; 3 C; 0 G; 3 T; 1 other;
  Query Match 1.1%; Score 12.6; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 7.9e+02;
  Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 68 GTATTGTAATGC 80
Db 13 GTATTGTAATGY 1

RESULT 1516
AAV10121/c
ID AAV10121 standard; cDNA; 14 BP.
XX
AC AAV10121;
XX
DT 29-MAY-1998 (first entry)
XX
DE Human retinoid receptor RRI T12MC primer.
XX
KW Retinoid receptor; RRI; steroid receptor; agonist; antagonist; cancer;
KW adrenal deficiency; skin disorder; inflammatory disorder;
KW immune response regulator; autoimmune disease; therapeutic antibody; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN US5728548-A.
XX
PD 17-MAR-1998.
XX
PF 29-JUN-1995; 95US-0496631.
XX
PR 29-JUN-1995; 95US-0496631.
XX
PA (GEMY ) GENETICS INST INC.
XX
PI Bowman M;
XX
DR WPI; 1998-206567/18.
XX
PT Human retinoid receptor protein RRI - useful for, e.g. drug
PT screening, therapy and antibody production
XX
PS Example 1; Column 10; 13pp; English.
XX
CC PCR primer AAV10121 is used in the amplification of a novel human
CC steroid receptor, the retinoid receptor protein or RRI. This protein can
CC be used in screening assays for steroid hormone receptor agonists and
CC antagonists and in pharmaceutical compositions for treating adrenal
CC deficiencies, e.g. Addison's disease, cancer, skin disorders, e.g. acne
CC and psoriasis, inflammatory disorders, e.g. arthritis and HIV infections.
CC The protein can also be used for regulating immune responses, e.g. as
CC antitumour agents, vaccine adjuvants, organ rejection inhibitors or
CC agents for treating autoimmune diseases. The protein can further be used
CC to produce therapeutic antibodies.
XX
SQ Sequence 14 BP; 0 A; 1 C; 0 G; 12 T; 1 other;
  Query Match 1.1%; Score 12.6; DB 1; Length 14;
  Best Local Similarity 92.3%; Pred. No. 8.4e+02;
  Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAJAAAJAAAJAA 1095
Db 13 KAAAJAAAJAAAJAA 1

RESULT 1517
AAZ89371/c
ID AAZ89371 standard; DNA; 14 BP.
XX
AC AAZ89371;
XX
DT 15-JUN-2000 (first entry)
XX
DE RNA detecting primer #1.
XX
KW Amplification; detection; gene expression; primer; ss.
XX
OS Unidentified.
XX
PN DE19840731-A1.
XX
PD 09-MAR-2000.

```

XX PF 07-SEP-1998; 98DE-1040731.
 XX PR 07-SEP-1998; 98DE-1040731.
 XX PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX DR WPI; 2000-257789/23.
 XX PT Analysis of RNA samples, useful for detection of differential gene
 PT expression uses two differentially labeled primers -
 XX PS Disclosure; Page 9; 10pp; German.
 XX CC This invention describes a novel method for analysis of an RNA sample
 CC which comprises amplifying cDNA with first and second differently
 CC labeled primers and analysis of the amplified labeled cDNA. The method
 CC is useful for analyzing differential gene expression, for identifying
 CC and/or characterizing pharmacological activities or for identifying
 CC target genes. The use of different primer combinations allow more cDNAs
 CC to be amplified. The method also provides a more detailed analysis than
 CC prior art methods. This sequence represents a primer used to illustrate
 CC the method of the invention.
 XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 12 T; 2 other;
 Query Match 1.1%; Score 12.6; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 8.4e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1095
 Db 13 KAAAAAATAAAAAA 1
 RESULT 1518
 ABK15060/c
 ID ABK15060 standard; DNA; 14 BP.
 XX AC ABK15060;
 XX DT 08-MAY-2002 (first entry)
 XX DE Reverse transcriptase PCR primer T12MN.
 XX KW Ligand-like protein; LPL1; ss; PCR; primer; pattern of division;
 KW orientation of elongation; organogenesis; differentiation pattern;
 KW plant development; environmental stimuli; T12MN.
 XX OS Synthetic.
 XX PN EP1164193-A1.
 XX PD 19-DEC-2001.
 XX PF 16-JUN-2000; 2000EP-0202118.
 XX PR 16-JUN-2000; 2000EP-0202118.
 XX PA (PLAN-) PLANT RES INT BV.
 XX PI Liu C, Fiers MA, Cordewener JHG, Joosen RVH;
 XX WPI; 2002-116056/16.
 XX PT Modulating plant phenotype, useful for influencing rate and pattern of
 PT division, orientation of elongation or organogenesis in plants,
 PT comprises providing a plant with a plant-signalling ligand-like protein
 PT -
 XX PS Example 5; Page 9; 78pp; English.
 XX CC The invention relates to modulating a plant phenotype comprising

CC providing a plant with a ligand-like protein (LLP) or its functional
 CC fragment at least comprising a box having an amino acid motif
 CC XRXRXGXXXXHX (LLP box) where: X = any amino acid. The method is useful
 CC for influencing architectural or phenotypical characteristics, such as
 CC plant rate and pattern of division, orientation of elongation,
 CC organogenesis or differentiation patterns in response to development or
 CC environmental stimuli. The present sequence is a T12M anchor RT-PCR
 CC (reverse transcriptase PCR) used to create B. napus cDNA library
 CC from which the cDNA encoding B. napus LPL1 protein was isolated.
 XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 12 T; 2 other;
 Query Match 1.1%; Score 12.6; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 8.4e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1095
 Db 13 KAAAAAATAAAAAA 1
 RESULT 1519
 ABA81571
 ID ABA81571 standard; DNA; 15 BP.
 XX AC ABA81571;
 XX DT 24-JAN-2002 (first entry)
 XX DE Human phospholipid transfer protein gene ASO probe SEQ ID NO: 20.
 XX KW Human; phospholipid transfer protein; PLTP; SNP; atherosclerosis;
 KW single nucleotide polymorphism; high-density lipoprotein metabolism;
 KW allele-specific oligonucleotide; probe; ss.
 XX OS Homo sapiens.
 XX PN WO200172761-A2.
 XX PD 04-OCT-2001.
 XX PF 15-MAR-2001; 2001WO-US08283.
 XX PR 24-MAR-2000; 2000US-192127P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Chew A, Choi JV, Koshiy B;
 XX WPI; 2001-662922/76.
 XX PT Genotyping phospholipid transfer protein gene of individual for
 PT haplotyping individual's gene, comprises determining identity of
 PT nucleotide pair at polymorphic sites for two copies of PLTP gene
 PT present in the individual -
 XX PS Claim 15; Page 13; 98pp; English.
 XX CC The present invention relates to a method for haplotyping the human
 CC phospholipid transfer protein (PLTP) gene, involving determining the
 CC identity of the nucleotide present at one or more of the 25 polymorphic
 CC sites within the gene. This can be used to aid drug development for the
 CC treatment of diseases associated with different haplotypes of the PLTP
 CC gene, possibly including atherosclerosis. The present sequence is an
 CC allele-specific probe used for detecting polymorphisms in the PLTP gene.
 XX SQ Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 1 other;
 Query Match 1.1%; Score 12.6; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 8.9e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 756 AAGGAGATGGCAG 768

Db 3 AAGGATGGCAG 15
|||||:|||||

RESULT 1520
AAS94583
ID AAS94583 standard; DNA; 15 BP.
XX
AC AAS94583;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human PLTP gene allele-specific oligonucleotide probe #17.
XX
KW Human; phospholipid transfer protein; PLTP; haplotyping; haplotype pair;
KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
KW binding affinity; atherosclerosis; ss; sequencing primer; PCR primer;
KW probe.
XX
OS Homo sapiens.
XX
PN WO200172966-A2.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-US09776.
XX
PR 24-MAR-2000; 2000US-192127P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshi B;
XX
DR WPI; 2002-010724/01.
XX
PT New isolated polynucleotide which is polymorphic variant of
PT phospholipid transfer protein (PLTP) gene, having any one of
PT polymorphic sites PS1-PS25, for studying function of PLTP, and
PT expressing PLTP protein -
XX
PS Claim 15; Page 70; 99pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human phospholipid transfer protein (PLTP). A method for
CC haplotyping the PLTP gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the PLTP haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC trait and a haplotype or haplotype pair of the PLTP gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype
CC or haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. PLTP and its corresponding DNA are used
CC for studying the expression and function of PLTP, for use in screening
CC for candidate drugs to treat diseases related to PLTP activity. The
CC sequences are also useful for studying the effect of variation on the
CC biological activity of PLTP as well as on the binding affinity of
CC candidate drugs targeting PLTP for treating atherosclerosis. Sequences
CC AAS94566-AAS94691 represent allele-specific oligonucleotide probes,
CC sequencing primers and PCR primers used for detecting PLTP gene
CC polymorphisms.
XX
SQ Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 1 other;

Query Match 1.1%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 8.9e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 756 AAGGATGGCAG 768
|||||:|||||

Db 3 AAGGATGGCAG 15

RESULT 1521
AAH45766/c
ID AAH45766 standard; DNA; 20 BP.
XX
AC AAH45766;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human E2F-2 gene PCR primer SEQ ID NO: 18.
XX
KW Nucleic acid amplification; adapter DNA; human; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200138572-A1.
XX
PD 31-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-JP08073.
XX
PR 19-NOV-1999; 99JP-0330726.
XX
PR 25-JUL-2000; 2000JP-0224663.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
PI Aoyagi K, Sasaki H, Terada M, Mineno J, Asada K, Kato I;
XX
DR WPI; 2001-355947/37.
XX
PT Amplifying nucleic acids with base sequences of mRNAs in sample while
PT sustaining the ratio among them used to monitor mRNA expression,
PT applicable in producing e.g. cRNA library and DNA microarrays -
XX
PS Example 1; Page 53; 67pp; Japanese.
XX
CC The present invention describes a method of amplifying nucleic acids,
CC involving forming a single-stranded DNA to an mRNA in a sample with a
CC primer, synthesising a DNA strand complementary to the single-stranded
CC DNA to form a double-stranded DNA, adding a single or double-stranded
CC adapter DNA to the double-stranded DNA, and amplifying the DNA strand
CC using a second primer with a nucleic acid sequence in the adapter DNA.
CC This can be used to amplify nucleic acids to monitor mRNA expression,
CC which is applicable in producing e.g. cRNA libraries, cDNA libraries, DNA
CC microarrays or membrane arrays in gene engineering and gene expression
CC analysis, and in drug development and health maintenance and
CC management. The present sequence is a PCR primer described in the
CC exemplification of the invention.
XX
SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 other;

Query Match 1.1%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 861 GGTGATGACCCCACTCCA 879
|||||:|||||
Db 19 GGTGATGACCCCACTCCA 1

RESULT 1522
AAQ45287/c
ID AAQ45287 standard; rRNA; 14 BP.
XX
AC AAQ45287;
XX
DT 25-MAR-2003 (updated)
DT 09-OCT-1994 (first entry)
XX
DE Sequence of minimal sequence required for anti-g10 antibody
DE recognition.

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XX KW D10 epitope; g10 antibody; control RNA; loop sequence; ss.
XX OS Synthetic.
XX PN WO9406934-A1.
XX PD 31-MAR-1994.
XX XX 31-AUG-1993; 93WO-US08210.
XX PF 11-SEP-1992; 92US-0944208.
XX PR 30-SEP-1992; 92US-0956693.
XX XX (UYDU-) UNIV DUKE.
XX PA Keene JD, Kenan DJ, Tsai DE;
XX XX WPI; 1994-118482/14.
XX DR Generating nucleic acid epitopes cross-reactive with non-nucleic
XX PT acid immunogens, pref. viruses and allergens - used to generate
XX PT immune responses in humans and animals
XX PS Example; page 34; 56pp; English.
XX XX
XX CC Anti-g10 antibody is specific for proteins contg. a g10 fusion
XX CC peptide (see AAR1052). However, whereas the g10 peptide is a useful
XX CC epitope tag for analysing complexes contg. protein, an RNA epitope
XX CC tag would be equally useful for studying complexes contg. RNA. The
XX CC anti-g10 serum was presented with a degenerate pool of RNA contg.
XX CC 1,048,576 species representing all possible RNA species. The
XX CC transcripts were immunoprecipitated with the anti-g10 serum.
XX CC A single RNA species, D10, was obt'd. The minimal sequence required
XX CC for antibody recognition is AAQ45287, in the context of a stem.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 14 BP; 2 A; 3 C; 7 G; 2 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 404 CCTGCTCCAGCAGG 417
Db 14 CCTGCTCCAGCAGG 1

RESULT 1523
AAT18608/C
ID AAT18608 standard; DNA; 14 BP.
XX AC AAT18608;
XX AC AAT18608;
XX DT 06-NOV-1996 (first entry)
XX DE Degenerate 3' oligo dt DDRT-PCR primer T12VT.
XX KW Differential display of mRNA; reverse transcription; DDRT-PCR;
XX KW human; chondrocyte; gene specific; primer; probe; isolation;
XX KW interleukin-beta; IL-beta; diagnosis; connective tissue disease;
XX KW osteoarthritis; rheumatoid arthritis;
XX KW polymerase chain reaction; ss.
XX OS Synthetic.
XX XX EP705842-A2.
XX XX 10-APR-1996.
XX XX
XX PF 02-OCT-1995; 95EP-0115510.
XX PR 06-OCT-1994; 94EP-0115751.

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```

XX PA (FARH ) HOECHST AG.
XX PI Bartnik E, Margerie D;
XX XX WPI; 1996-181045/19.
XX DR
XX PT Diagnosis and treatment of IL-1 mediated connective tissue diseases
XX PT - using osteopontin, calnexin, TSG-6 gene prod., genes encoding them
XX PT or antibodies to them
XX PS Example; Page 15; 31pp; English.
XX XX
XX CC The present sequence is 1 of 4 degenerate 3' oligo dt primers,
XX CC which were used along with 25 arbitrary 5' oligodecamer primers for
XX CC the differential display of human chondrocyte mRNA by reverse
XX CC transcription and PCR (DDRT-PCR). Sequence analysis revealed the
XX CC sequences of 52 cDNA clones, which were then searched against DNA
XX CC databases for homology to known human genes. The cDNA mols. can be
XX CC used for the prodn. of gene specific primers and probes to isolate
XX CC genes induced by treating (esp. human) chondrocytes with
XX CC interleukin-beta (IL-1beta), and for the diagnosis of IL-1beta
XX CC related connective tissue diseases, in partic. osteoarthritis or
XX CC rheumatoid arthritis.
XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 1 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1097
Db 14 AAAAAAAAAAAAAA 1

RESULT 1524
AAT91861/C
ID AAT91861 standard; DNA; 14 BP.
XX AC AAT91861;
XX AC AAT91861;
XX DT 20-MAR-1998 (first entry)
XX DE 3' primer for DUB-1 (T14) cDNA amplification.
XX KW DUB; ubiquitin-specific; thiol protease; deubiquitinating enzyme; murine;
XX KW cytokine-induced; conserved domain; CYS; HIS; haematopoietic cell;
XX KW cell growth arrest; proliferation; cancer; leukaemia; lymphoma;
XX KW PCR primer; amplify; ss.
XX OS Synthetic.
XX OS Mus sp.
XX XX WO9706247-A2.
XX XX 20-FEB-1997.
XX XX
XX PF 07-AUG-1996; 96WO-US12884.
XX PR 14-JUN-1996; 96US-0019787.
XX PR 09-AUG-1995; 95US-0002066.
XX XX
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX XX Dandrea AD, Zhu Y;
XX XX WPI; 1997-154255/14.
XX XX
XX PT Nucleic acids encoding deubiquitinating enzymes - useful for
XX PT inhibiting or stimulating growth of haematopoietic cells, e.g. for
XX PT treatment of cancers
XX XX

```

PS Disclosure; Page 39; 94pp; English.

XX CC Primers AAT91860-61 were used for PCR amplification of DUB-1 (T14) cDNA.
XX CC DUB enzymes are ubiquitin-specific thiol proteases or Deubiquitinating
XX CC (DUB) enzymes. The DUB enzymes are induced by at least one cytokine and
XX CC include two conserved domains (Cys and His domains). DUB-1 is
XX CC interleukin (IL)-3, IL-5 and/or GM-CSF inducible and is expressed in
XX CC haematopoietic cells and induces growth arrest of the cell in the G0/G1
XX CC phase of the cell cycle. The enzymes of the invention can be used to
XX CC arrest proliferation of preferably haematopoietic cells for treating or
XX CC preventing e.g. cancer especially leukaemias or lymphomas. The enzymes
XX CC can also be used to stimulate preferably haematopoietic cell
XX CC proliferation e.g. to produce blood cells for replacing blood cell
XX CC depletion due to disease or condition e.g. immune suppression from AIDS
XX CC or therapy such as chemotherapy or dialysis. The enzymes may also be
XX CC used to suppress the immune system e.g. during organ or cell
XX CC transplantation. The nucleic acid can be used to transform cells for
XX CC screening agents which inhibit DUB enzyme activity.

XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
Db 14 AAAAAAAAAAAAAA 1

RESULT 1525

AAV09226/c
ID AAV09226 standard; DNA; 14 BP.

XX AC AAV09226;

XX DT 07-JUL-1998 (first entry)

XX DE 3' poly(T) primer 2.

XX KW 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
XX KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.

XX OS Synthetic.

XX PN WO9749832-A2.

XX PD 31-DEC-1997.

XX PF 23-JUN-1997; 97WO-CA00488.

XX PR 01-OCT-1996; 96US-0724466.

XX PR 21-JUN-1996; 96US-0667546.

XX XX (TOOH) UNIV QUEENS KINGSTON.

XX PA Petkovich PM;

XX PI WPI; 1998-077193/07.

XX DR Identifying DNA encoding inducible or suppressible cytochrome P450 -
XX PT by screening for drugs which reduce the catabolism of retinoic acid,
XX PT useful in cancer chemotherapy and the treatment of acne and
XX PT psoriasis

XX PS Example 1; Page 49; 113pp; English.

XX CC This is a 3' poly(T) PCR primer used in the amplification of the
XX CC inducible cytochrome P450RAI gene which specifically metabolises a
XX CC derivative of the retinoic acid (RA). The cytochrome P450 gene in
XX CC general produces enzymes involved in the oxidative metabolism of
XX CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
XX CC sequence can be used to induce or suppress the expression of its

CC protein. P450RAI is highly induced by RA in cell lines and tissues.
CC This allows for the development of a drug screen using promoters and
CC nucleotide sequences to identify drugs which are useful for reducing
CC the catabolism of RA.

XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAA 1095
Db 14 TCAAAAAAAAAAAAAA 1

RESULT 1526

AAV09227/c
ID AAV09227 standard; DNA; 14 BP.

XX AC AAV09227;

XX DT 07-JUL-1998 (first entry)

XX DE 3' poly(T) primer 3.

XX KW 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
XX KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.

XX OS Synthetic.

XX PN WO9749832-A2.

XX PD 31-DEC-1997.

XX PF 23-JUN-1997; 97WO-CA00488.

XX PR 01-OCT-1996; 96US-0724466.

XX PR 21-JUN-1996; 96US-0667546.

XX XX (TOOH) UNIV QUEENS KINGSTON.

XX PA Petkovich PM;

XX PI WPI; 1998-077193/07.

XX DR Identifying DNA encoding inducible or suppressible cytochrome P450 -
XX PT by screening for drugs which reduce the catabolism of retinoic acid,
XX PT useful in cancer chemotherapy and the treatment of acne and
XX PT psoriasis

XX PS Example 1; Page 50; 113pp; English.

XX CC This is a 3' poly(T) PCR primer used in the amplification of the
XX CC inducible cytochrome P450RAI gene which specifically metabolises a
XX CC derivative of the retinoic acid (RA). The cytochrome P450 gene in
XX CC general produces enzymes involved in the oxidative metabolism of
XX CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
XX CC sequence can be used to induce or suppress the expression of its
XX CC protein. P450RAI is highly induced by RA in cell lines and tissues.
XX CC This allows for the development of a drug screen using promoters and
XX CC nucleotide sequences to identify drugs which are useful for reducing
XX CC the catabolism of RA.

XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
Db 14 AAAAAAAAAAAAAA 1

```

RESULT 1527
AAV09234/c
ID AAV09234 standard; DNA; 14 BP.
XX AC AAV09234;
XX DT 07-JUL-1998 (first entry)
XX DE 3' poly(T) primer 10.
XX DE 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
XX OS Synthetic.
XX PN WO9749832-A2.
XX PD 31-DEC-1997.
XX PF 23-JUN-1997; 97WO-CA00488.
XX PR 01-OCT-1996; 96US-0724466.
XX PR 21-JUN-1996; 96US-0667546.
XX PA (TOOH ) UNIV QUEENS KINGSTON.
XX PI Petkovich PM;
XX PI WPI; 1998-077193/07.
XX PT Identifying DNA encoding inducible or suppressible cytochrome P450 -
PT by screening for drugs which reduce the catabolism of retinoic acid,
PT useful in cancer chemotherapy and the treatment of acne and
PT psoriasis
XX PS Example 1; Page 51; 113pp; English.
XX CC This is a 3' poly(T) PCR primer used in the amplification of the
CC inducible cytochrome P450RAI gene which specifically metabolises a
CC derivative of the retinoic acid (RA). The cytochrome P450 gene in
CC general produces enzymes involved in the oxidative metabolism of
CC endogenous and exogenous compounds. The cytochrome P450 nucleotide
CC sequence can be used to induce or suppress the expression of its
CC protein. P450RAI is highly induced by RA in cell lines and tissues.
CC This allows for the development of a drug screen using promoters and
CC nucleotide sequences to identify drugs which are useful for reducing
CC the catabolism of RA.
XX SQ Sequence 14 BP; 0 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
DB 14 TGAATAAAAAAAAAA 1

RESULT 1528
AAV09235/c
ID AAV09235 standard; DNA; 14 BP.
XX AC AAV09235;
XX DT 07-JUL-1998 (first entry)
XX DE 3' poly(T) primer 11.
XX DE 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.

```

PR 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX
 XX Beckett BR, Jones G, Petkovich PM, White JA;
 XX WPI; 1998-077178/07.
 DR
 XX Retinoid metabolising protein - useful to develop products to treat,
 PT e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
 PT ichthyosis
 XX
 XX Disclosure; Page 14; 110pp; English.
 XX
 CC PolyT oligonucleotides (see AAV12217-28) were used in reverse
 CC transcription reactions on polyA+ RNA isolated from the fins of
 CC control or retinoic acid-treated zebrafish (Danio rerio). Several
 CC combinations of the polyT primers were used with degenerate
 CC upstream primers (see AAV12229-33) for differential display PCR.
 CC Bands demonstrating reproducible differential amplifications were
 CC found using the primers given in AAV12221 and AAV12231. This PCR
 CC product was reamplified (see AAV12234-35). A differential display
 CC of retinoic acid for its expression was isolated, and was used to
 CC isolate a full-length clone (see AAV12203) coding for a novel
 CC retinoid metabolising protein (see AAW44159), designated zF45ORAI.
 XX
 SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAA 1095
 Db 14 TGAATAAAAAAAAAA 1
 RESULT 1530
 AAV12227/C
 ID AAV12227 standard; DNA; 14 BP.
 AC AAV12227;
 XX
 DT 22-JUN-1998 (first entry)
 XX
 DE Poly(T) oligonucleotide used in differential display PCR.
 XX
 KW Retinoid metabolising protein; P45ORAI; retinoid oxidase;
 KW retinoic acid; zebrafish; inhibitor; antisense; cancer;
 KW actinic keratosis; oral leukoplakia; head tumour; neck tumour;
 KW non-small cell lung carcinoma; basal cell carcinoma;
 KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
 KW ichthyosis; therapy; diagnosis; screening; differential display;
 KW PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9749815-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 23-JUN-1997; 97WO-CA00440.
 XX
 XX 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX
 XX Beckett BR, Jones G, Petkovich PM, White JA;
 XX WPI; 1998-077178/07.
 XX
 PT Retinoid metabolising protein - useful to develop products to treat,
 PT e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
 PT ichthyosis
 XX
 XX Disclosure; Page 14; 110pp; English.
 XX
 CC PolyT oligonucleotides (see AAV12217-28) were used in reverse
 CC transcription reactions on polyA+ RNA isolated from the fins of
 CC control or retinoic acid-treated zebrafish (Danio rerio). Several
 CC combinations of the polyT primers were used with degenerate
 CC upstream primers (see AAV12229-33) for differential display PCR.
 CC Bands demonstrating reproducible differential amplifications were
 CC found using the primers given in AAV12221 and AAV12231. This PCR
 CC product was reamplified (see AAV12234-35). A differential display
 CC of retinoic acid for its expression was isolated, and was used to
 CC isolate a full-length clone (see AAV12203) coding for a novel
 CC retinoid metabolising protein (see AAW44159), designated zF45ORAI.
 XX
 SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAA 1095
 Db 14 TGAATAAAAAAAAAA 1
 RESULT 1530
 AAV12227/C
 ID AAV12227 standard; DNA; 14 BP.
 AC AAV12227;
 XX
 DT 22-JUN-1998 (first entry)
 XX
 DE Poly(T) oligonucleotide used in differential display PCR.
 XX
 KW Retinoid metabolising protein; P45ORAI; retinoid oxidase;
 KW retinoic acid; zebrafish; inhibitor; antisense; cancer;
 KW actinic keratosis; oral leukoplakia; head tumour; neck tumour;
 KW non-small cell lung carcinoma; basal cell carcinoma;
 KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
 KW ichthyosis; therapy; diagnosis; screening; differential display;
 KW PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9749815-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 23-JUN-1997; 97WO-CA00440.
 XX
 XX 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX
 XX Beckett BR, Jones G, Petkovich PM, White JA;
 XX WPI; 1998-077178/07.
 XX

XX Retinoid metabolising protein - useful to develop products to treat,
 PT e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
 PT ichthyosis
 XX
 XX Disclosure; Page 14; 110pp; English.
 XX
 CC PolyT oligonucleotides (see AAV12217-28) were used in reverse
 CC transcription reactions on polyA+ RNA isolated from the fins of
 CC control or retinoic acid-treated zebrafish (Danio rerio). Several
 CC combinations of the polyT primers were used with degenerate
 CC upstream primers (see AAV12229-33) for differential display PCR.
 CC Bands demonstrating reproducible differential amplifications were
 CC found using the primers given in AAV12221 and AAV12231. This PCR
 CC product was reamplified (see AAV12234-35). A differential display
 CC of retinoic acid for its expression was isolated, and was used to
 CC isolate a full-length clone (see AAV12203) coding for a novel
 CC retinoid metabolising protein (see AAW44159), designated zF45ORAI.
 XX
 SQ Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 14 AGAAAAAAAAAAAAA 1
 RESULT 1531
 AAV12218/C
 ID AAV12218 standard; DNA; 14 BP.
 XX
 AC AAV12218;
 XX
 DT 22-JUN-1998 (first entry)
 XX
 DE Poly(T) oligonucleotide used in differential display PCR.
 XX
 KW Retinoid metabolising protein; P45ORAI; retinoid oxidase;
 KW retinoic acid; zebrafish; inhibitor; antisense; cancer;
 KW actinic keratosis; oral leukoplakia; head tumour; neck tumour;
 KW non-small cell lung carcinoma; basal cell carcinoma;
 KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
 KW ichthyosis; therapy; diagnosis; screening; differential display;
 KW PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9749815-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 23-JUN-1997; 97WO-CA00440.
 XX
 XX 01-OCT-1996; 96US-0724466.
 PR 21-JUN-1996; 96US-0667546.
 XX
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX
 XX Beckett BR, Jones G, Petkovich PM, White JA;
 XX WPI; 1998-077178/07.
 XX
 PT Retinoid metabolising protein - useful to develop products to treat,
 PT e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
 PT ichthyosis
 XX
 XX Disclosure; Page 14; 110pp; English.
 XX
 CC PolyT oligonucleotides (see AAV12217-28) were used in reverse

transcription reactions on polyA+ RNA isolated from the fins of control or retinoic acid-treated zebrafish (Danio rerio). Several combinations of the polyT primers were used with degenerate upstream primers (see AAV12229-33) for differential display PCR. Bands demonstrating reproducible differential amplifications were found using the primers given in AAV12221 and AAV12231. This PCR product was reamplified (see AAV12234-35). A differential display product (see AAV12213) which exhibited a dependence on the presence of retinoic acid for its expression was isolated, and was used to isolate a full-length clone (see AAV12203) coding for a novel retinoid metabolising protein (see AAW44159), designated zp450RAI.

Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
DB 14 TCAAAAAAAAAA 1

RESULT 1532
AAV12219/c
ID AAV12219 standard; DNA; 14 BP.

XX AAV12219;

AC AAV12219;

DT 22-JUN-1998 (first entry)

XX Poly(T) oligonucleotide used in differential display PCR.

XX Retinoid metabolising protein; P450RAI; retinoid oxidase;
KW retinoic acid; zebrafish; inhibitor; antisense; cancer;
KW actinic keratosis; oral leukoplakia; head tumour; neck tumour;
KW non-small cell lung carcinoma; basal cell carcinoma;
KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
KW ichthyosis; therapy; diagnosis; screening; differential display;
KW PCR; primer; ss.

XX Synthetic.

OS WO9749815-A1.

XX 31-DEC-1997.

XX 23-JUN-1997; 97WO-CA00440.

XX 01-OCT-1996; 96US-0724466.

XX 21-JUN-1996; 96US-0667546.

XX (TOOH) UNIV QUEENS KINGSTON.

XX Beckett BR, Jones G, Petkovich PM, White JA;

XX WPI; 1998-077178/07.

XX Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or ichthyosis

XX Disclosure; Page 14; 110pp; English.

XX PolyT oligonucleotides (see AAV12217-28) were used in reverse transcription reactions on polyA+ RNA isolated from the fins of control or retinoic acid-treated zebrafish (Danio rerio). Several combinations of the polyT primers were used with degenerate upstream primers (see AAV12229-33) for differential display PCR. Bands demonstrating reproducible differential amplifications were found using the primers given in AAV12221 and AAV12231. This PCR product was reamplified (see AAV12234-35). A differential display product (see AAV12213) which exhibited a dependence on the presence

CC of retinoic acid for its expression was isolated, and was used to isolate a full-length clone (see AAV12203) coding for a novel retinoid metabolising protein (see AAW44159), designated zp450RAI.

XX Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1097
DB 14 AAAAAAAAAAAAAA 1

RESULT 1533
AAT99552/c
ID AAT99552 standard; DNA; 14 BP.

XX AAT99552;

AC AAT99552;

DT 08-JUN-1998 (first entry)

XX Oligo-dT primer used in epoxide hydrolase MEH gene RT-PCR.

XX Cell growth regulatory gene; MEH; microsomal epoxide hydrolase;
KW rat; tumour; cancer; diagnosis; gene therapy; RT-PCR; primer; ss.
XX Synthetic.

OS WO9745542-A2.

XX 04-DEC-1997.

XX 29-MAY-1997; 97WO-US09584.

XX 29-MAY-1996; 96US-0018557.

XX (PHAR-) PHARMAGENICS INC.

XX Beaudry GA, Bertelsen AH, Galella E, Madden SI;

XX WPI; 1998-032649/03.

XX DNA encoding mammalian growth response protein CGR11 or CGR19 - useful to suppress or diagnose cancer, also similar use of SM20 or MEH protein

XX Example 2; Page 16; 46pp; English.

XX This oligo-dT primer was used with a random 10-mer primer (see AAT99553) in an RT-PCR amplification of rat embryo fibroblast REF-112 cell RNA. This was performed in order to identifying p53 regulated genes. One transcript that was upregulated specifically in cells harboring wild-type p53 protein was characterised. A previously known gene, MEH (microsomal epoxide hydrolase), was identified. 2 Novel cell growth regulatory genes, CGR11 (see AAV04008) and CGR19 (see AAV04010), were also isolated. These genes and the novel CGR11 and CGR19 growth regulatory proteins (see AAW38423 and AAW38425) can be used in methods for the diagnosis and treatment of cancer.

XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
DB 14 TCAAAAAAAAAA 1

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RESULT 1534
AAAX34947/c
ID AAX34947 standard; DNA; 14 BP.
XX
XX AC AAX34947;
XX
DT 28-JUN-1999 (first entry)
XX
DE PCR primer for DNA encoding a dehiscence zone protein designated DZ15.
XX
KW Dehiscence zone protein; DZ15; dehiscence regulation;
XX pre-harvest seed loss; cell separation; PCR primer; ss.
XX
OS Synthetic.
OS Brassica napus.
XX
XX WO9915681-A1.
XX
PN 01-APR-1999.
XX
XX 21-SEP-1998; 98WO-GB02850.
XX
PR 19-SEP-1997; 97GB-0020039.
XX
XX (BIOG-) BIOGEMMA UK LTD.
XX
PI Paul W, Roberts JA, Whitelaw C;
XX
XX WPI; 1999-244428/20.
XX
PT Control of pod dehiscence or shatter
XX
XX Example 1; Page 11; 21pp; English.
XX
CC PCR primers AAX34947-48 were used to amplify DNA encoding a dehiscence
CC zone protein designated DZ15. The dehiscence zone protein DZ15 and
CC polynucleotide can be used to regulate dehiscence in all crops that
CC lose seed pre-harvest because of cell separation events. The invention
CC especially applies to Brassica napus, but is relevant to plants that
CC develop dry fruits, including Brassica, Synapis, and other genera of
CC the Brassicaceae, soybean, and other leguminous species, Cuphea and
CC sesame.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAATAAAAAAAAAA 1095
Db 14 TCAAAAAAAAAA 1
RESULT 1535
AAAX19475/c
ID AAX19475 standard; DNA; 14 BP.
XX
XX AC AAX19475;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:17.
XX
KW Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9907893-A1.
XX
PN 18-FEB-1999.
XX
XX
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XX
PF 05-AUG-1998; 98WO-US16343.
XX
PR 08-AUG-1997; 97US-0908873.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Hosier S, Kubbies M, Swissshelm K;
XX
XX WPI; 1999-167454/14.
XX
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT polypeptide - useful for inducing a senescence phenotype in a cell
XX
XX Example 1; Page 18; 44pp; English.
XX
CC The present invention describes human senescence factor p23. An
CC expression vector for p23 is useful for inducing a senescent phenotype
CC in a cell (preferably eukaryotic). This may help in regulating diseases,
CC including cancer, persistent inflammation, and various proliferative and
CC degenerative disorders. These transgenic cells are useful in gene
CC therapy for treating cancer, particularly where antisense
CC oligonucleotides are useful for blocking normal or mutant p23 expression
CC in cancer cells or other proliferating cells. Transgenic cells are also
CC useful for producing the p23 polypeptide in large quantities. The
CC antibodies are useful for raising antiserum against p23, and for
CC identifying senescent cells in culture and tissue biopsies. The p23
CC polynucleotides are useful for modulating or altering p23 activity in a
CC cell, and for identifying and isolating the whole gene encoding p23,
CC and variants of p23. Assays based on p23 elements, which detect p23
CC levels and activity are useful as diagnostic markers for staging tumours,
CC determining prognosis, and/or predicting therapeutic success. These
CC elements also provide an assay for detecting chromosomal rearrangements
CC in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
CC permits the manipulation of malignant growth in cancer. The present
CC sequence represents a primer used in an example from the present
CC invention.
XX
SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
Db 14 ACAAAAAAAAAAAAAA 1
RESULT 1536
AAAX19476/c
ID AAX19476 standard; DNA; 14 BP.
XX
XX AC AAX19476;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:18.
XX
KW Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9907893-A1.
XX
PN 18-FEB-1999.
XX
XX
PF 05-AUG-1998; 98WO-US16343.
XX
PR 08-AUG-1997; 97US-0908873.
XX
XX
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PA (UNIW ) UNIV WASHINGTON.
XX
XX Hosier S, Kubbies M, Swissshelm K;
XX
XX WPI; 1999-167454/14.
XX
XX Newly isolated nucleic acid molecule (designated p23) encoding a p23
XX polypeptide - useful for inducing a senescence phenotype in a cell
XX
XX Example 1; Page 18; 44pp; English.
XX
XX The present invention describes human senescence factor p23. An
XX expression vector for p23 is useful for inducing a senescent phenotype
XX in a cell (preferably eukaryotic). This may help in regulating diseases,
XX including cancer, persistent inflammation, and various proliferative and
XX degenerative disorders. These transgenic cells are useful in gene
XX therapy for treating cancer, particularly where antisense
XX oligonucleotides are useful for blocking normal or mutant p23 expression
XX in cancer cells or other proliferating cells. Transgenic cells are also
XX useful for producing the p23 polypeptide in large quantities. The
XX antibodies are useful for raising antiserum against p23, and for
XX identifying senescent cells in culture and tissue biopsies. The p23
XX polynucleotides are useful for modulating or altering p23 activity in a
XX cell, and for identifying and isolating the whole gene encoding p23,
XX levels and activity are useful as diagnostic markers for staging tumours,
XX determining prognosis, and/or predicting therapeutic success. These
XX elements also provide an assay for detecting chromosomal rearrangements
XX in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
XX permits the manipulation of malignant growth in cancer. The present
XX sequence represents a primer used in an example from the present
XX invention.
XX
XX Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 other;
SQ
XX
XX Query Match 1.1%; Score 12.4; DB 1; Length 14;
XX Best Local Similarity 92.9%; Pred. No. 9.1e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1097
XX Db | |||||
XX 14 AAAAAAAAAAAAAA 1
XX
XX RESULT 1537
XX AAX19466/c
XX ID AAX19466 standard; DNA; 14 BP.
XX AC AAX19466;
XX
XX DT 21-MAY-1999 (first entry)
XX DE Human senescence factor p23 T12 anchor primer SEQ ID NO:8.
XX
XX KW Human; senescence factor; p23; cancer; persistent inflammation;
XX proliferative disorder; degenerative disorder; primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9907893-A1.
XX
XX PD 18-FEB-1999.
XX
XX PF 05-AUG-1998; 98WO-US16343.
XX
XX PR 08-AUG-1997; 97US-0908873.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI Hosier S, Kubbies M, Swissshelm K;
XX
XX WPI; 1999-167454/14.
XX
XX Newly isolated nucleic acid molecule (designated p23) encoding a p23
XX polypeptide - useful for inducing a senescence phenotype in a cell
XX
XX Example 1; Page 18; 44pp; English.
XX
XX The present invention describes human senescence factor p23. An
XX expression vector for p23 is useful for inducing a senescent phenotype
XX in a cell (preferably eukaryotic). This may help in regulating diseases,
XX including cancer, persistent inflammation, and various proliferative and
XX degenerative disorders. These transgenic cells are useful in gene
XX therapy for treating cancer, particularly where antisense
XX oligonucleotides are useful for blocking normal or mutant p23 expression
XX in cancer cells or other proliferating cells. Transgenic cells are also
XX useful for producing the p23 polypeptide in large quantities. The
XX antibodies are useful for raising antiserum against p23, and for
XX identifying senescent cells in culture and tissue biopsies. The p23
XX polynucleotides are useful for modulating or altering p23 activity in a
XX cell, and for identifying and isolating the whole gene encoding p23,
XX levels and activity are useful as diagnostic markers for staging tumours,
XX determining prognosis, and/or predicting therapeutic success. These
XX elements also provide an assay for detecting chromosomal rearrangements
XX in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
XX permits the manipulation of malignant growth in cancer. The present
XX sequence represents a primer used in an example from the present
XX invention.
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
SQ
XX
XX Query Match 1.1%; Score 12.4; DB 1; Length 14;
XX Best Local Similarity 92.9%; Pred. No. 9.1e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1082 TTTAAAAAAAAAAAAA 1095
XX Db | |||||
XX 14 TCAAAAAAAAAAAAAA 1
XX
XX RESULT 1538
XX AAX19467/c
XX ID AAX19467 standard; DNA; 14 BP.
XX AC AAX19467;
XX
XX DT 21-MAY-1999 (first entry)
XX DE Human senescence factor p23 T12 anchor primer SEQ ID NO:9.
XX
XX KW Human; senescence factor; p23; cancer; persistent inflammation;
XX proliferative disorder; degenerative disorder; primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9907893-A1.
XX
XX PD 18-FEB-1999.
XX
XX PF 05-AUG-1998; 98WO-US16343.
XX
XX PR 08-AUG-1997; 97US-0908873.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI Hosier S, Kubbies M, Swissshelm K;
XX
XX WPI; 1999-167454/14.
XX
XX Newly isolated nucleic acid molecule (designated p23) encoding a p23
XX polypeptide - useful for inducing a senescence phenotype in a cell
XX
XX Example 1; Page 18; 44pp; English.
XX
XX The present invention describes human senescence factor p23. An
XX expression vector for p23 is useful for inducing a senescent phenotype
XX in a cell (preferably eukaryotic). This may help in regulating diseases,
XX including cancer, persistent inflammation, and various proliferative and
XX degenerative disorders. These transgenic cells are useful in gene
XX therapy for treating cancer, particularly where antisense
XX oligonucleotides are useful for blocking normal or mutant p23 expression
XX in cancer cells or other proliferating cells. Transgenic cells are also
XX useful for producing the p23 polypeptide in large quantities. The
XX antibodies are useful for raising antiserum against p23, and for
XX identifying senescent cells in culture and tissue biopsies. The p23
XX polynucleotides are useful for modulating or altering p23 activity in a
XX cell, and for identifying and isolating the whole gene encoding p23,
XX levels and activity are useful as diagnostic markers for staging tumours,
XX determining prognosis, and/or predicting therapeutic success. These
XX elements also provide an assay for detecting chromosomal rearrangements
XX in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
XX permits the manipulation of malignant growth in cancer. The present
XX sequence represents a primer used in an example from the present
XX invention.
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 other;
SQ

```


XX The present invention describes human senescence factor p23. An
 CC expression vector for p23 is useful for inducing a senescent phenotype
 CC in a cell (preferably eukaryotic). This may help in regulating diseases,
 CC including cancer, persistent inflammation, and various proliferative and
 CC degenerative disorders. These transgenic cells are useful in gene
 CC therapy for treating cancer, particularly where antisense
 CC oligonucleotides are useful for blocking normal or mutant p23 expression
 CC in cancer cells or other proliferating cells. Transgenic cells are also
 CC useful for producing the p23 polypeptide in large quantities. The
 CC antibodies are useful for raising antiserum against p23, and for
 CC identifying senescent cells in culture and tissue biopsies. The p23
 CC polynucleotides are useful for modulating or altering p23 activity in a
 CC cell, and for identifying and isolating the whole gene encoding p23,
 CC and variants of p23. Assays based on p23 elements, which detect p23
 CC levels and activity are useful as diagnostic markers for staging tumors,
 CC determining prognosis, and/or predicting therapeutic success. These
 CC elements also provide an assay for detecting chromosomal rearrangements
 CC in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
 CC permits the manipulation of malignant growth in cancer. The present
 CC sequence represents a primer used in an example from the present
 CC invention.

XX SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAAATAAAAA 1095
 DB 14 TGAATAAAAAAATAAAAA 1

RESULT 1539

AAAX02696/c

ID AAX02696 standard; DNA; 14 BP.

XX AC AAX02696;

DT 10-MAY-1999 (first entry)

XX DE Barley HPPD primer #2.

XX HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
 KW transgenic; plant cell; callus tissue; protoplast; electroporation;
 KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
 KW sunflower; tobacco; ss.

XX OS Hordeum vulgare.

XX PN DE19730066-A1.

XX PD 21-JAN-1999.

XX PF 14-JUL-1997; 97DE-1030066.

XX PR 14-JUL-1997; 97DE-1030066.

XX PA (BADI) BASF AG.

XX PI Falk J, Kurpinska K, Lerchl J, Schmidt R, Seulberger H;

XX DR WPI; 1999-096742/09.

XX DNA encoding barley hydroxyphenylpyruvate dioxygenase - for
 PT producing plants with increased vitamin E content, etc.

XX PS Example 1; Page 9; 26pp; German.

XX AAX02695-X02708 are primers used in the isolation of a novel barley
 CC (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
 CC protein is useful for plant transformation to produce transgenic plants

CC especially where an expression cassette is introduced into a plant cell,
 CC callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
 CC transformation, electroporation or particle bombardment and where the
 CC plants are selected from soya, barley, wheat, oilseed rape, maize and
 CC sunflower, or where the DNA is expressed in tobacco plants, especially
 CC in leaves or seeds.

XX SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAAATAAAAA 1095
 DB 14 TGAATAAAAAAATAAAAA 1

RESULT 1540

AAAX02698/c

ID AAX02698 standard; DNA; 14 BP.

XX AC AAX02698;

DT 10-MAY-1999 (first entry)

XX DE Barley HPPD primer #4.

XX HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
 KW transgenic; plant cell; callus tissue; protoplast; electroporation;
 KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
 KW sunflower; tobacco; ss.

XX OS Hordeum vulgare.

XX PN DE19730066-A1.

XX PD 21-JAN-1999.

XX PF 14-JUL-1997; 97DE-1030066.

XX PR 14-JUL-1997; 97DE-1030066.

XX PA (BADI) BASF AG.

XX PI Falk J, Kurpinska K, Lerchl J, Schmidt R, Seulberger H;

XX DR WPI; 1999-096742/09.

XX DNA encoding barley hydroxyphenylpyruvate dioxygenase - for
 PT producing plants with increased vitamin E content, etc.

XX PS Example 1; Page 9; 26pp; German.

XX AAX02695-X02708 are primers used in the isolation of a novel barley
 CC (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
 CC protein is useful for plant transformation to produce transgenic plants
 CC especially where an expression cassette is introduced into a plant cell,
 CC callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
 CC transformation, electroporation or particle bombardment and where the
 CC plants are selected from soya, barley, wheat, oilseed rape, maize and
 CC sunflower, or where the DNA is expressed in tobacco plants, especially
 CC in leaves or seeds.

XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAATAAAAA 1097
 DB 14 ACAATAAAAAAATAAAAA 1

```
RESULT 1541
AAC88538/C
ID AAC88538 standard; RNA; 14 BP.
XX
XX AC AAC88538;
XX
XX AC (first entry)
XX
XX 02-MAR-2001 (first entry)
XX
XX DE Anti-gammaPDE coding sequence fragment #2.
XX
XX KW Ribozyme; retinal degradation; retinal disease; learning; memory;
XX KW amyotrophic lateral sclerosis; tumour suppression; ss.
XX
XX OS Mus sp.
XX
XX PN WO200066780-A2.
XX
XX PD 09-NOV-2000.
XX
XX PF 28-APR-2000; 2000WO-US11509.
XX
XX PR 30-APR-1999; 99US-0131942.
XX
XX PA (UYFL ) UNIV FLORIDA.
XX
XX PI Lewin AS, Muzyczka N, Hauswirth WW, Teschendorf C, Burger C;
XX
XX DR WPI; 2000-687548/67.
XX
XX PT Novel methods for identifying genes with selected functions comprising
XX PT contacting genes with a library of ribozymes, useful for identifying
XX PT genes involved in, e.g. retinal disease, learning or memory and tumor
XX PT suppression -
XX
XX PS Claim 16; Fig 17; 11pp; English.
XX
XX CC The present invention relates to a method for identifying a gene with a
XX CC selected function comprising contacting genes with a library of ribozymes
XX CC and identifying at least 1 ribozyme that alters the selected function of
XX CC the gene. The present sequence is a target sequence used in the present
XX CC invention. The methods (and ribozymes) are useful for identifying novel
XX CC genes involved in retinal degradation, retinal disease, learning or
XX CC memory, amyotrophic lateral sclerosis or tumour suppression, and for
XX CC producing non-human animal models of diseases.
XX
XX SQ Sequence 14 BP; 6 A; 3 C; 4 G; 1 U; 0 other;
XX
XX Query Match 1.1%; Score 12.4; DB 1; Length 14;
XX Best Local Similarity 92.9%; Pred. No. 9.1e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 540 CTTCTGACACTCTGT 553
XX Db ||||| |||||
XX 14 CTTCTGACACTCTGT 1
XX
XX RESULT 1542
AAC83822
ID AAC83822 standard; RNA; 14 BP.
XX
XX AC AAC83822;
XX
XX 28-FEB-2001 (first entry)
XX
XX DE RNA oligonucleotide #2 used in a binding assay.
XX
XX KW L-ribo-configurated Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.
XX
XX OS Unidentified.
XX
XX PN WO200066604-A2.
```

```
XX 09-NOV-2000.
XX
XX 04-MAY-2000; 2000WO-DK00225.
XX
XX 04-MAY-1999; 99DK-0000603.
XX 01-SEP-1999; 99DK-0001225.
XX 11-JAN-2000; 2000DK-0000032.
XX
XX (EXIQ-) EXIQON AS.
XX
XX Wengel J;
XX
XX WPI; 2001-060972/07.
XX
XX Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides,
XX useful for therapeutic purposes e.g. in the construction of
XX oligonucleotides, as substrates for nucleic acids polymerases and in
XX RNA mediated catalytic processes -
XX
XX Example 11; Page 56; 79pp; English.
XX
XX The present invention relates to an oligomer comprising
XX L-ribo-configurated Locked Nucleoside Analogues (L-ribo-LNA analogues).
XX The present sequence is an RNA oligonucleotide. Binding studies of the
XX L-ribo-LNA analogues towards the present sequence were carried out, to
XX determine the thermostability of the L-ribo-LNA analogues. The analogs of
XX the present invention have a variety of uses e.g. in the preparation of
XX conjugates of the L-ribo-LNA modified oligonucleotides (oligomers).
XX
XX SQ Sequence 14 BP; 13 A; 1 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.1%; Score 12.4; DB 1; Length 14;
XX Best Local Similarity 92.9%; Pred. No. 9.1e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1097
XX Db ||||| |||||
XX 1 AAAAAAAAAAAAAA 14
XX
XX RESULT 1543
ABQ83273
ID ABQ83273 standard; DNA; 14 BP.
XX
XX AC ABQ83273;
XX
XX 18-JAN-2003 (first entry)
XX
XX EGI cDNA tag related oligonucleotide SEQ ID NO:46.
XX
XX cDNA tag; identification; gene expression analysis; linker;
XX expressed gene identification; EGI; ss.
XX
XX Synthetic.
XX
XX WO200274951-A1.
XX
XX 26-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-JP02338.
XX
XX 15-MAR-2001; 2001JP-0073959.
XX
XX (KURE ) KUREHA CHEM IND CO LTD.
XX (YAMA/) YAMAMOTO M.
XX (YAMA/) YAMAMOTO N.
XX
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX
XX WPI; 2002-759896/82.
XX
XX Construction of cDNA tags for identifying expressed genes with specific
```

PT linkers and recognition sequences, applicable in gene expression
 PT analysis, disease diagnosis and identifying target for gene therapy -
 PS Example 1; Page 24; 59pp; Japanese.
 XX
 CC The present invention describes a method for constructing a cDNA tag for
 CC identifying an expressed gene. The method comprises: (a) preparation of
 CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
 CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
 CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
 CC linker Y ligated material; and (e) cleaving the amplification product.
 CC The method can be used for the construction of cDNA tags for identifying
 CC expressed genes, which is applicable in gene expression analysis, disease
 CC diagnosis and identifying target for gene therapy, including the
 CC clarification of difference in function or morphology of cells under
 CC physiological or pathological conditions. The cDNA or cells for assay can
 CC be specifically expressed, with reproducibility and accuracy in the
 CC detection of genes. The present sequence represents an expressed gene
 CC identification (EGI) cDNA tag related oligonucleotide which is used in
 CC an example from the present invention.
 XX
 SQ Sequence 14 BP; 13 A; 1 C; 0 G; 0 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 1 AAAAAAAAAAAAAA 14
 RESULT 1544
 ABQ83274/c
 ID ABQ83274 standard; DNA; 14 BP.
 AC ABQ83274;
 XX
 DT 18-JAN-2003 (first entry)
 DE
 DE EGI cDNA tag related oligonucleotide SEQ ID NO:47.
 XX
 XX cDNA tag; identification; gene expression analysis; linker;
 KW expressed gene identification; EGI; ss.
 XX Synthetic.
 OS
 XX WO200274951-A1.
 PN
 XX 26-SEP-2002.
 PD
 XX 13-MAR-2002; 2002WO-JP02338.
 PF
 XX 15-MAR-2001; 2001JP-0073959.
 PR
 XX (KURE) KUREHA CHEM IND CO LTD.
 PA (YAMA/) YAMAMOTO M.
 PA (YAMA/) YAMAMOTO N.
 XX
 PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
 XX WPI; 2002-759896/82.
 DR
 XX Construction of cDNA tags for identifying expressed genes with specific
 PT linkers and recognition sequences, applicable in gene expression
 PT analysis, disease diagnosis and identifying target for gene therapy -
 XX Example 1; Page 24; 59pp; Japanese.
 PS
 XX The present invention describes a method for constructing a cDNA tag for
 CC identifying an expressed gene. The method comprises: (a) preparation of
 CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
 CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA

CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
 CC linker Y ligated material; and (e) cleaving the amplification product.
 CC The method can be used for the construction of cDNA tags for identifying
 CC expressed genes, which is applicable in gene expression analysis, disease
 CC diagnosis and identifying target for gene therapy, including the
 CC clarification of difference in function or morphology of cells under
 CC physiological or pathological conditions. The cDNA or cells for assay can
 CC be specifically expressed, with reproducibility and accuracy in the
 CC detection of genes. The present sequence represents an expressed gene
 CC identification (EGI) cDNA tag related oligonucleotide which is used in
 CC an example from the present invention.
 XX
 SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 Db 14 AAAAAAAAAAAAAA 1

RESULT 1545
 AAD44153/c
 ID AAD44153 standard; DNA; 14 BP.
 XX
 AC AAD44153;
 XX
 DT 13-DEC-2002 (first entry)
 DE
 DE PCR primer #2 used to illustrate the method of the invention.
 XX
 XX Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase;
 KW PCR; primer; ss.
 XX Unidentified.
 OS
 XX US6277571-B1.
 PN
 XX 21-AUG-2001.
 PD
 XX 30-SEP-1998; 98US-0163485.
 PF
 XX 03-OCT-1997; 97US-108152P.
 PR
 XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 PA
 XX Fillmore H, Broadus W, Gillies G;
 PI
 XX WPI; 2002-412824/44.
 DR
 XX Sequential consensus region-directed amplification for sorting mixture
 PT of DNAs into 2 or more subsets or distinguishing gene expression
 PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
 XX Example; Fig 1E; 19pp; English.
 PS
 XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC a PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 1 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 1545
 AAD44153/c
 ID AAD44153 standard; DNA; 14 BP.
 XX
 AC AAD44153;
 XX
 DT 13-DEC-2002 (first entry)
 DE
 DE PCR primer #2 used to illustrate the method of the invention.
 XX
 XX Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase;
 KW PCR; primer; ss.
 XX Unidentified.
 OS
 XX US6277571-B1.
 PN
 XX 21-AUG-2001.
 PD
 XX 30-SEP-1998; 98US-0163485.
 PF
 XX 03-OCT-1997; 97US-108152P.
 PR
 XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 PA
 XX Fillmore H, Broadus W, Gillies G;
 PI
 XX WPI; 2002-412824/44.
 DR
 XX Sequential consensus region-directed amplification for sorting mixture
 PT of DNAs into 2 or more subsets or distinguishing gene expression
 PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
 XX Example; Fig 1E; 19pp; English.
 PS
 XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC a PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 1 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 1547

```

KW retinoid-regulated gene; ss.
XX Unidentified.
XX US6306624-B1.
XX 23-OCT-2001.
XX 25-JUN-1997; 97US-0882164.
XX 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX (TOOH ) UNIV QUEENS KINGSTON.
XX PA Petkovich PM, White JA, Beckett BR, Jones G;
XX WPI; 2002-033254/04.
XX New DNA fragments having promoter activity, useful in retinoid
XX metabolism, as well as in producing retinoic acid metabolizing
XX cytochrome P450s that are useful as targets for the treatment of
XX certain cancers -
XX Disclosure; Column 13; 75pp; English.
XX The present invention relates to retinoid (e.g., retinoic acid (RA),
XX vitamin A) metabolising proteins and nucleic acid sequences encoding
XX them. RA metabolising proteins contain a haeme-binding motif which is
XX characteristic of the group of proteins known as cytochrome P450s. The
XX sequences of the invention are useful in retinoid metabolism and in
XX producing retinoic acid metabolising cytochrome P450s. They are
XX particularly useful as targets for the treatment of certain cancers
XX such as prostate cancer. The invention also relates to a method of
XX screening drugs for their effect on activity of RA inducible proteins.
XX The present DNA sequence is poly(T) PCR primer which is used for
XX isolating retinoid regulating genes by differential display of mRNAs.
XX Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;
SQ
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. NO. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
Db | | | | | | | | | | | | | | | |
14 AAAAAAAAAAAAAA 1
RESULT 1549
AAD24496/c
ID AAD24496 standard; DNA; 14 BP.
XX AC AAD24496;
XX 07-MAR-2002 (first entry)
XX Retinoid-regulated gene isolating poly(T) PCR primer #10.
XX Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
XX cytochrome P450; prostate cancer; drug screening; PCR primer;
XX retinoid-regulated gene; ss.
XX Unidentified.
XX US6306624-B1.
XX 23-OCT-2001.
XX 25-JUN-1997; 97US-0882164.
XX 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX (TOOH ) UNIV QUEENS KINGSTON.
XX PA Petkovich PM, White JA, Beckett BR, Jones G;
XX WPI; 2002-033254/04.
XX New DNA fragments having promoter activity, useful in retinoid
XX metabolism, as well as in producing retinoic acid metabolizing
XX cytochrome P450s that are useful as targets for the treatment of
XX certain cancers -
XX Disclosure; Column 13; 75pp; English.
XX The present invention relates to retinoid (e.g., retinoic acid (RA),
XX vitamin A) metabolising proteins and nucleic acid sequences encoding
XX them. RA metabolising proteins contain a haeme-binding motif which is
XX characteristic of the group of proteins known as cytochrome P450s. The
XX sequences of the invention are useful in retinoid metabolism and in
XX producing retinoic acid metabolising cytochrome P450s. They are
XX particularly useful as targets for the treatment of certain cancers
XX such as prostate cancer. The invention also relates to a method of
XX screening drugs for their effect on activity of RA inducible proteins.
XX The present DNA sequence is poly(T) PCR primer which is used for
XX isolating retinoid regulating genes by differential display of mRNAs.
XX Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 other;
SQ
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. NO. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
Db | | | | | | | | | | | | | | | |
14 AAAAAAAAAAAAAA 1
RESULT 1550
AAD24497/c
ID AAD24497 standard; DNA; 14 BP.
XX AC AAD24497;
XX 07-MAR-2002 (first entry)
XX Retinoid-regulated gene isolating poly(T) PCR primer #11.
XX Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
XX cytochrome P450; prostate cancer; drug screening; PCR primer;
XX retinoid-regulated gene; ss.
XX Unidentified.
XX US6306624-B1.
XX 23-OCT-2001.
XX 25-JUN-1997; 97US-0882164.
XX 21-JUN-1996; 96US-0667546.
PR 01-OCT-1996; 96US-0724466.
PR 23-JUN-1997; 97WO-CA00440.
XX (TOOH ) UNIV QUEENS KINGSTON.
XX PA Petkovich PM, White JA, Beckett BR, Jones G;
XX WPI; 2002-033254/04.
XX New DNA fragments having promoter activity, useful in retinoid
XX metabolism, as well as in producing retinoic acid metabolizing
XX cytochrome P450s that are useful as targets for the treatment of
XX certain cancers -
XX Disclosure; Column 13; 75pp; English.
XX The present invention relates to retinoid (e.g., retinoic acid (RA),
XX vitamin A) metabolising proteins and nucleic acid sequences encoding
XX them. RA metabolising proteins contain a haeme-binding motif which is
XX characteristic of the group of proteins known as cytochrome P450s. The
XX sequences of the invention are useful in retinoid metabolism and in
XX producing retinoic acid metabolising cytochrome P450s. They are
XX particularly useful as targets for the treatment of certain cancers
XX such as prostate cancer. The invention also relates to a method of
XX screening drugs for their effect on activity of RA inducible proteins.
XX The present DNA sequence is poly(T) PCR primer which is used for
XX isolating retinoid regulating genes by differential display of mRNAs.
XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 other;
SQ
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. NO. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAATAAAAAAAAA 1095
Db | | | | | | | | | | | | | | | |
14 TGAATAAAAAAAAA 1

```

PT cytochrome P450s that are useful as targets for the treatment of
PT Certain cancers -
XX
PS Disclosure; Column 13; 75pp; English.
XX
XX The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers
CC such as prostate cancer. The invention also relates to a method of
CC screening drugs for their effect on activity of RA inducible proteins.
CC The present DNA sequence is poly(T) PCR primer which is used for
CC isolating retinoid regulating genes by differential display of mRNAs.
XX
SQ Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
DB 14 AGAAAAAAAAAAAAA 1
RESULT 1551
ABX79985
ID ABX79985 standard; cDNA; 14 BP.
AC ABX79985;
XX
XX 17-APR-2003 (first entry)
DE EST polymorphic DNA repeat polynucleotide #310.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
OS
XX
XX US6472154-B1.
XX
XX 29-OCT-2002.
XX
XX 31-DEC-1999; 99US-0475947.
XX
XX 31-DEC-1999; 99US-0475947.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW,
XX WFI; 2003-208818/20.
XX
XX Identifying a candidate polymorphic repeat within a coding sequence,
PT for understanding or treating genetic disease, comprises detecting
PT tandem repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability -
XX
XX Examples; Column 1147; 588pp; English.
XX
XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a

CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs.
XX
SQ Sequence 14 BP; 13 A; 1 C; 0 G; 0 U; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1097
DB 1 AAAAAAAAAAACAA 14
RESULT 1552
AAT55113/C
ID AAT55113 standard; RNA; 15 BP.
XX
XX AAT55113;
XX
XX 25-MAR-2003 (updated)
DT 21-APR-1997 (first entry)
XX
XX Human relA hammerhead ribozyme target sequence (nt. position 1005).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW myocardial rejection; rheumatoid arthritis; psoriasis;
KW transplant ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome;
KW AIDS; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB00156.
XX
XX 30-JAN-1995; 95US-0380734.
XX 23-FEB-1994; 94US-0201109.
XX 29-MAR-1994; 94US-0218934.
XX 04-APR-1994; 94US-0222795.
XX 07-APR-1994; 94US-0224483.
XX 15-APR-1994; 94US-0227958.
XX 18-MAY-1994; 94US-0228041.
XX 06-JUL-1994; 94US-0245736.
XX 15-AUG-1994; 94US-0291932.
XX 16-AUG-1994; 94US-0291433.
XX 17-AUG-1994; 94US-0292620.
XX 19-AUG-1994; 94US-0293520.
XX 02-SEP-1994; 94US-0300000.
XX 08-SEP-1994; 94US-0303039.
XX 23-SEP-1994; 94US-0311486.
XX 28-SEP-1994; 94US-0311749.
XX 03-OCT-1994; 94US-0314397.
XX 07-OCT-1994; 94US-0316771.
XX 07-OCT-1994; 94US-0319492.

PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334647.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX DR WPI; 1995-351090/45.
 XX PT Ribozymes having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX PS Claim 2; Page 229; 407pp; English.
 XX CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves rela
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC The rela gene product is a subunit of the transcriptional
 CC regulator NF-kappaB and is implicated specifically in the induction
 CC of inflammatory responses. Regions of the mRNA that do not form
 CC secondary folding structures and that contain potential hammerhead
 CC and hairpin ribozyme cleavage sites were identified by computer
 CC analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the
 CC target sequences and thereby inhibit rela expression, making them
 CC potentially useful for treating rheumatoid arthritis, restenosis
 CC and asthma as well as for increasing tolerance to transplanted
 CC tissues. The potential immunosuppressive properties of a ribozyme
 CC that cleaves rela mRNA means that uses are limited to local
 CC delivery, acute indications or ex vivo treatment.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 15 BP; 5 A; 4 C; 4 G; 2 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 245 GCTCTTGAAGGACT 258
 Db |||||
 15 GCTCTTGAAGGTC 2
 RESULT 1553
 AAT5115/C
 ID AAT5115 standard; RNA; 15 BP.
 XX AC AAT5115;
 XX DT 25-MAR-2003 (updated)
 XX DT 21-APR-1997 (first entry)
 XX DE Human rela hammerhead ribozyme target sequence (nt. position 1006).
 XX KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

XX OS Homo sapiens.
 XX PN W09523225-A2.
 XX PD 31-AUG-1995.
 XX PF 23-FEB-1995; 95WO-IB00156.
 XX PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX PT Ribozymes having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX PS Claim 2; Page 229; 407pp; English.
 XX CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves rela
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC The rela gene product is a subunit of the transcriptional
 CC regulator NF-kappaB and is implicated specifically in the induction
 CC of inflammatory responses. Regions of the mRNA that do not form
 CC secondary folding structures and that contain potential hammerhead
 CC and hairpin ribozyme cleavage sites were identified by computer
 CC analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the
 CC target sequences and thereby inhibit rela expression, making them
 CC potentially useful for treating rheumatoid arthritis, restenosis
 CC and asthma as well as for increasing tolerance to transplanted
 CC tissues. The potential immunosuppressive properties of a ribozyme
 CC that cleaves rela mRNA means that uses are limited to local
 CC delivery, acute indications or ex vivo treatment.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 15 BP; 6 A; 4 C; 3 G; 2 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 245 GCTCTTGAAGGACT 258
 Db |||||
 15 GCTCTTGAAGGTC 2
 RESULT 1553
 AAT5115/C
 ID AAT5115 standard; RNA; 15 BP.
 XX AC AAT5115;
 XX DT 25-MAR-2003 (updated)
 XX DT 21-APR-1997 (first entry)
 XX DE Human rela hammerhead ribozyme target sequence (nt. position 1006).
 XX KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 245 GCTCTGAGGACT 258
 DB 14 GCTCTGAGGACT 1

RESULT 1554
 ID AAT52144/c
 AC AAT52144 standard; RNA; 15 BP.
 XX AAT52144;
 XX 25-MAR-2003 (updated)
 DT 25-MAR-1997 (first entry)
 XX Human ICAM hammerhead ribozyme target sequence (nt. position 2914).

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 intercellular adhesion molecule; rel A; tumour necrosis factor;
 TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 translocation; chronic myelogenous leukaemia; CML; cancer;
 Philadelphia chromosome; inflammation; autoimmune disease;
 atherosclerosis; myocardial infarction; stroke; restenosis;
 transplant rejection; rheumatoid arthritis; psoriasis;
 myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 human immunodeficiency virus; acquired immune deficiency syndrome;
 AIDS; ss.

OS Homo sapiens.
 XX
 XX WO9523225-A2.
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.

XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowira B, Dorenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpisky A, Kisch K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Favco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR

XX Ribozymes having modified bases and methods for producing them -
 PT for use in inhibiting disease related genes
 XX
 PS Claim 2; Page 175; 407pp; English.

XX The present sequence represents a preferred target sequence for
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and
 CC thereby inhibit ICAM-1 expression, making them useful for reducing
 CC transplant rejection and alleviating symptoms in patients with
 CC rheumatoid arthritis, asthma and other inflammatory disorders.
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 15 BP; 1 A; 1 C; 1 G; 12 U; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAA 1095
 DB 14 TGAATAAAAAAAAAA 1

RESULT 1555
 AAX79429/c
 ID AAX79429 standard; DNA; 15 BP.
 XX
 AC AAX79429;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE HLA-DR typing probe F67DR70.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation; ss.
 XX
 OS Synthetic.
 XX
 XX US5468611-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 08-APR-1993; 93US-0045530.
 XX
 PR 27-JUN-1990; 90US-0544218.
 PR 08-APR-1993; 93US-0045530.
 XX
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 XX Baxter-Lowe LA, Gorski JA;
 XX WPI; 1996-010091/01.

PT Improved method for HLA typing - by DNA amplification and
 PT sequence-specific oligonucleotide hybridisation, used to select
 PT bone marrow donors
 XX
 XX Disclosure; Column 21-22; 20pp; English.

XX A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,

Db 2 TGCTTCCAGGAG 15

RESULT 1558
AAV48765
ID AAV48765 standard; DNA; 15 BP.
XX
AC AAV48765;
XX
DT 15-OCT-1998 (first entry)
XX
DE ErbbB-2 gene antisense oligonucleotide ErbbB-2-57.
XX
KW ErbbB-2; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-0101531.
XX
PR 31-JAN-1997; 97EP-0101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Brysch W, Schlingensiepen K;
XX
DR WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of
PT residues able to form two or three hydrogen bonds, have greater
PT activity and reduced toxicity, used therapeutically or to modulate
PT growth of cells in culture
XX
XX Claim 10; Fig 6b; 286pp; English.
XX
CC AAV48709-886 represent antisense oligonucleotides directed against the
CC ErbbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted
CC in significant reduction in ErbbB-2 protein expression, while
CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in
CC cases of cancer or (targeting TGF) for stimulating the immune system.
XX
SQ Sequence 15 BP; 4 A; 5 C; 4 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 671 GAAGCTCACAGATG 684
| | | | | | | | | |
Db 1 GCAGCTCACAGATG 14

RESULT 1559
AAV48595/c

ID AAV48595 standard; DNA; 15 BP.
XX
AC AAV48595;
XX
DT 15-OCT-1998 (first entry)
XX
DE junD gene antisense oligonucleotide JunD-12.
XX
KW junB; junD; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-0101531.
XX
PR 31-JAN-1997; 97EP-0101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Brysch W, Schlingensiepen K;
XX
DR WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of
PT residues able to form two or three hydrogen bonds, have greater
PT activity and reduced toxicity, used therapeutically or to modulate
PT growth of cells in culture
XX
XX Claim 10; Fig 5a; 286pp; English.
XX
CC AAV48564-708 represent antisense oligonucleotides directed against the
CC junB and junD genes. Of these, only oligonucleotides AAV48565-614
CC resulted in effective downregulation of negative growth control by JunB
CC or JunD, while AAV48615-708 had little effect. The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErbbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in
CC cases of cancer or (targeting TGF) for stimulating the immune system.
XX
SQ Sequence 15 BP; 3 A; 6 C; 4 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 825 GGTGCTGAAGCTGG 838
| | | | | | | | | |
Db 15 GGTGCTGAAGCTGG 2

RESULT 1560
AAV16667/c
ID AAV16667 standard; DNA; 15 BP.
XX
AC AAV16667;
XX
DT 12-JUN-1998 (first entry)

```

XX DE Probe F67DR70 used to identify HLA-DR sequences.
XX DR region; major histocompatibility complex; HLA-DR; HLA-typing;
KW HLA-DR beta consensus sequence; allelic polymorphism;
KW HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
XX Synthetic.
OS Homo sapiens.
XX US5702885-A.
XX 30-DEC-1997.
XX 08-APR-1993; 93US-0057957.
XX 27-JUN-1990; 90US-0544218.
XX (BLOO-) BLOOD CENT RES FOUND INC.
XX Baxter-Lowe LA, Gorski JA;
XX WPI; 1998-076408/07.
XX Oligo:nucleotide probes and primers and methods for HLA typing -
XX particularly for tissue typing for bone marrow transplants
XX Disclosure; Column 20; 20pp; English.
XX The present probe is used to identify differences in the DR region of
XX human major histocompatibility complex (HLA-DR). The specification
XX describes a method for HLA-typing, which includes an oligonucleotide
XX probe which undergoes sequence-specific hybridisation with an HLA-DR
XX beta consensus sequence at positions 61-64. The probe contains a
XX labelling substance other than a nucleotide sequence, which facilitates
XX detection of the probe. The HLA sequence of a subject is PCR amplified,
XX and a probe that recognises an allelic polymorphism at a selected HLA
XX locus is contacted with the amplified product. This first probe
XX recognises a HLA-DR beta-allelic polymorphism. A second (different)
XX probe is brought into contact with a second sample of the amplified DNA
XX in a separate reaction, and hybridisation detected. The probes and
XX primers are used for HLA typing, e.g. for tissue, especially bone
XX marrow, transplants.
XX Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e-02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 452 TGCCCTCCAGGAAG 465
DB 14 TGCTCTCCAGGAAG 1
RESULT 1561
AAT86601
ID AAT86601 standard; DNA; 15 BP.
XX AC AAT86601;
XX 04-JUN-1998 (first entry)
XX DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX Synthetic.
OS WO9745721-A1.
XX 04-DEC-1997.
XX PF 23-MAY-1997; 97WO-EP02647.
XX XX
XX PF 23-MAY-1997; 97WO-EP02647.
XX XX
XX 24-MAY-1996; 96CH-0001320.
XX (NOVS ) NOVARTIS AG.
XX Muscate A, Natt F, Paulus A;
XX WPI; 1998-041763/04.
XX Separation of electrically charged target molecules - by capillary
XX affinity gel electrophoresis using polymer-gel to which receptors
XX for target molecules are bound
XX Example D2; Page 25; 41pp; English.
XX A mixture of oligonucleotides (AAT86601-3) were separated by a new
XX process using capillary affinity gel electrophoresis. The invention
XX relates to selective separation of electrically charged target molecules
XX in an analytical mixture. It comprises capillary affinity gel
XX electrophoresis using a capillary tube which is at least partly filled
XX with a polymer gel. Receptors for target molecules are covalently bound
XX to the polymer. An electric field of at least 50 volts/cm is applied.
XX The capillary tube is charged with the analytical mixture. In a first
XX separation stage, the target molecules in the mixture are bound to the
XX receptors and the remaining components are eluted, optionally whilst
XX splitting open. In a second stage, the elution conditions are changed,
XX the receptor is eliminated and the target molecules are eluted and
XX detected, optionally whilst splitting open. The process is useful for
XX selective separation and/or determination of charged organic compounds,
XX such as oligonucleotides, peptides or carbohydrates. It may be used,
XX e.g. for isolation of specific proteins and DNA molecules, purification
XX of antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity
XX than prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods.
XX Sequence 15 BP; 12 A; 0 C; 0 G; 3 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e-02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1083 TAAAAAATAAAAAA 1096
DB 1 TAAAAAATAAAAAA 14
RESULT 1562
AAT86602
ID AAT86602 standard; DNA; 15 BP.
XX AC AAT86602;
XX 04-JUN-1998 (first entry)
XX DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX Synthetic.
OS WO9745721-A1.
XX 04-DEC-1997.
XX PF 23-MAY-1997; 97WO-EP02647.
XX XX

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PR 24-MAY-1996; 96CH-0001320.
 XX (NOVS) NOVARTIS AG.
 PA Muscate A, Natt F, Paulus A;
 XX WPI; 1998-041763/04.
 XX Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors
 PT for target molecules are bound
 XX
 XX Example D2; Page 25; 41pp; English.
 XX
 XX A mixture of oligonucleotides (AAT8601-3) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel
 CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied.
 CC The capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC optionally in stages, so that the affinity of the target molecules for
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used,
 CC e.g. for isolation of specific proteins and DNA molecules, purification
 CC of antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity
 CC than prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods.
 XX
 XX Sequence 15 BP; 13 A; 0 C; 0 G; 2 T; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1097
 DB 1 AAAAAAAAAAAAAA 14
 RESULT 1563
 AAX31568/c
 ID AAX31568 standard; DNA; 15 BP.
 AC AAX31568;
 XX
 XX 21-MAY-1999 (first entry)
 DE Tag sequence of a transcript increased in pancreatic cancer.
 DE Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW Homo sapiens.
 OS WO9853319-A2.
 PN 26-NOV-1998.
 PD 20-MAY-1998; 98WO-US10277.
 XX Tag sequence of a transcript increased in pancreatic cancer.
 XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW Homo sapiens.
 OS WO9853319-A2.
 PN 26-NOV-1998.
 PD 20-MAY-1998; 98WO-US10277.
 XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW Homo sapiens.
 OS (UYJO) UNIV JOHNS HOPKINS.
 PA Claim 2; Page 29; 120pp; English.
 XX AAX30947-31815 represent tag sequences of transcripts that are

XX Kinzler KW, Vogelstein B;
 PI WPI; 1999-070161/06.
 DR
 XX Use of isolated gene transcripts - useful for developing products
 PT for the diagnosis, prognosis and treatment of cancers, particularly
 PT colon and pancreatic cancer
 XX
 XX Claim 13; Page 61; 120pp; English.
 PS
 XX AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic
 CC cancer, or in both. The tag sequences can be used to identify
 CC genes by matching the tag to a gen data base member, or by using
 CC the tag sequences as probes to isolate unidentified genes from
 CC cDNA libraries. The tag sequences can also be used in a method
 CC for diagnosing colon or pancreatic cancer in a sample suspected
 CC of being neoplastic. The method comprises comparing the level of
 CC at least one transcript in a first sample of a tissue to a second
 CC sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic
 CC tissue. The transcript is identified by a tag selected from
 CC AAX30947-31815. The methods of the invention can be used in the
 CC diagnosis, prognosis and treatment of cancer.
 XX
 XX Sequence 15 BP; 1 A; 6 C; 1 G; 7 T; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 121 GGGAGAGAAAGGATG 134
 DB 14 GGGAGAGAAAGGATG 1
 RESULT 1564
 AAX31059
 ID AAX31059 standard; DNA; 15 BP.
 XX
 XX AAX31059;
 AC
 XX 21-MAY-1999 (first entry)
 DT Tag sequence of a transcript increased in colorectal cancer.
 DE Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW Homo sapiens.
 OS WO9853319-A2.
 PN 26-NOV-1998.
 PD 20-MAY-1998; 98WO-US10277.
 XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW Homo sapiens.
 OS (UYJO) UNIV JOHNS HOPKINS.
 PA Kinzler KW, Vogelstein B;
 PI WPI; 1999-070161/06.
 DR
 XX Use of isolated gene transcripts - useful for developing products
 PT for the diagnosis, prognosis and treatment of cancers, particularly
 PT colon and pancreatic cancer
 XX
 XX Claim 2; Page 29; 120pp; English.
 PS
 XX AAX30947-31815 represent tag sequences of transcripts that are

CC differentially expressed in colorectal cancer, in pancreatic
 CC cancer, or in both. The tag sequences can be used to identify
 CC genes by matching the tag to a gen data base member, or by using
 CC the tag sequences as probes to isolate unidentified genes from
 CC cDNA libraries. The tag sequences can also be used in a method
 CC for diagnosing colon or pancreatic cancer in a sample suspected
 CC of being neoplastic. The method comprises comparing the level of
 CC at least one transcript in a first sample of a tissue to a second
 CC sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic
 CC tissue. The transcript is identified by a tag selected from
 CC AAX30947-31815. The methods of the invention can be used in the
 CC diagnosis, prognosis and treatment of cancer.

XX Sequence 15 BP; 12 A; 1 C; 1 G; 1 T; 0 other;
 SQ

Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA AAAA 1094
 |||||
 2 ATGAATAAAAAA 15

Db

RESULT 1565
 AAX30987
 ID AAX30987 standard; DNA; 15 BP.
 XX
 AC AAX30987;
 XX
 DT 21-MAY-1999 (first entry)
 DE
 DE Tag sequence of a transcript increased in colorectal cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 OS Homo sapiens.
 XX WO9853319-A2.
 XX 26-NOV-1998.
 PD
 PF 20-MAY-1998; 98WO-US10277.
 XX
 PR 21-MAY-1997; 97US-0047352.
 XX
 PA (UJO) UNIV JOHNS HOPKINS.
 XX
 FI Kinzler KW, Vogelstein B;
 XX
 DR WPI; 1999-070161/06.
 XX
 PT Use of isolated gene transcripts - useful for developing products
 PT for the diagnosis, prognosis and treatment of cancers, particularly
 PT colon and pancreatic cancer
 XX
 PS Claim 2; Page 24; 120pp; English.
 XX
 CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic
 CC cancer, or in both. The tag sequences can be used to identify
 CC genes by matching the tag to a gen data base member, or by using
 CC the tag sequences as probes to isolate unidentified genes from
 CC cDNA libraries. The tag sequences can also be used in a method
 CC for diagnosing colon or pancreatic cancer in a sample suspected
 CC of being neoplastic. The method comprises comparing the level of
 CC at least one transcript in a first sample of a tissue to a second
 CC sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic
 CC tissue. The transcript is identified by a tag selected from
 CC AAX30947-31815. The methods of the invention can be used in the

CC diagnosis, prognosis and treatment of cancer.
 XX
 SQ Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 ATGCAACTGTGGTT 90
 |||||
 2 ATGAACACTGTGGTT 15

Db

RESULT 1566
 AAZ64263/C
 ID AAZ64263 standard; RNA; 15 BP.
 XX
 AC AAZ64263;
 XX
 DT 28-MAR-2000 (first entry)
 DE
 DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 6973.
 XX
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9955847-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 26-APR-1999; 99WO-US09027.
 XX
 PR 27-APR-1998; 98US-0083217.
 PR 18-SEP-1998; 98US-0100842.
 PR 25-FEB-1999; 99US-0257608.
 PR 23-MAR-1999; 99US-0274553.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
 XX
 XX WPI; 2000-062023/05.
 DR
 XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection -
 PT
 PS Claim 1; Page 86; 123pp; English.
 XX
 CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given
 CC in the descriptor line.
 CC The HCV sequence was screened for optimal ribozyme target sites using
 CC a computer folding algorithm and regions of the mRNA which did not form
 CC secondary folding structures and contained potential ribozyme cleavage
 CC sites were identified. Ribozymes were synthesised to target these sites
 CC and their activities optimised by either varying the length of the
 CC binding arms or by modification to prevent degradation by nucleases.
 CC The ribozymes of the invention inhibit gene expression and/or viral
 CC replication, and are used to treat diseases associated with Hepatitis C
 CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
 CC carcinoma. The ribozymes may be used in combination with interferon to
 CC treat HCV infection, other infectious diseases, autoimmune diseases, and
 CC cancer.

XX Sequence 15 BP; 3 A; 5 C; 3 G; 4 U; 0 other;
 SQ

Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 452 TGCCTTCCAGGAG 465
 DB 15 TGCCTTCAAGGAAG 2

RESULT 1567

AAZ64408/C
 ID AAZ64408 standard; RNA; 15 BP.

XX AC AAZ64408;

XX 28-MAR-2000 (first entry)

XX Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8884.
 XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.

XX Hepatitis C virus.

XX WO9955847-A2.

XX 04-NOV-1999.

XX 26-APR-1999; 99WO-US09027.

XX 27-APR-1998; 98US-0083217.

XX 18-SEP-1998; 98US-0100842.

XX 25-FEB-1999; 99US-0257608.

XX 23-MAR-1999; 99US-0274553.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;

XX WPI; 2000-062023/05.

XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection -
 XX Claim 1; Page 91; 123pp; English.

XX The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given
 CC in the descriptor line.
 CC The HCV sequence was screened for optimal ribozyme target sites using
 CC a computer folding algorithm and regions of the mRNA which did not form
 CC secondary folding structures and contained potential ribozyme cleavage
 CC sites were identified. Ribozymes were synthesized to target these sites
 CC and their activities optimised by either varying the length of the
 CC binding arms or by modification to prevent degradation by nucleases.
 CC The ribozymes of the invention inhibit gene expression and/or viral
 CC replication, and are used to treat diseases associated with Hepatitis C
 CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
 CC carcinoma. The ribozymes may be used in combination with interferon to
 CC treat HCV infection, other infectious diseases, autoimmune diseases, and
 CC cancer.

SQ Sequence 15 BP; 2 A; 7 C; 0 G; 6 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 9.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 773 GGAGAGAGAGTGTG 786

DB 15 GGAGAGAGAGTGTG 2

RESULT 1568

AAF92685/C
 ID AAF92685 standard; DNA; 15 BP.

XX AAF92685;

XX 16-MAY-2001 (first entry)

XX HLA-DR typing probe #65.

XX Human; leukocyte antigen; HLA; typing; sequence specific probe;
 KW SSOPH; ss.

XX Homo sapiens.

XX US6194147-B1.

XX 27-FEB-2001.

XX 30-DEC-1997; 97US-0000805.

XX 27-JUN-1990; 90US-0544218.

XX 08-APR-1993; 93US-0057957.

XX (BLOO-) BLOOD CENT RES FOUND INC.

XX Baxter-Lowe LA, Gorski JA;

XX WPI; 2001-217923/22.

XX Human leukocyte antigen typing by amplifying a sample followed by
 PT sequence specific oligonucleotide hybridization with labeled
 PT oligonucleotide probes that hybridize with a series of known control
 PT DNA sequences -
 XX Disclosure; Column 11-14; 15pp; English.
 XX The present invention relates to human leukocyte antigen (HLA) typing.
 CC The method involves detecting polymorphic residues by sequence
 CC specific oligonucleotide probe hybridization (SSOPH) with labeled
 CC oligonucleotide probes.
 XX Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 9.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 452 TGCCTTCCAGGAG 465

DB 14 TGCCTTCCAGGAG 1

RESULT 1569

AAF95031

ID AAF95031 standard; DNA; 15 BP.

XX AAF95031;

XX 23-MAY-2001 (first entry)

XX Mutant capture oligonucleotide #24.

XX Tubercle bacillus; drug sensitivity; drug resistance; rifampicin;
 KW streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene;
 KW rpsL gene; inhA gene; katG gene; emsB gene; probe; PCR primer; ss.
 XX Mycobacterium tuberculosis.

XX EP1076099-A2.

XX 14-FEB-2001.

XX 02-AUG-2000; 2000EP-0306563.

XX 03-AUG-1999; 99JP-0220357.
XX (NISN) NISSHINBO IND INC.
XX PA (SYST-) SYSTEM RES INC.
XX PI Suzuki Y, Nishida M, Takenishi S;
XX WPI; 2001-246696/26.
XX
XX New oligonucleotides, nucleic acid probes and primers are useful for
PT differentiating drug-resistance and determining infection with tubercle
PT bacilli -
XX
XX Claim 10; Page 25; 114pp; English.
XX
XX The present invention relates to oligonucleotides based on nucleotide
CC sequences obtained from both wild-type tubercle bacilli (wTB) that are
CC susceptible to a drug and mutant-type tubercle bacilli (mtTB) that are
CC resistant to a drug. The drugs used in the present invention are
CC rifampicin (RFP), streptomycin (SM), kanamycin (KM), isoniazid (INH) and
CC ethambutol (EB). The rpoB gene is responsible for resistance to RFP; the
CC rrs gene is responsible for resistance to SM and KM; the rpsL gene is
CC responsible for resistance to SM; the inhA gene is responsible for
CC resistance to INH; the katG gene is responsible for resistance to INH;
CC and the emsB gene is responsible for resistance to EB. The present
CC invention also relates to nucleic acid probes having part of a nucleotide
CC sequence of tubercle bacilli (TB) responsible for drug resistance and
CC primers used to generate the probes. The present sequence is an
CC oligonucleotide of the present invention. The oligonucleotides of the
CC present invention can be used to enable the differentiation of drug
CC resistance and the determination of infection with tubercle bacilli
CC simultaneously.
XX
XX Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 other;
SQ

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 723 CAGGAGCTGCGGTA 736
DB |||||
2 CAGGAGCTGCGGTA 15

RESULT 1570
AAF60455/c
ID AAF60455 standard; DNA; 15 BP.
XX
XX AAF60455;
XX
XX 27-APR-2001 (first entry)
XX
XX Oligonucleotide clamp #10.
XX
XX Oligonucleotide clamp; ds.
XX
XX Unidentified.
XX
XX US6180777-B1.
XX
XX 30-JAN-2001.
XX
XX 03-JAN-1997; 97US-0787321.
XX
XX 12-JAN-1996; 96US-0009918.
XX
XX (FARB) BAYER CORP.
XX
XX Horn T;
XX
XX WPI; 2001-201911/20.
XX

PT Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
XX second units having thiol or phosphorothioate groups -
XX
XX Example 5; Column 17-18; 20pp; English.
XX
XX The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the
CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention.
XX
XX Sequence 15 BP; 1 A; 2 C; 0 G; 12 T; 0 other;
SQ

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAA 1095
DB |||||
14 TCAAAAAAATAAAAA 1

RESULT 1571
AAF81000/c
ID AAF81000 standard; DNA; 15 BP.
XX
XX AAF81000;
XX
XX 02-MAY-2001 (first entry)
XX
XX PTGS2 allele specific oligonucleotide primer SEQ ID 106.
XX
XX Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
KW inflammation; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200107662-A1.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-US20114.
XX
XX 22-JUL-1999; 99US-0145170.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Denton RR, Mandabalan K, Sanchis A, Stephens JC, Tanguay DA;
XX WPI; 2001-182805/18.
XX
XX New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
PT for gene therapy of inflammation and for establishing a genotype or
PT haplotype -
XX
XX Disclosure; Page 23; 118pp; English.
XX
XX This invention relates to a polynucleotide sequence that is a polymorphic
CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
CC protein is represented by AAB72199. The invention includes PCR and
CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
CC are used to isolate and characterise the PTGS2 gene sequence, and to
CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide

CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
CC especially for determining association between a particular trait, e.g. a
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
CC effects of therapeutic agents.

SQ Sequence 15 BP; 1 A; 7 C; 2 G; 5 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 999 CTGAGGCTGGAGAA 1012
Db 14 CTGAGGCTGGAGAA 1

RESULT 1572
AAF46502
ID AAF46502 standard; DNA; 15 BP.

XX AAF46502;

XX 30-MAR-2001 (first entry)

DE IGFBP2 oligonucleotide #1341.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU00693.

XX 21-JUN-1999; 99US-0140345.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -

XX Example 6; Page 42; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

SQ Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 725 GGAGCTGGGTACA 738
Db 2 GGAGCTGGGTACA 15

RESULT 1573

AAF46504

ID AAF46504 standard; DNA; 15 BP.

XX AAF46504;

XX 30-MAR-2001 (first entry)

XX IGFBP2 oligonucleotide #1343.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU00693.

XX 21-JUN-1999; 99US-0140345.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -

XX Example 6; Page 42; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of

CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 other;
SQ Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 726 GAGCTGGGTACAG 739
Db 1 GAGCTGGGTACAG 14

RESULT 1574
AAF49043/C
ID AAF49043 standard; DNA; 15 BP.

XX AC AAF49043;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #3.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU00693.

XX 21-JUN-1999; 99US-0140345.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -

XX Example 8; Page 60; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other

CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 1 A; 0 C; 2 G; 12 T; 0 other;

XX Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1082 TTAATAAAAAAAAAA 1095
Db 14 TCAAAAAAAAAAAAAA 1

RESULT 1575
AAF51980
ID AAF51980 standard; DNA; 15 BP.

XX AC AAF51980;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-I oligonucleotide #2940.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU00693.

XX 21-JUN-1999; 99US-0140345.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -

XX Example 8; Page 80; 201pp; English.

XX The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1002 AGGCTGGGAGATGG 1015
 |||||
 Db 2 AGGCTGGGAGATGG 15

RESULT 1576
 AAF51981
 ID AAF51981 standard; DNA; 15 BP.

XX AC AAF51981;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGF-I oligonucleotide #2941.

XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX FN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU00693.

XX PR 21-JUN-1999; 99US-0140345.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -

XX PS Example 8; Page 80; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.

XX SQ Sequence 15 BP; 4 A; 1 C; 8 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1002 AGGCTGGGAGATGG 1015
 |||||
 Db 1 AGGCTGGGAGATGG 14

RESULT 1577
 AAF53299/c
 ID AAF53299 standard; DNA; 15 BP.

XX AC AAF53299;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGF-I oligonucleotide #4259.

XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX FN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU00693.

XX PR 21-JUN-1999; 99US-0140345.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -

XX PS Example 8; Page 88; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.

XX SQ Sequence 15 BP; 2 A; 5 C; 2 G; 6 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 764 GGCAGAACTGGAGA 777
 |||||
 Db 15 GGCAGAACTGGAGA 2

RESULT 1578
AA53300/c
ID AAF53300 standard; DNA; 15 BP.
XX AC AAF53300;
XX AC AAF53300;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4260.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX OS WO200078341-A1.
XX PN 28-DEC-2000.
XX PD 21-JUN-2000; 2000WO-AU00693.
XX PF 21-JUN-1999; 99US-0140345.
XX PR (MURD-) MURDOCH CHILDRENS RES INST.
XX PA Wright CJ, Werther GA, Edmondson SR;
XX PI WPI; 2001-041421/05.
XX DR Ameliorating the effects of a disorder, e.g. psoriasis, by
XX PT administering UV (ultra-violet) treatment (optional) and an antisense
XX PT nucleic acid that inhibits or reduces growth factor mediated cell
XX PT proliferation and/or inflammation -
XX PS Example 8; Page 88; 201pp; English.
XX CC The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-P45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic disease, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX SQ Sequence 15 BP; 1 A; 6 C; 2 G; 6 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 764 GGCAGAACTGGAGA 777
DB 14 GGCAGAACTGGAGA 1
RESULT 1579
ABX01316/c
ID AAF53300 standard; RNA; 15 BP.
XX AC ABX01316;
XX DT 23-DEC-2002 (first entry)
XX DE Hepatitis C virus substrate #1098 for HCV hammerhead ribozyme #1098.
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX OS Hepatitis C virus.
XX OS US2002082225-A1.
XX PN 27-JUN-2002.
XX PD 23-MAR-1999; 99US-0274553.
XX PF 23-MAR-1999; 99US-0274553.
XX PR (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;
XX DR WPI; 2002-617759/66.
XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit
XX viral replication and are useful to treat hepatitis C virus infections
XX and cirrhosis, liver failure or hepatocellular carcinoma -
XX PS Claim 1; Page 52; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or
XX hairpin (HP) motif where the binding arms comprise sequences
XX complementary to one of the substrate sequences defined in the
XX specification. The HCV ribozymes are useful for modulating the
XX expression and/or replication of HCV. They can be used to treat
XX cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV
XX ribozymes are also useful for treating a condition associated with
XX HCV infection in conjunction with one or more other drug therapies,
XX particularly type I interferon, especially interferon alpha, beta or
XX gamma or consensus interferon. The present sequence represents a
XX substrate for a HCV hammerhead (HH) ribozyme.
XX Note: Some of the sequence data for this patent did not form part of
XX the printed specification. The complete sequence data for this patent
XX was obtained in electronic format directly from the USPTO web site
XX at seqdata.uspto.gov/psipdbEntry.html.
XX SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 U; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 452 TGCCTTCAGGAAG 465
DB 15 TGCCTTCAGGAAG 2
RESULT 1580
ABX01461/c
ID ABX01461 standard; RNA; 15 BP.

XX AC ABX01461;
XX DT 23-DEC-2002 (first entry)
XX DE Hepatitis C virus substrate #1243 for HCV hammerhead ribozyme #1243.
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX KW type I interferon; interferon alpha; interferon beta; cytosolic;
XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX OS Hepatitis C virus.
XX PN US2002082225-A1.
XX PD 27-JUN-2002.
XX PF 23-MAR-1999; 99US-0274553.
XX PR 23-MAR-1999; 99US-0274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVCO/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit
XX viral replication and are useful to treat hepatitis C virus infections
XX and cirrhosis, liver failure or hepatocellular carcinoma -
XX Claim 1; Page 56; 80pp; English.
XX The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or
XX hairpin (HP) motif where the binding arms comprise sequences
XX complementary to one of the substrate sequences defined in the
XX specification. The HCV ribozymes are useful for modulating the
XX expression and/or replication of HCV. They can be used to treat
XX cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV
XX ribozymes are also useful for treating a condition associated with
XX HCV infection in conjunction with one or more other drug therapies,
XX particularly type I interferon, especially interferon alpha, beta or
XX gamma or consensus interferon. The present sequence represents a
XX substrate for a HCV hammerhead (HH) ribozyme.
XX Note: Some of the sequence data for this patent did not form part of
XX the printed specification. The complete sequence data for this patent
XX was obtained in electronic format directly from the USPTO web site
XX at seqdata.uspto.gov/psipds/IDEntry.html.
XX SQ Sequence 15 BP; 2 A; 7 C; 0 G; 6 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 773 GGAGAGAGAGTGTG 786
|||
Dd 15 GGAGAGAGAGTGTG 2

RESULT 1581
ABK41344
ID ABK41344 standard; RNA; 15 BP.
XX

AC ABK41344;
XX 21-MAY-2002 (first entry)
XX Human eIF2Bgamma ribozyme sequence tag #9.
XX DE
XX KW Human; ss; translation initiation factor 2B gamma subunit;
XX KW eIF2Bgamma; ribozyme; ribozyme sequence tag; RST; TST;
XX KW target sequence tag; HCV; hepatitis C virus infection; virucide;
XX KW hepatotropic; antiinflammatory; proteasome alpha subunit; PMSA1.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200183754-A2.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US14337.
XX PR 02-MAY-2000; 2000US-0563794.
XX PA (IMMU-) IMMUSOL INC.
XX PI Kruger M, Welch PJ, Barber JR;
XX WPI; 2002-034514/04.
XX Identifying cellular regulators essential in pathogenesis of infectious
XX agents, useful for treatment of infectious diseases preferably viral
XX diseases especially hepatitis C virus (HCV) -
XX Claim 16; Fig 4D; 74pp; English.

The invention relates to a randomised ribozyme gene vector library
which is introduced into a population of cells expressing negative
selection marker gene operatively linked to viral nucleic acid acted on
by cellular regulator of virus replication or expression (e.g. the
human translation initiation factor 2B gamma subunit, eIF2Bgamma,
and proteasome alpha subunit 1, PMSA1, acting on Hepatitis C virus, HCV,
sequences) and a target recognition sequence of recovered ribozymes are
sequenced to identify the cellular regulator. Also included are target
sequence tags, TST, derived from eIF2Bgamma and PMSA1, the ribozyme
in the specification), methods of identifying the ribozyme sequences
and other compounds having a positive or negative effect on viral
replication via interaction with the cellular regulator.
The methods are useful for identifying a cellular regulator of virus
replication or expression, for identifying a compound that
modulates the activity of a viral cellular regulator, identifying
a ribozyme reactive with a cellular regulator of virus replication or
expression, and for treating an HCV infection by inhibiting the activity
of a cellular regulator involved in HCV replication. The ribozymes
and inhibitory compounds identified by the above screening methods are
used to reduce the severity of such an infection. The methods allow rapid
and efficient identification of cellular genes involved in the
propagation or pathogenesis of infectious agents. The present
sequence is a ribozyme sequence tag, RST, of the invention.

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 9.6e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 760 AGATGGCAGAACTG 773
|||
Dd 1 AGCUGGCGAGACUG 14

RESULT 1582
ABK31940
ID ABK31940 standard; DNA; 15 BP.


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CC SAGE tags of the invention.
XX Sequence 15 BP; 1 A; 6 C; 1 G; 7 T; 0 other;
SQ
    Query Match      1.1%; Score 12.4; DB 1; Length 15;
    Best Local Similarity 92.9%; Pred. No. 9.6e+02;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 GGAAGAAGGATG 134
Db 14 GGAAGAAGGATG 1

RESULT 1585
ABZ76549/c
ID ABZ76549 standard; DNA; 15 BP.
XX
AC ABZ76549;
XX
29-APR-2003 (first entry)
XX
Lactobacillus brevis PCR primer ORF3 SEQ ID NO:52.
XX
Lactobacillus brevis; beer turbidity; beer clouding; beer; detection;
KW lactic acid bacteria; brewing; probe; PCR primer; ss.
XX
Lactobacillus brevis.
XX
WO200295028-A1.
XX
28-NOV-2002.
XX
23-MAY-2002; 2002WO-JP05022.
XX
23-MAY-2001; 2001JP-0154085.
XX (KIRI) KIRIN BEER KK.
XX
Fujii T;
XX
WPI; 2003-120803/11.
XX
Polynucleotide probes and primers for detecting beer-clouding lactic
PT acid bacteria, for quality control during beer production applicable in
PT brewing industry -
XX
Claim 7; Page 30; 94pp; Japanese.
XX
The present invention describes a polynucleotide probe, or primer, for
CC detecting beer-clouding lactic acid bacteria containing a nucleotide
CC sequence of (I) with 8056 base pairs (see ABZ76501), or a nucleotide made
CC from not less than 15 nucleotides hybridisable with its complementary
CC sequence. Probes and primers from the present invention can be used for
CC detecting beer-clouding lactic acid bacteria (lactobacillus brevis) for
CC quality control during beer production, which is applicable in the
CC brewing industry. The present sequence represents a PCR primer for
CC Lactobacillus brevis which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 15 BP; 2 A; 5 C; 5 G; 3 T; 0 other;
    Query Match      1.1%; Score 12.4; DB 1; Length 15;
    Best Local Similarity 92.9%; Pred. No. 9.6e+02;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 384 CTGCTGCGGCAC 397
Db 14 CTGCTGCGGCAC 1

RESULT 1586
AAV14166
ID AAV14166 standard; DNA; 16 BP.

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```

XX AC AAV14166;
XX
19-MAY-1998 (first entry)
XX
Probe HBPr21 for genotype specific target of HBV.
XX
Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KW mutation detection; ss.
XX
Synthetic.
OS Hepatitis b virus.
XX
WO9740193-A2.
XX
30-OCT-1997.
XX
21-APR-1997; 97WO-EP02002.
XX
19-APR-1996; 96EP-0870053.
XX (INNO-) INNOGENETICS NV.
XX
Maertens G, Rossau R, Stuyver L;
XX
WPI; 1997-535867/49.
XX
Detection and/or genetic analysis of hepatitis B virus -
PT specifically genotype, preCore mutations, vaccine escape mutations
PT and RT gene mutations selected by treatment with drugs
XX
Claim 5; Page 26; 80pp; English.
XX
This sequence is a probe for a genotype specific target of hepatitis
b virus (HBV). This sequence can be used in the method of the invention
CC for detection and/or genetic analysis of hepatitis B virus (HBV) in a
CC sample. The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to known locations on a solid
CC support and hybridise specifically to mutant target sequences chosen from
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and inferring
CC the HBV genotype and/or mutants present in the sample from the
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and
CC RT gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir.
XX
SQ Sequence 16 BP; 2 A; 7 C; 3 G; 4 T; 0 other;
    Query Match      1.1%; Score 12.4; DB 1; Length 16;
    Best Local Similarity 92.9%; Pred. No. 1e+03;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 208 GTTCCCGAGCCCTCT 221
Db 1 GTTCCCGAGCCCTCT 14

RESULT 1587
AAT48906
ID AAT48906 standard; DNA; 16 BP.
XX
AAT48906;
AC
XX
17-SEP-1997 (first entry)
XX
Complementary human MDR1 oligonucleotide OL(1Wb)mdr.
DE

```

XX Human multidrug resistance-1; MRP; inhibition; aptameric;
 KW human multidrug resistance-associated protein; antisense;
 KW cytotoxic; chemotherapeutic; cancer; ss.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT misc_feature 1..16
 FT /*tag= a
 FT /note= "Backbone selected from: phosphorothioate;
 FT dithioate; methylphosphonate; phosphodiester;
 FT morpholino backbone; polyamide backbone;
 FT and any combination of these backbone types;
 FT the backbone may be modified to incorporate
 FT a ribozyme structure, or a pendant group"
 XX
 PN WO9640715-A1.
 XX
 XX 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US09388.
 XX
 XX 07-JUN-1995; 95US-0487141.
 XX
 XX (UYNE-) UNIV NEBRASKA.
 XX
 XX Smith LJ;
 XX
 XX WPI; 1997-052217/05.
 XX
 XX Oligo-nucleotide(s) able to inhibit multi:drug resistant phenotype -
 PT either by anti:sense or aptameric effects, useful for enhancing
 PT cytotoxic effects of chemotherapeutic agents on multi:drug resistant
 PT cancer cells
 XX
 XX Claim 5; Page 14; 74pp; English.
 XX
 XX The present sequence represents a novel oligonucleotide OL(1WB)mdr
 CC that specifically hybridises in a human cell with a complementary
 CC sequence of human multidrug resistance-1 (MDR1) gene. Hybridisation
 CC causes inhibition of expression of the multidrug resistance phenotype
 CC by the cell, due to the oligonucleotide having an aptameric inhibitory
 CC effect as well as an antisense inhibitory effect. The oligonucleotide
 CC is administered to cancer patients to prevent development of the
 CC multidrug resistant phenotype. When co-administered with
 CC chemotherapeutic agents, the oligonucleotide is useful for potentiating
 CC elimination of multidrug resistant tumour cells from bone marrow or
 CC peripheral stem cell grafts. Also, the oligonucleotide can be used as
 CC an immunosuppressive agent. All MDR-aptamers are useful for treating
 CC cancer patients by sensitising the tumour to chemotherapeutic agents,
 CC as probes to discover the target to which the aptamers bind and which
 CC is critical for maintaining multidrug resistant phenotype, and as
 CC prototypes for development of other aptameric molecules.
 XX
 SQ Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 875 CTCGATTCGGTCC 888
 DB 1 CTCGATTCGGTCC 14
 RESULT 1588
 AAX57828/c
 ID AAX57828 standard; DNA; 16 BP.
 XX
 XX AAX57828;
 AC
 XX 15-JUL-1999 (first entry)
 DT

XX PCR primer for G. oxydans autonomous replication domain.
 DE Autonomous replication domain; plasmid pF4; L-sorbose dehydrogenase;
 XX L-sorbose dehydrogenase production; 2-keto-L-gulononic acid; PCR primer;
 KW ss.
 XX Synthetic.
 OS Gluconobacter oxydans.
 XX WO9920772-A1.
 PN 29-APR-1999.
 XX
 XX 13-OCT-1998; 98WO-JP04611.
 PF
 XX 16-OCT-1997; 97JP-0303395.
 PR
 XX (FUJI) FUJISAWA PHARM CO LTD.
 PA
 XX Noguchi Y, Saito Y, Soeda S, Yoshikawa K;
 PI WPI; 1999-302744/25.
 DR
 XX Gluconobacter-originated plasmid pF4 DNAs, useful for producing
 PT biologically active substance e.g. L-sorbose dehydrogenase and
 PT 2-keto-L-gulononic acid
 XX
 XX Example; Page 15; 57pp; Japanese.
 XX
 XX This sequence represents a PCR primer for the autonomous replication
 CC domain of Gluconobacter oxydans.
 CC The invention relates to a DNA originating in plasmid pF4 with a domain
 CC controlling the autonomous replication in Gluconobacter and a domain from
 CC which polynucleotides in the region unnecessary in the autonomous
 CC replication have been wholly or partly deleted, with exception of the pF4
 CC body. Transformsants transformed with the vector can be used to produce
 CC physiologically active substances, particularly L-sorbose dehydrogenase
 CC and/or L-sorbose dehydrogenase and 2-keto-L-gulononic acid. The DNAs
 CC contain the domain controlling the autonomous replication in a bacterium
 CC and a domain with polynucleotides in the region unnecessary for this
 CC function completely or partially removed to cut down the size, while
 CC other domains of the vector can be enlarged by integrating a greater
 CC variety of structural genes to impart more functions.
 XX
 SQ Sequence 16 BP; 4 A; 1 C; 9 G; 2 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 209 TTCCGAGCCCTCTC 222
 DB 14 TTCCGAGCCCTCTC 1
 RESULT 1589
 AAX3683/c
 ID AAX3683 standard; DNA; 16 BP.
 XX
 XX AAX3683;
 AC
 XX 13-JUL-1999 (first entry)
 DT
 XX PCR primer for marker D6S1677.
 DE
 XX PCR primer; detection; glaucoma allele; haplotype analysis; human; GLC1B;
 KW chromosome 2; chromosome 6; GLC6P25; haplotype profile;
 KW presymptomatic glaucoma; symptomatic glaucoma; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX

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PN WO9916899-A2.
XX
XX
PD 08-APR-1999.
XX
PF 29-SEP-1998; 98WO-CA00924.
XX
XX 30-SEP-1997; 97CA-2217097.
XX
XX (UYLA-) UNIV LAVAL.
XX
PI Anttil J, Cote G, Falardeau P, Morissette J, Raymond V;
XX
XX WPI; 1999-263704/22.
XX
XX Haplotype analyses for indirect detection of glaucoma
XX
XX Claim 18; Page 28; 41pp; English.
XX
CC This sequence represents a PCR primer used in the method of the
CC invention. The method is for detecting the presence of alleles for
CC glaucoma comprising haplotype analysis of human chromosome 2 and 6
CC respectively, where the haplotypes are associated with loci GLC1B and
CC GLC6p25 respectively. The primers are used to amplify gene sequences to
CC generate information necessary to compile haplotype profiles. The
CC haplotype profiles can be used to detect presymptomatic and symptomatic
CC glaucoma. They can also be used to localise, isolate and identify the
CC GLC1B and GLC6p25 loci so that detection of individuals with glaucoma is
CC enhanced. The haplotype analyses also provide means for identification
CC and following of mutant alleles in pedigrees or populations.
CC Identification of presymptomatic individuals using the methods allows
CC intervention in the disease process and obviates the impact of inheriting
CC a mutant allele causing disease, by medically disrupting the initiation
CC or progression of the disease.
XX
SQ Sequence 16 BP; 2 A; 3 C; 7 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 983 CTCAGCCCTTGGAA 996
Db | ||||| |||||
16 CCCAGCCCTTGGAA 3

RESULT 1590
AAX23000/c
ID AAX23000 standard; DNA; 16 BP.
XX
XX
AC AAX23000;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human HLA-A/HLA-B primer S2.
XX
KW HLA-A; HLA-B; subtyping; reverse-transcription; human; amplification;
KW detection; polymorphism; locus specific PCR; DNA sequencing; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN DE19740339-A1.
XX
XX 18-MAR-1999.
XX
PF 13-SEP-1997; 97DE-1040339.
XX
PR 13-SEP-1997; 97DE-1040339.
XX
XX (WERN/) WERNET P.
XX
PI Enczmann J, Knipper A;
XX

WO9916899-A2.
XX
XX Oligonucleotides for human HLA-A and HLA-B subtyping - by reverse
XX transcription, amplification and sequencing
XX
XX Claim 1; Page 3; 4pp; German.
XX
CC This invention describes a method for the reverse-transcription of human
CC HLA-A and HLA-B RNA and for amplification and sequencing of the resulting
CC cDNA and for HLA-A and HLA-B subtyping by detecting polymorphisms. The
CC invention describes oligonucleotides for reverse transcription, for locus
CC specific PCR and for DNA sequencing.
XX
SQ Sequence 16 BP; 1 A; 6 C; 3 G; 6 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1005 CTGAGAGATGGAA 1018
Db | ||||| |||||
14 CTGAGAGATGGAA 1

RESULT 1591
AAA46246
ID AAA46246 standard; DNA; 16 BP.
XX
XX
AC AAA46246;
XX
XX
DT 04-SEP-2000 (first entry)
XX
DE Interphotoreceptor matrix proteoglycan IPM200 acceptor site of exon 2.
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome q13-q15; ocular disease; retinal detachment;
KW chorioretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis; rod-
KW cone dystrophy; cone-rod dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO200026367-A2.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US25440.
XX
XX 29-OCT-1998; 98US-0183972.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2000-365616/31.
XX
XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful
XX for preventing, diagnosing and treating ocular disorders such as
XX retinal detachment and chorioretinal degeneration -
XX
XX Disclosure; Page 120; 183pp; English.
XX
XX AAA46245-76 represent donor and acceptor sites of human
XX interphotoreceptor matrix (IPM) proteoglycan, designated IPM200. The
XX protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and
XX IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15,
XX between markers CHLC.GATA11F10 and D6S284. The IPM proteins may be used
XX to supplement a patient's own production of the protein or to rectify
XX alterations in their nucleic acids that result in expression of an
XX inactive protein. The IPM nucleic acids may be used in this way to
XX treat ocular diseases such as retinal detachment, chorioretinal
XX degeneration, retinal degeneration, age related macular degeneration,

```


CC photoreceptor degeneration, RPE (retinal pigment epithelium)
 CC degeneration, cone degeneration, mucopolysaccharidosis, rod-cone
 CC dysrophy and cone-rod dystrophy. The nucleic acids and proteins may
 CC also be used to assay for other modulators of IPM proteoglycan
 CC expression and activity that may be used to treat ocular diseases. The
 CC nucleic acids and proteins may also be used as diagnostic reagents to
 CC detect the presence of IPM nucleic acids and their products in samples
 CC from patients according to standard methodologies.

XX Sequence 16 BP; 6 A; 5 C; 2 G; 3 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 547 ACTCTGTAGCCCAA 560
 Db 2 ACTCTGTAGCCCAA 15

RESULT 1592
 AAZ36573/C
 ID AAZ36573 standard; DNA; 16 BP.

AC AAZ36573;

DT 22-FEB-2000 (first entry)

DE Probe hybridising to nucleotides of human c-erb-B-2 (HER-2).

XX Human; c-erb-B-2; HER-2; chromosome aberration; probe;
 KW peptide nucleic acid; haemopoietic malignancy; cancer;
 KW inborn constitutiel disease; herbicide resistance gene; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9957309-A1.

PN 11-NOV-1999.

XX 04-MAY-1999; 99WO-DK00245.

XX 04-MAY-1998; 98DK-0000615.

XX (DAKO-) DAKO AS.

XX Pluzek K, Nielsen KV, Adelhurst K;

XX WPI; 2000-038821/03.

XX Detection of chromosome aberrations, used for detecting diseases and
 PT disorders, infections, and plant alterations related to e.g. herbicide
 PT resistance -

PS Example 1; Page 44; 63pp; English.

XX Oligonucleotides AAZ36562-97 represent a set of probes hybridising to
 CC the human c-erb-B-2 (HER-2) gene. The probes are used to demonstrate
 CC the method of the invention. The specification describes a method
 CC for the detection of chromosome aberrations in eukaryotic samples
 CC uses sets of peptide nucleic acid (PNA) probes in hybridisation
 CC reactions. The method comprises using at least 2 sets of hybridisation
 CC probes, where at least one set comprises one or more PNA probes capable
 CC of hybridising to specific nucleic acid sequences related to a potential
 CC aberration in a chromosome. The methods can be used for the detection of
 CC chromosome aberrations. They can be used for the diagnosis of disorders
 CC and diseases related to chromosomal aberrations or abnormalities such as
 CC e.g. haemopoietic malignancies, cancers and inborn constitutiel diseases.
 CC The method may be used for detecting viral sequences and their
 CC localization in the chromosome. In plant biology, the methods can be
 CC used for monitoring the efficiency of transferring herbicide resistance
 CC genes to a plant.

XX Sequence 16 BP; 4 A; 3 C; 9 G; 0 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 423 CGGCTGCCCCCTGC 436
 Db 14 CGTCTGCCCCCTGC 1

RESULT 1593
 AAH91937
 ID AAH91937 standard; DNA; 16 BP.

AC AAH91937;

DT 09-OCT-2001 (first entry)

XX Human inflammatory bowel disease associated polymorphic site #1012.

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 KW chromosome 5q31-33; forensic test; gene therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT misc_feature 8

FT /*tag= a

FT /note= "SNP, optionally A or G at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33632.

XX 10-DEC-1999; 99US-0170257.

XX 10-APR-2000; 2000US-0196046.

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory
 PT bowel disease, using a hybridization assay -

XX Claim 1; Page 81; 463pp; English.

XX The present invention describes a method for detecting the presence of
 CC polymorphisms associated with inflammatory bowel diseases such as
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect
 CC the presence of genetic polymorphisms associated with inflammatory bowel
 CC disease and correlating their occurrence with disease states. They may be
 CC used in this way for phenotypic correlations, forensics, paternity
 CC testing, medicine and genetic analysis. The present sequence is a
 CC polymorphic site described in the exemplification of the invention.

XX Sequence 16 BP; 4 A; 1 C; 3 G; 7 T; 1 other;

Query Match 1.1%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. No. 1e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 TCAGGTTTGTGTTTA 945
 Db 2 TCAGGTTTGTGTTTA 16

ACA58253;
 09-JUN-2003 (first entry)
 Human familial bipolar affective disorder chromosome marker primer #201.
 Human; genotype determination; familial bipolar affective disorder;
 chromosomal region linked; locus associated with resistance; D4S402;
 D4S424; D4S431; D4S404; D11S394; D11S29; chromosome marker;
 primer; ss.
 Homo sapiens.
 OS
 XX
 PN US2002192655-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 13-JUN-2001; 2001US-0881012.
 XX
 PR 29-MAR-1996; 96US-014334P.
 PR 20-OCT-1997; 97US-062924P.
 PR 19-OCT-1998; 98US-0175158.
 XX
 PA (GINN/) GINNS E I.
 PA (EGEL/) EGELAND J A.
 PA (PAUL/) PAUL S M.
 XX
 PI Ginns EI, Egeland JA, Paul SM;
 XX
 PF WPI; 2003-352708/33.
 XX
 PT Determining a genotype associated with increased or decreased
 PT resistance to familial bipolar affective disorder in a family comprises
 PT determining the genotype of e.g., chromosomal regions D4S402 and D4S424
 PT -
 XX
 PS Disclosure; Page 12; 79pp; English.
 XX
 CC The present invention relates to a method of determining a genotype
 CC associated with increased or decreased resistance to familial bipolar
 CC affective disorder. The method comprises determining the genotype
 CC with at least one marker of at least one chromosomal region linked
 CC to a locus associated with resistance to bipolar affective disorder,
 CC where the chromosomal regions are included of and localised between,
 CC D4S402 and D4S424, D4S431 and D4S404, or D11S394 and D11S29. The
 CC invention also discloses a kit for determining a genotype associated
 CC with increased or decreased resistance to familial bipolar affective
 CC disorder, where the kit comprises markers for two or more of the
 CC chromosomal regions cited. The method and kit are useful for
 CC determining a genotype associated with increased or decreased
 CC resistance to familial bipolar affective disorder in a family
 CC affected by bipolar affective disorder, for determining the
 CC contribution of these chromosomal regions to bipolar affective
 CC disorder in an affective family member, and for assessing an
 CC increased or decreased risk of developing bipolar illness for a
 CC tested individual from an affected family. ACA58053-ACA58292
 CC represent primers used in the present invention.
 XX
 SQ Sequence 16 BP; 2 A; 3 C; 7 G; 4 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 983 CTCAGCCCTTGAA 996
 Db 16 CCCAGCCCTTGAA 3
 RESULT 1597
 AAQ26112
 ID AAQ26112 standard; DNA; 17 BP.
 XX

AC AAQ26112;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-JAN-1993 (first entry)
 XX
 DE HLA-DR beta sub-type tailed probe DRB03 hybridising region.
 XX
 KW Tissue typing; identity determination; disease susceptible; ss.
 KW
 XX Synthetic.
 OS
 XX WO9210589-A1.
 PN
 XX 25-JUN-1992.
 PD
 PF 06-DEC-1991; 91WO-US09294.
 XX
 PR 06-DEC-1990; 90US-0623098.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Apple RJ, Begovich AB, Bugawan T, Erlich HA, Griffith RL;
 PI Scharf SJ;
 XX
 DR WFI; 1992-234644/28.
 XX
 XX Method for determining HLA-DR beta sub-type in DNA sample -
 PT comprises amplification and hybridisation with probes and
 PT primers, useful in tissue typing
 PT
 XX Example; Page 37; 90pp; English.
 XX
 CC The sequence is that of the hybridising region of tailed probe DRB03 for
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid
 CC sample. The method allows specific nucleic acid sequences of the second
 CC exon of HLA-DR beta genes to be amplified then probed for identification
 CC of polymorphic sequences. The amplified DNA is useful for typing
 CC homozygous or heterozygous samples from a variety of sources and for
 CC detecting allelic variants not distinguishable by serological methods.
 CC The typing system can be used in a reverse dot blot format which is
 CC simple and rapid to perform, produces detectable signals in minutes and
 CC can be utilised in tissue typing, determination of individual identity
 CC and identifying disease susceptible individuals. The probe is used with
 CC the HRP-labelled, untailled probe CRX35. See also AAQ26092-Q26367.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 452 TGCCCTCCAGGAAG 465
 Db 3 TGCTCTCCAGGAAG 16
 RESULT 1598
 AAQ26233/c
 ID AAQ26233 standard; DNA; 17 BP.
 XX
 AC AAQ26233;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-JAN-1993 (first entry)
 XX
 DE HLA-DR beta sub-type tailed probe DRB129 hybridising region.
 XX
 KW Tissue typing; identity determination; disease susceptible; ss.
 KW
 XX Synthetic.
 OS
 PN WO9210589-A1.

XX PD 25-JUN-1992.
 XX PF 06-DEC-1991; 91WO-US09294.
 XX PR 06-DEC-1990; 90US-0623098.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Apple RJ, Begovich AB, Bugawan T, Erlich HA, Griffith RL;
 XX PI Scharf SJ;
 XX DR WPI; 1992-234644/28.
 XX PT Method for determining HLA-DR beta sub-type in DNA sample -
 XX PT comprises amplification and hybridisation with probes and
 XX PT primers, useful in tissue typing
 XX PS Example; Page 40; 90pp; English.
 XX CC The sequence is that of the hybridising region of tailed probe DRB129
 CC for use in a method for determining HLA-DR beta sub-type in a nucleic
 CC acid sample. The method allows specific nucleic acid sequences of the
 CC second exon of HLA-DR beta genes to be amplified then probed for
 CC identification of polymorphic sequences. The amplified DNA is useful for
 CC typing homozygous or heterozygous samples from a variety of sources and
 CC for detecting allelic variants not distinguishable by serological
 CC methods. The typing system can be used in a reverse dot blot format which
 CC is simple and rapid to perform, produces detectable signals in minutes
 CC and can be utilised in tissue typing, determination of individual
 CC identity and identifying disease susceptible individuals. It has not yet
 CC been tested. See also AAQ26092-Q26367.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 452 TGCCTTCCAGGAG 465
 Db 15 TGCTTCCAGGAG 2
 RESULT 1599
 AAQ26331/c
 ID AAQ26331 standard; DNA; 17 BP.
 XX AC AAQ26331;
 XX DT 25-MAR-2003 (updated)
 XX DT 04-JAN-1993 (first entry)
 XX DE HLA-DR beta sub-type tailed probe DRB229 hybridising region.
 XX KW Tissue typing; identity determination; disease susceptible; ss.
 XX OS Synthetic.
 XX PN WO9210589-A1.
 XX PD 25-JUN-1992.
 XX PF 06-DEC-1991; 91WO-US09294.
 XX PR 06-DEC-1990; 90US-0623098.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Apple RJ, Begovich AB, Bugawan T, Erlich HA, Griffith RL;
 XX PI Scharf SJ;
 XX PD 25-JUN-1992.
 XX PF 06-DEC-1991; 91WO-US09294.
 XX PR 06-DEC-1990; 90US-0623098.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Apple RJ, Begovich AB, Bugawan T, Erlich HA, Griffith RL;
 XX PI Scharf SJ;

DR WPI; 1992-234644/28.
 XX Method for determining HLA-DR beta sub-type in DNA sample -
 XX PT comprises amplification and hybridisation with probes and
 XX PT primers, useful in tissue typing
 XX PS Example; Page 43; 90pp; English.
 XX CC The sequence is that of the hybridising region of tailed probe DRB229
 CC for use in a method for determining HLA-DR beta sub-type in a nucleic
 CC acid sample. The method allows specific nucleic acid sequences of the
 CC second exon of HLA-DR beta genes to be amplified then probed for
 CC identification of polymorphic sequences. The amplified DNA is useful for
 CC typing homozygous or heterozygous samples from a variety of sources and
 CC for detecting allelic variants not distinguishable by serological
 CC methods. The typing system can be used in a reverse dot blot format which
 CC is simple and rapid to perform, produces detectable signals in minutes
 CC and can be utilised in tissue typing, determination of individual
 CC identity and identifying disease susceptible individuals.
 CC See also AAQ26092-Q26367.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 452 TGCCTTCCAGGAG 465
 Db 15 TGCTTCCAGGAG 2
 RESULT 1600
 AAQ47606/c
 ID AAQ47606 standard; cDNA to mRNA; 17 BP.
 XX AC AAQ47606;
 XX DT 25-MAR-2003 (updated)
 XX DT 26-JAN-1994 (first entry)
 XX DE Human D HUMJUNDR/C2147 c-jun specific probe.
 XX KW Probe; quantification; human; GTP binding protein; G protein;
 KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
 KW pathophysiology; disease state; hereditary; cancer; infectious;
 KW osteodystrophy; pituitary tumour; acromegaly; melanoma cells;
 KW diabetes; PCR; polymerase chain reaction; ss.
 XX OS Synthetic.
 XX PN WO9315221-A1.
 XX PD 05-AUG-1993.
 XX PF 29-JAN-1993; 93WO-US00977.
 XX PR 29-JAN-1992; 92US-0827208.
 XX PR 24-MAR-1992; 92US-0857059.
 XX PR 12-NOV-1992; 92US-0974409.
 XX PA (HITB) HITACHI CHEM CO LTD.
 XX PA (HITB) HITACHI CHEM RES CENT INC.
 XX PI Akitaya T, Cooper A, Mitsuhashi M;
 XX DR WPI; 1993-258695/32.
 XX PT Quantitating messenger RNA in sample - using immobilised-poly-
 XX PT nucleotide having sequence complementary to sequence unique to
 XX PT the mRNA

PS Example 9; Page 72; 177pp; English.

XX The sequences given in AA047605-11 show regions of homology between
CC jun sequences and the c-jun specific probe C2147 which may be of
CC use as c-jun specific probes. They were used in the method of the
CC invention for the detection and quantification of mRNAs in a sample
CC without the need to purify the mRNA from cells. The claimed method
CC comprises identifying a polynucleotide sequence unique to the mRNA,
CC and immobilising an oligomer complementary to this sequence to an
CC insoluble support. The sample is then incubated with the insoluble
CC support such that the unique sequence will hybridise to the bound
CC oligomer and be immobilised. Non-immobilised components are washed
CC from the support and bound RNA is labelled in such a way that the
CC label is incorporated onto the support relative to the amount of
CC mRNA on the support. The amount of bound label is then determined.
CC This method can be used for the reliable, rapid, simultaneous
CC quantification of multiple varieties of mRNA. It may be used for
CC diagnosing and recognition of pathophysiology of various disease
CC states, eg. hereditary diseases, cancer, and infectious diseases.
CC G proteins are thought to be involved in causing various disease
CC states. A genetic deficiency of Gs protein is the molecular basis of
CC hereditary osteodystrophy. Pituitary tumours in acromegalic patients
CC have been shown to contain mutant Gs proteins. G proteins are also
CC involved in invasive and metastatic melanoma cells, and diabetes.
CC See also AA047381-666.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 411 CAGCAGGCTCG 424
DB 17 CAGCAGGCTCG 4

RESULT 1601

AAW71613/C
ID AAX71613 standard; RNA; 17 BP.

AC AAX71613;

DT 28-JUL-1999 (first entry)

DE Human KDR VEGF receptor hammerhead ribozyme substrate #625.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW fetal liver kinase 1; ss.

OS Homo sapiens.

PN WO9715662-A2.

XX 01-MAY-1997.

PF 25-OCT-1996; 96WO-US17480.

PR 11-JAN-1996; 96US-0584040.

XX 26-OCT-1995; 95US-0005974.

PA (CHIR) CHIRON CORP.

XX (RIBO-) RIBOZYME PHARM INC.

PI Escobedo J, McSwiggan J, Pavco P, Stinchcomb D;

XX WPI; 1997-259017/23.

PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or

PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient

PS Claim 4; Page 116; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or fetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.

XX Sequence 17 BP; 4 A; 6 C; 3 G; 4 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1000 TCAGGCTGGAGAT 1013

DB 17 TCAGGCTGGAGAT 4

RESULT 1602

AAV14179/C

ID AAV14179 standard; DNA; 17 BP.

AC AAV14179;

DT 19-MAY-1998 (first entry)

DE Probe HBPr50 for genotype specific target of HBV.

XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KW mutation detection; ss.

OS Synthetic.

XX Hepatitis b virus.

PN WO9740193-A2.

XX 30-OCT-1997.

XX 21-APR-1997; 97WO-EP02002.

PR 19-APR-1996; 96EP-0870053.

XX (INNO-) INNOGENETICS NV.

XX Maertens G, Rossau R, Stuyver L;

XX WPI; 1997-535867/49.

PT Detection and/or genetic analysis of hepatitis B virus -
PT specifically genotype, preCore mutations, vaccine escape mutations
PT and RT gene mutations selected by treatment with drugs

PS Claim 5; Page 27; 80pp; English.

XX This sequence is a probe for a genotype specific target of hepatitis
CC b virus (HBV). This sequence can be used in the method of the invention
CC for detection and/or genetic analysis of hepatitis B virus (HBV) in a
CC sample. The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to known locations on a solid
CC support and hybridise specifically to mutant target sequences chosen from

CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and
 CC RT gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir.

SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 208 GTTCCCAAGCCCTCT 221
 Db 17 GTTCCCAAGCCCTCT 4

RESULT 1603
 AAV97635/c
 ID AAV97635 standard; RNA; 17 BP.

AC AAV97635;

DT 17-MAR-1999 (first entry)

DE Human EGF-R target sequence nucleotide position 3560.

KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.

OS Homo sapiens.

PN WO9833893-A2.

PD 06-AUG-1998.

PF 14-JAN-1998; 98WO-US00730.

PR 04-DEC-1997; 97US-0985162.

PR 31-JAN-1997; 97US-0036476.

PA (RIBO-) RIBOZYME PHARM INC.
 PA (UYAS-) UNIV ASTON.

PI Akhtar S, Fell P, McSwiggen JA;

PI WPI; 1998-437449/37.

PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and
 PT for treating cancers

PS Claim 5; Page 76; 109pp; English.

CC The present invention describes enzymatic nucleic acid molecules (NAMs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell.

SQ Sequence 17 BP; 5 A; 9 C; 2 G; 1 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 813 CCTGGTACTGTGGG 826
 Db 14 CCTGGTACTGTGGG 1

RESULT 1604

AAV95304

ID AAV95304 standard; RNA; 17 BP.

AC AAV95304;

DT 24-FEB-1999 (first entry)

DE Human c-fos target sequence nucleotide position 356.

KW Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;
 KW cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
 KW mutation; diseased cell; ss.

OS Homo sapiens.

PN WO9832846-A2.

PD 30-JUL-1998.

PF 20-JAN-1998; 98WO-US01017.

PR 23-JAN-1997; 97US-0037658.

PA (RIBO-) RIBOZYME PHARM INC.

PI Jarvis T, McSwiggen JA, Stinchcomb DT;

PI WPI; 1998-427942/36.

PT Enzymatic nucleic acid molecules which specifically cleave RNA
 PT derived from a c-fos gene - useful for treating conditions related
 PT to levels of c-fos, especially cancer

PS Claim 2; Page 50; 72pp; English.

CC The present invention describes an enzymatic nucleic acid molecule which
 CC specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540
 CC and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
 CC ribozymes, respectively, which specifically cleave human c-fos. AAV95261
 CC to AAV95400 and AAV95585 to AAV95628 represent human c-fos target
 CC sequences. The enzymatic nucleic acid molecules can be used for treating
 CC cancer associated with elevated levels of c-fos oncogene, especially
 CC leukaemias, neuroblastomas and lung, breast and colon cancers. The
 CC ribozymes may also be used as diagnostic tools to examine genetic drift
 CC and mutations within diseased cells, or to detect the presence of c-fos
 CC RNA in a cell.

SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 78.6%; Pred. No. 1.1e+03;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 615 GCCATCTCAACCAG 628
 Db 4 GCCAUCUCGACCAG 17

RESULT 1605

AAV95305

ID AAV95305 standard; RNA; 17 BP.

AC AAV95305;

XX DT 24-FEB-1999 (first entry)
 XX DE Human c-fos target sequence nucleotide position 358.
 XX KW Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;
 XX KW cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
 XX KW mutation; diseased cell; ss.
 XX OS Homo sapiens.
 XX PN WO9832846-A2.
 XX PD 30-JUL-1998.
 XX PF 20-JAN-1998; 98WO-US01017.
 XX PR 23-JAN-1997; 97US-0037658.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Jarvis T, McSwiggen JA, Stinchcomb DT;
 XX WPI; 1998-427942/36.
 XX PT Enzymatic nucleic acid molecules which specifically cleave RNA
 XX PT derived from a c-fos gene - useful for treating conditions related
 XX PT to levels of c-fos, especially cancer
 XX PS Claim 2; Page 50; 72pp; English.
 XX CC The present invention describes an enzymatic nucleic acid molecule which
 XX CC specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540
 XX CC and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
 XX CC ribozymes, respectively, which specifically cleave human c-fos. AAV95261
 XX CC to AAV95400 and AAV95585 to AAV95628 represent human c-fos target
 XX CC sequences. The enzymatic nucleic acid molecules can be used for treating
 XX CC cancer associated with elevated levels of c-fos oncogene, especially
 XX CC leukaemias, neuroblastomas and lung, breast and colon cancers. The
 XX CC ribozymes may also be used as diagnostic tools to examine genetic drift
 XX CC and mutations within diseased cells, or to detect the presence of c-fos
 XX CC RNA in a cell.
 XX SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 78.6%; Pred. No. 1.1e+03;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 615 GCCATCTCAACGAG 628
 ||||:|:|
 Db 2 GCCAUCUGGACGAG 15
 RESULT 1606
 AAV96425
 ID AAV96425 standard; RNA; 17 BP.
 XX AC AAV96425;
 XX DT 01-MAR-1999 (first entry)
 XX DE Potato citrate synthase target sequence position 207.
 XX KW Solanidine; glucosyltransferase; potato; citrate synthase; target;
 XX KW hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
 XX KW flower formation; cleavage; solanaceous plant; ss.
 XX OS Solanum tuberosum.
 XX PN WO9832843-A2.
 XX PD 30-JUL-1998.

XX PF 14-JAN-1998; 98WO-US00738.
 XX PR 24-NOV-1997; 97US-0979416.
 XX PR 28-JAN-1997; 97US-0036545.
 XX PR 28-JAN-1997; 97US-0036599.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI McSwiggen JA, Zwick MG;
 XX WPI; 1998-427939/36.
 XX PR New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid
 XX PT biosynthesis or regulating flowering
 XX PS Claim 53; Page 52; 79pp; English.
 XX CC The present invention describes enzymatic nucleic acid molecules with
 XX CC RNA-cleaving activity (e.g. ribozymes) which are capable of modulating
 XX CC the expression of plant genes: (i) involved in biosynthesis of
 XX CC alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334,
 XX CC and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase
 XX CC hammerhead and hairpin ribozymes, respectively. AAV95829 to AAV95981,
 XX CC and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase
 XX CC target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195
 XX CC represent potato citrate synthase hammerhead and hairpin ribozymes,
 XX CC respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent
 XX CC potato citrate synthase target sequences. Ribozymes of the present
 XX CC invention can be used to inhibit the synthesis of toxic alkaloids in
 XX CC solanaceous plants, particularly potato but also tomato, pepper,
 XX CC aubergine and dicura or to inhibit flowering in potato, lettuce, spinach,
 XX CC cabbage, brussels sprouts, arugula, kale, collards, chard, beet, turnip,
 XX CC sweet potato and turf grass. Also the ribozymes can be used for RNA
 XX CC manipulation in the same way that restriction endonucleases are for DNA,
 XX CC as well as to examine genetic drift and mutations in plants and to
 XX CC detect specific RNA. The ribozymes can be targeted to specific genes or
 XX CC to consensus sequences within a family of related genes, and being
 XX CC catalytic need to be present at only very low concentrations.
 XX SQ Sequence 17 BP; 6 A; 2 C; 5 G; 4 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 78.6%; Pred. No. 1.1e+03;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 833 AGCTGGTACACGAA 846
 ||||:|:|
 Db 2 AGCUGGUACAAGAA 15
 RESULT 1607
 AAV48869
 ID AAV48869 standard; DNA; 17 BP.
 XX AC AAV48869;
 XX DT 15-OCT-1998 (first entry)
 XX DE ErBB-2 gene antisense oligonucleotide ErBB-2-N-78.
 XX KW ErBB-2; antisense oligonucleotide; modulate; gene expression; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN EP856579-A1.
 XX PD 05-AUG-1998.
 XX PF 31-JAN-1997; 97EP-0101531.
 XX PR 31-JAN-1997; 97EP-0101531.

XX PA (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.
XX PI Brysch W, Schlingensiepen K;
XX DR WPI; 1998-400910/35.
XX PT Preparation of antisense oligonucleotide(s) which lack long runs of
XX PT consecutive guanosine or inosine - and have specific ratio of
XX PT residues able to form two or three hydrogen bonds, have greater
XX PT activity and reduced toxicity, used therapeutically or to modulate
XX PT growth of cells in culture
XX PS Example 4; Fig 6d; 286pp; English.
XX CC AAV48709-886 represent antisense oligonucleotides directed against the
XX CC ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted
XX CC in significant reduction in ErbB-2 protein expression, while
XX CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
XX CC exemplify the invention. The specification describes oligonucleotides
XX CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
XX CC can each form three hydrogen bonds to cytosine; do not contain four
XX CC consecutive nucleotides able to form three H-bonds each to four
XX CC consecutive cytosines; do not contain two sequences of three consecutive
XX CC nucleotides each able to form three H-bonds to three consecutive
XX CC cytosines, and the ratio between residues able to form two H-bonds each
XX CC (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The
XX CC oligonucleotides are used to modulate expression of genes, particularly
XX CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
XX CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
XX CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
XX CC oligonucleotides can also be used to analyse function of proteins (by
XX CC altering their expression or activity) and therapeutically, e.g. in
XX CC cases of cancer or (targeting TGF) for stimulating the immune system.
XX SQ Sequence 17 BP; 11 A; 3 C; 0 G; 3 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTTAAAAAATAAAA 1095
DB 3 TTTAAAAAATAAAA 16

RESULT 1608
AAV20388/c
ID AAA20388 standard; RNA; 17 BP.
AC AAA20388;
XX 19-JUN-2000 (first entry)
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3614.
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
XX tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
XX WO9950403-A2.
XX 07-OCT-1999.
XX 24-MAR-1999; 99WO-US06507.

XX PR 27-MAR-1998; 98US-0079678.
XX XX (RIBO-) RIBOZYME PHARM INC.
XX PA Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX WPI; 1999-591315/50.
XX PT Novel ribozymes for modulating the synthesis, expression and/or
XX PT stability of an mRNA encoding an angiogenic factors
XX PS Claim 55; Page 142; 305pp; English.
XX CC The present invention describes enzymatic cleavage of nucleic acid molecules with
XX CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
XX CC hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3
XX CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA21688 represent their corresponding target sequences;
XX CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
XX CC for integrin subunit beta 3, and AAA22476 to AAA23282, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX CC the invention are used for modulating the synthesis, expression and/or
XX CC stability of an mRNA encoding angiogenic factor, especially ARNT,
XX CC especially used to treat cancer, diabetic retinopathy, age related
XX CC macular degeneration (ARMD), inflammation, and arthritis, as well as
XX CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX CC angioblastoma of tuberculous sclerosis, pot-wine stains, Sturge Weber
XX CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX CC integrin subunit alpha-6, or integrin subunit beta-3.
XX SQ Sequence 17 BP; 0 A; 4 C; 8 G; 5 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACGAGCCACAGCC 15
DB 16 CACGAGCCACAGCC 3

RESULT 1609
AAV91019
ID AAV91019 standard; RNA; 17 BP.
XX AC AAV91019;
XX 18-FEB-1999 (first entry)
XX Human C-raf target site nucleotide position 644.
XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene;
XX delivery; screening; identification; synthesis; deprotection;
XX purification; cancer; inflammation; psoriasis; non-hepatic ascites;
XX infection; genetic drift; restenosis; rheumatoid arthritis; ss.
XX Homo sapiens.
XX WO9850530-A2.
XX 12-NOV-1998.


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PF 05-MAY-1998; 98WO-US09249.
XX 19-DEC-1997; 97US-0068212.
PR 09-MAY-1997; 97US-0046059.
PR 09-JUN-1997; 97US-0049002.
PR 03-JUL-1997; 97US-0051718.
PR 22-AUG-1997; 97US-0056808.
PR 02-OCT-1997; 97US-0061321.
PR 02-OCT-1997; 97US-0061324.
PR 05-NOV-1997; 97US-0064866.
XX (RIBO-) RIBOZYME PHARM INC.
XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
PI Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
XX WPI; 1999-009494/01.
XX Identifying new catalytic nucleic acid that modulates selected
PT processes - especially ribozymes that cleave Raf RNA for treating
PT cancer, restenosis, and also new ribozymes and modified nucleoside
PT triphosphates used as antiviral agents and synthons
XX Claim 177; Page 147; 259pp; English.
XX A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules
CC with endonuclease activity and catalytic activity, from the present
CC invention, are used to modulate gene expression in plant and mammalian
CC cells and to cleave target nucleic acid, particularly for treating
CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
CC psoriasis, non-hepatic ascites and infection. They may also be used to
CC detect genetic drift and mutations in diseased cells and to determine
CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
CC expression of the Raf gene, are used to treat cancer, restenosis,
CC psoriasis or rheumatoid arthritis, or generally any condition associated
CC with the level of c-raf. Introduction of sugar/phosphate modifications
CC increases stability against nuclease and activity. AAV90922 to AAV93877
CC represent NACs that can be used in the method, specifically for
CC modulating the expression of a Raf gene.
XX Sequence 17 BP; 6 A; 4 C; 2 G; 5 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 716 CAAATTTTCAGGAGC 729
DB 4 CAAAUUUCAGAGC 17

RESULT 1610
AAV91020
ID AAV91020 standard; RNA; 17 BP.
XX AAV91020;
AC AAV91020;
XX Human C-raf target site nucleotide position 645.
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene;
XX delivery; screening; identification; synthesis; deprotection;
XX purification; cancer; inflammation; psoriasis; non-hepatic ascites;
XX infection; genetic drift; restenosis; rheumatoid arthritis; ss.

PF 05-MAY-1998; 98WO-US09249.
XX 19-DEC-1997; 97US-0068212.
PR 09-MAY-1997; 97US-0046059.
PR 09-JUN-1997; 97US-0049002.
PR 03-JUL-1997; 97US-0051718.
PR 22-AUG-1997; 97US-0056808.
PR 02-OCT-1997; 97US-0061321.
PR 02-OCT-1997; 97US-0061324.
PR 05-NOV-1997; 97US-0064866.
XX (RIBO-) RIBOZYME PHARM INC.
XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
PI Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
XX WPI; 1999-009494/01.
XX Identifying new catalytic nucleic acid that modulates selected
PT processes - especially ribozymes that cleave Raf RNA for treating
PT cancer, restenosis, and also new ribozymes and modified nucleoside
PT triphosphates used as antiviral agents and synthons
XX Claim 177; Page 147; 259pp; English.
XX A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules
CC with endonuclease activity and catalytic activity, from the present
CC invention, are used to modulate gene expression in plant and mammalian
CC cells and to cleave target nucleic acid, particularly for treating
CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
CC psoriasis, non-hepatic ascites and infection. They may also be used to
CC detect genetic drift and mutations in diseased cells and to determine
CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
CC expression of the Raf gene, are used to treat cancer, restenosis,
CC psoriasis or rheumatoid arthritis, or generally any condition associated
CC with the level of c-raf. Introduction of sugar/phosphate modifications
CC increases stability against nuclease and activity. AAV90922 to AAV93877
CC represent NACs that can be used in the method, specifically for
CC modulating the expression of a Raf gene.
XX Sequence 17 BP; 6 A; 4 C; 2 G; 5 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 716 CAAATTTTCAGGAGC 729
DB 4 CAAAUUUCAGAGC 17

RESULT 1610
AAV91020
ID AAV91020 standard; RNA; 17 BP.
XX AAV91020;
AC AAV91020;
XX Human C-raf target site nucleotide position 645.
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene;
XX delivery; screening; identification; synthesis; deprotection;
XX purification; cancer; inflammation; psoriasis; non-hepatic ascites;
XX infection; genetic drift; restenosis; rheumatoid arthritis; ss.

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DE Human C-raf target site nucleotide position 646.
 XX Human: c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene;
 KW delivery; screening; identification; synthesis; deprotection;
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.
 XX Homo sapiens.
 XX
 XX WO9850530-A2.
 XX 12-NOV-1998.
 XX 05-MAY-1998; 98WO-US09249.
 XX 19-DEC-1997; 97US-0068212.
 XX 03-MAY-1997; 97US-0046059.
 XX 09-JUN-1997; 97US-0049002.
 XX 03-JUL-1997; 97US-0051718.
 XX 22-AUG-1997; 97US-0056808.
 XX 02-OCT-1997; 97US-0061321.
 XX 02-OCT-1997; 97US-0061324.
 XX 05-NOV-1997; 97US-0064866.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
 PI Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
 XX WPI; 1999-009494/01.
 XX Identifying new catalytic nucleic acid that modulates selected
 PT processes - especially ribozymes that cleave Raf RNA for treating
 PT cancer, restenosis, and also new ribozymes and modified nucleoside
 PT triphosphates used as antiviral agents and synthons
 XX
 PS Claim 177; Page 147; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD) comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules
 CC with endonuclease activity and catalytic activity, from the present
 CC invention, are used to modulate gene expression in plant and mammalian
 CC cells and to cleave target nucleic acid, particularly for treating
 CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
 CC psoriasis, non-hepatic ascites and infection. They may also be used to
 CC detect genetic drift and mutations in diseased cells and to determine
 CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
 CC expression of the Raf gene, are used to treat cancer, restenosis,
 CC psoriasis or rheumatoid arthritis, or generally any condition associated
 CC with the level of c-raf. Introduction of sugar/phosphate modifications
 CC increases stability against nuclease and activity. AAV90922 to AAV93877
 CC represent NACs that can be used in the method, specifically for
 CC modulating the expression of a Raf gene.
 XX
 SQ Sequence 17 BP; 7 A; 4 C; 2 G; 4 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 716 CAAATTTCAGGAGC 729
 DB 2 CAAAUUUCAGGAGC 15
 RESULT 1612

AAC66363/c
 ID AAC66363 standard; DNA; 17 BP.
 XX
 AC AAC66363;
 XX
 DT 22-FEB-2001 (first entry)
 XX
 DE PCR primer used to amplify B. pertussis S1 DNA.
 XX
 KW Protection; pathogen infection; vaccination; immunisation; poliovirus;
 KW Bordetella pertussis; respiratory syncytial virus; Mycoplasma pneumoniae;
 KW meningococcus; pneumococcus; rotavirus; influenza; parainfluenza;
 KW Corynebacterium diphtheriae; Clostridium tetani; hepatitis B virus;
 KW Chlamydia pneumoniae; Chlamydia trachomatis; Moraxella catarrhalis;
 KW PCR primer; ss.
 XX
 OS Bordetella pertussis.
 XX WO200064457-A1.
 XX 02-NOV-2000.
 XX 21-APR-2000; 2000WO-US10954.
 XX 23-APR-1999; 99US-0298135.
 XX (UYDA-) UNIV DALHOUSIE.
 XX Lee SF, Halperin SA;
 XX WPI; 2000-687261/67.
 XX
 CC Composition having genetically modified live oral commensal bacteria
 PT which express immunogenic fragments of mucosal pathogens, used as oral
 PT vaccines to treat host against Bordetella pertussis, poliovirus
 PT infection -
 XX
 PS Example 1; Page 25; 52pp; English.
 XX
 CC A composition for stimulating protection against infection by a pathogen,
 CC comprises a live commensal oral organism genetically modified to express
 CC multiple immunogenic fragments of the pathogen. The composition has
 CC antibacterial and antiviral activity and acts as a vaccine. The
 CC composition which is administered orally or intranasally, is used for
 CC prophylactically treating a host against infection by a pathogen such as
 CC Bordetella pertussis, respiratory syncytial virus, poliovirus, Mycoplasma
 CC pneumoniae, meningococcus, pneumococcus, rotavirus, influenza,
 CC parainfluenza, Corynebacterium diphtheriae, Clostridium tetani, hepatitis
 CC B virus, Neisseria gonorrhoeae non-typeable Haemophilus influenzae
 CC Chlamydia pneumoniae, Chlamydia trachomatis, Moraxella catarrhalis, or
 CC their combinations. The composition can also be used for chronic
 CC immunisation of a host against infection by a pathogen. The present
 CC sequence represents a PCR primer used to amplify a Bordetella pertussis
 CC DNA sequence, which is used in an example illustrating the use of the
 CC composition of the invention.
 XX
 SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 597 CGGTGGCGGGTGA 610
 DB 16 CGGTGGCGGGAGGA 3
 RESULT 1613
 AAF02281
 ID AAF02281 standard; DNA; 17 BP.
 XX
 XX AAF02281;
 AC
 XX

DT 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #576.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO200061729-A2.
 PN 19-OCT-2000.
 PD 11-APR-2000; 2000WO-US09721.
 XX 12-APR-1999; 99US-0129390.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, McSwiggen J;
 PI WPI; 2000-647423/62.
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX Claim 37; Page 69; 164pp; English.
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX Sequence 17 BP; 3 A; 9 C; 3 G; 2 T; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 213 CAGCCCTCTCCAGA 226
 DB 2 CCGCCCTCTCCAGA 15
 RESULT 1614
 AAF02453
 ID AAF02453 standard; DNA; 17 BP.
 XX AC AAF02453;
 XX 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #748.
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO200061729-A2.
 PN 19-OCT-2000.
 PD 11-APR-2000; 2000WO-US09721.
 XX 12-APR-1999; 99US-0129390.
 XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX Claim 37; Page 73; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX Sequence 17 BP; 4 A; 3 C; 3 G; 7 T; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 433 CTGCTAGTCTAAAG 446
 DB 4 CTGCTAGTCTTAAG 17
 RESULT 1615
 AAF02454
 ID AAF02454 standard; DNA; 17 BP.
 XX AC AAF02454;
 XX 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #749.
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO200061729-A2.
 PN 19-OCT-2000.
 PD 11-APR-2000; 2000WO-US09721.
 XX 12-APR-1999; 99US-0129390.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, McSwiggen J;
 PI WPI; 2000-647423/62.
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX Claim 37; Page 73; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor

```

CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 other;

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 433 CTGCTAGTCTTAAG 446
Db 1 CTGCTAGTCTTAAG 14

RESULT 1616
AAFO2692
ID AAF02692 standard; DNA; 17 BP.
XX
AC AAF02692;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #987.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
useful for producing e.g. granulocyte colony stimulating factor
protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 78; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
molecules that act as inhibitors of the expression of repressor genes
encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
transcription factor gene, IRF-2 and/or the CAAT Displacement
Protein (CDP). Inhibition of the repressors removes prevents
inhibition (and consequently increases expression of) genes involved in
the production of erythropoietin, granulocyte colony stimulating factor
protein and interferon alpha.
XX
SQ Sequence 17 BP; 8 A; 2 C; 4 G; 3 T; 0 other;

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 287 GAACTTGTAAGTCG 300
Db 3 GAACTTGTAAGTCG 16

RESULT 1617
AAFO3223/c
ID AAF03223 standard; DNA; 17 BP.
XX
AC AAF03223;

```

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XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1518.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
useful for producing e.g. granulocyte colony stimulating factor
protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 90; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
molecules that act as inhibitors of the expression of repressor genes
encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
transcription factor gene, IRF-2 and/or the CAAT Displacement
Protein (CDP). Inhibition of the repressors removes prevents
inhibition (and consequently increases expression of) genes involved in
the production of erythropoietin, granulocyte colony stimulating factor
protein and interferon alpha.
XX
SQ Sequence 17 BP; 4 A; 0 C; 1 G; 12 T; 0 other;

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAAATAAAAA 1095
Db 17 TTCAAAAAAATAAAAA 4

RESULT 1618
AAFO6312/c
ID AAF06312 standard; DNA; 17 BP.
XX
AC AAF06312;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #3109.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX

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PA (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, McSwiggen J;
 PI WPI; 2000-647423/62.
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 XX useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 PT Claim 42; Page 127; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX Sequence 17 BP; 3 A; 1 C; 1 G; 12 U; 0 Other;
 SQ

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1096
 DB 17 TAAAAAATAAAAAA 4

RESULT 1619
 AAF06313/c
 ID AAF06313 standard; DNA; 17 BP.
 XX
 AC AAF06313;
 XX
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #3110.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 OS
 XX WO200061729-A2.
 PN
 XX 19-OCT-2000.
 PD
 XX 11-APR-2000; 2000WO-US09721.
 PF
 XX 12-APR-1999; 99US-0129390.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Zwick M, Pavco P, McSwiggen J;
 PI WPI; 2000-647423/62.
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 XX useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 PT Claim 42; Page 127; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in

CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX Sequence 17 BP; 2 A; 1 C; 1 G; 13 U; 0 Other;
 SQ

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1096
 DB 16 TAAAAAATAAAAAA 3

RESULT 1620
 AAA46231
 ID AAA46231 standard; DNA; 17 BP.
 XX
 AC AAA46231;
 XX
 DT 04-SEP-2000 (first entry)
 DE Primer IPM7F for interphotoreceptor matrix proteoglycan IPM150 cDNA.
 XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPW200;
 KW chromosome 6q13-q15; ocular disease; retinal detachment;
 KW choriorretinal degeneration; retinal degeneration; cone degeneration;
 KW age related macular degeneration; photoreceptor degeneration;
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis; rod-
 KW cone dystrophy; cone-rod dystrophy; PCR primer; ss.
 XX Unidentified.
 OS
 XX WO200026367-A2.
 PN
 XX 11-MAY-2000.
 PD
 XX 29-OCT-1999; 99WO-US25440.
 PF
 XX 29-OCT-1998; 98US-0183972.
 PR (IOWA) UNIV IOWA RES FOUND.
 PA Hageman GS, Kuehn MH;
 PI WPI; 2000-365616/31.
 DR Nucleic acids encoding interphotoreceptor matrix proteoglycans useful
 XX for preventing, diagnosing and treating ocular disorders such as
 PT retinal detachment and chorioretinal degeneration -
 PT Claim 43; Page 44; 183pp; English.
 PS
 XX PCR primers AAA46209-42 were used to amplify cDNA encoding an
 CC interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The
 CC protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150
 CC and IPM200, exist. The human IPM150 gene is located on chromosome
 CC 6q13-q15, between markers CHLC.GAT11F10 and B6S284. The IPM proteins
 CC may be used to supplement a patient's own production of the protein or
 CC to rectify alterations in their nucleic acids that result in
 CC expression of an inactive protein. The IPM nucleic acids may be used
 CC in this way to treat ocular diseases such as retinal detachment,
 CC choriorretinal degeneration, retinal degeneration, age related macular
 CC degeneration, photoreceptor degeneration, RPE (retinal pigment
 CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis,
 CC rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and
 CC proteins may also be used to assay for other modulators of IPM
 CC proteoglycan expression and activity that may be used to treat ocular
 CC diseases. The nucleic acids and proteins may also be used as diagnostic
 CC reagents to detect the presence of IPM nucleic acids and their products
 CC in samples from patients according to standard methodologies.
 XX Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 Other;
 SQ

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. NO. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 329 AGCTGTGGAGCAAC 342
 ||||| ||||| |||||
 Db 4 AGCTGTGGAGCAAC 17

RESULT 1621
 AAA36001
 ID AAA36001 standard; DNA; 17 BP.
 AC AAA36001;
 XX
 XX 26-JUL-2000 (first entry)
 XX
 DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:58.
 XX
 KW Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200018960-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US22283.
 XX
 PR 25-SEP-1998; 98US-0101757.
 XX
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA Landers JE, Jordan B, Housman DE, Charest A;
 PI WPI; 2000-293181/25.
 XX
 DR
 XX
 PT Detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs
 XX
 PS Disclosure; Page 55; 11pp; English.
 XX
 CC A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a
 CC SNP allele. The method can be used to characterise a tumour, to generate
 CC a genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be
 CC used to perform linkage analysis. AAA35944 to AAA35947 represent
 CC sequences used in the exemplification of the present invention. AAA35948
 CC to AAA36632 represent nucleotide sequences containing SNPs.
 XX
 SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. NO. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 831 GAAGCTGGTACCAG 844
 ||||| ||||| |||||
 Db 2 GAAGTGGTACCAG 15

RESULT 1622
 AAZ24112/C

ID AAZ24112 standard; DNA; 17 BP.
 XX
 AC AAZ24112;
 XX
 DT 03-FEB-2000 (first entry)
 XX
 DE Human frataxin gene PCR primer 1.
 XX
 KW Frataxin; human; diagnosis; arteriosclerosis; rheumatic disease; NIDDM;
 KW cardiovascular risk factor; soft rheumatism; diabetes mellitus type 2;
 KW Non-insulin dependent diabetes mellitus; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN DE19820201-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 06-MAY-1998; 98DE-1020201.
 XX
 PR 06-MAY-1998; 98DE-1020201.
 XX
 PA (KRON/) KRONE W.
 PA (MUEL/) MUELLER-WIELAND D.
 XX
 PI Krone W, Mueller-Wieland D;
 XX
 DR WPI; 2000-000421/01.
 XX
 PT Diagnostic test for cardiovascular risk factors and their complications
 XX
 PS Claim 5; Column 4; 8pp; German.
 XX
 CC This invention describes a novel diagnostic test to diagnose
 CC arteriosclerosis and its complications, for cardiovascular risk factors
 CC and rheumatic diseases, especially soft rheumatism, comprising
 CC characterizing the GAA-repeats of the frataxin gene. The risks and
 CC complications of arteriosclerosis are 5-times higher in diabetics than
 CC non-diabetics. The diagnostic test is used to predict cardiovascular risk
 CC factors and their complications for example in diabetes mellitus type 2
 CC (Non-insulin dependent diabetes mellitus, NIDDM). This sequence
 CC represents a PCR primer used in the amplification of the frataxin gene
 CC which is used in the method of the invention.
 XX
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. NO. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1013 TGGGAAGTGTAAAGC 1026
 ||||| ||||| |||||
 Db 15 TGGGAAGTGTAAAGC 2

RESULT 1623
 ABA79372
 ID ABA79372 standard; DNA; 17 BP.
 XX
 AC ABA79372;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Factor VIII mutation correcting oligonucleotide SEQ ID NO: 2218.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;

KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 KW antilepemic; ss.
 OS Homo sapiens.
 XX
 XX WO200173002-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO-US09761.
 XX
 XX 27-MAR-2000; 2000US-192176P.
 XX 27-MAR-2000; 2000US-192176P.
 XX 01-JUN-2000; 2000US-208538P.
 XX 30-OCT-2000; 2000US-244989P.
 XX
 XX (UYDE) UNIV DELAWARE.
 XX
 XX Kniec EB, Gampier HB, Rice MC;
 XX WPI; 2001-639230/73.
 XX
 XX Oligonucleotide for targeted alterations of genetic sequences and for
 XX treating cystic fibrosis, comprises at least one mismatch and chemical
 XX modification -
 XX
 XX Claim 7; Page 171; 294pp; English.
 XX
 XX The present invention provides single-stranded oligonucleotides which can
 XX be used for the targeted alteration of genomic sequences, where the
 XX oligonucleotide has at least one mismatch compared with the genomic
 XX sequence to be altered. In particular, these sequences are directed at
 XX the following genes: adenosine deaminase, p53, beta-globin,
 XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 XX various syndromes. The present sequence is one of the gene correcting
 XX oligonucleotides of the invention.
 XX
 XX Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 568 GATCCTCGTGCCT 581
 |||||
 Db 3 GATCCTCGTGCCT 16

RESULT 1624
 ABA79373/c
 ID ABA79373 standard; DNA; 17 BP.
 XX
 XX ABA79373;
 XX
 XX 24-JAN-2002 (first entry)
 XX
 XX Factor VIII mutation correcting oligonucleotide SEQ ID NO: 2219.
 XX
 XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;

KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 KW antilepemic; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200173002-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO-US09761.
 XX
 XX 27-MAR-2000; 2000US-192176P.
 XX 27-MAR-2000; 2000US-192176P.
 XX 01-JUN-2000; 2000US-208538P.
 XX 30-OCT-2000; 2000US-244989P.
 XX
 XX (UYDE) UNIV DELAWARE.

Kniec EB, Gampier HB, Rice MC;

WPI; 2001-639230/73.

Oligonucleotide for targeted alterations of genetic sequences and for
 treating cystic fibrosis, comprises at least one mismatch and chemical
 modification -

Claim 7; Page 171; 294pp; English.

The present invention provides single-stranded oligonucleotides which can
 be used for the targeted alteration of genomic sequences, where the
 oligonucleotide has at least one mismatch compared with the genomic
 sequence to be altered. In particular, these sequences are directed at
 the following genes: adenosine deaminase, p53, beta-globin,
 retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 various syndromes. The present sequence is one of the gene correcting
 oligonucleotides of the invention.

Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 GATCCTCGTGCCT 581
 |||||
 Db 15 GATCCTCGTGCCT 2

RESULT 1625
 AAH95047
 ID AAH95047 standard; RNA; 17 BP.
 XX
 XX AAH95047;
 XX

09-OCT-2001 (first entry)

Human Chk1 ribozyme substrate SEQ ID NO: 472.

Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 RNA cleavage; cancer; ss.
 XX
 XX Homo sapiens.

XX PN WO200157206-A2.
XX PD 09-AUG-2001.
XX PF 02-FEB-2001; 2001WO-US03504.
XX PR 03-FEB-2000; 2000US-0179983.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (FATT/) FATTAEY A R.
XX PI Fattaey AR, Jarvis T, McSwiggen J, Bocher RN, Holman PS;
XX WPI; 2001-496922/54.
XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT molecules, which downregulates expression of a checkpoint kinase-1
PT gene, useful for treating colorectal, lung, breast or prostate cancers
PT -
XX Claim 4; Page 62; 115pp; English.
XX The present invention provides nucleic acid molecules capable of
CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC gene. These may be antisense or ribozyme sequences, and are useful in the
CC treatment of diseases associated with conditions affected by Chk1 levels,
CC including cancer. The present sequence is an oligonucleotide described in
CC the exemplification of the invention.
XX Sequence 17 BP; 6 A; 6 C; 2 G; 3 U; 0 other;
XX Query Match 1.1%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 71.4%; Pred. No. 1.1e+03;
XX Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 983 CTCAGCCCTTGGAA 996
DB 2 CUCAACCCUUGGAA 15
RESULT 1626
AAH95048
ID AAH95048 standard; RNA; 17 BP.
XX AC AAH95048;
XX DT 09-OCT-2001 (first entry)
XX DE Human Chk1 ribozyme substrate SEQ ID NO: 473.
XX KW Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
XX KW RNA cleavage; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157206-A2.
XX PD 09-AUG-2001.
XX PF 02-FEB-2001; 2001WO-US03504.
XX PR 03-FEB-2000; 2000US-0179983.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (FATT/) FATTAEY A R.
XX PI Fattaey AR, Jarvis T, McSwiggen J, Bocher RN, Holman PS;
XX WPI; 2001-496922/54.
XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT molecules, which downregulates expression of a checkpoint kinase-1
PT gene, useful for treating colorectal, lung, breast or prostate cancers
PT -

PT Gene, useful for treating colorectal, lung, breast or prostate cancers
PT -
XX Claim 4; Page 62; 115pp; English.
XX The present invention provides nucleic acid molecules capable of
CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC gene. These may be antisense or ribozyme sequences, and are useful in the
CC treatment of diseases associated with conditions affected by Chk1 levels,
CC including cancer. The present sequence is an oligonucleotide described in
CC the exemplification of the invention.
XX Sequence 17 BP; 7 A; 5 C; 2 G; 3 U; 0 other;
XX Query Match 1.1%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 71.4%; Pred. No. 1.1e+03;
XX Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 983 CTCAGCCCTTGGAA 996
DB 1 CUCAACCCUUGGAA 14
RESULT 1627
AAH80144
ID AAH80144 standard; cDNA; 17 BP.
XX AC AAH80144;
XX DT 19-SEP-2001 (first entry)
XX DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 108.
XX KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX KW disease diagnosis; ss.
XX OS Oryctolagus cuniculus.
XX PN US6251588-B1.
XX PD 26-JUN-2001.
XX PF 10-FEB-1998; 98US-0021701.
XX PR 10-FEB-1998; 98US-0021701.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX WPI; 2001-424456/45.
XX Predicting the potential of an oligonucleotide to hybridize to a target
PT nucleotide sequence, useful for evaluating oligonucleotide probe
PT sequences, by identifying a oligonucleotides based on the evaluation of
PT parameters -
XX Example 1; Column 49; 342pp; English.
XX The present invention describes a method for predicting the potential of
CC an oligonucleotide to hybridize to a (complementary) target nucleotide
CC sequence, involving identifying a subset of oligonucleotides within the
CC predetermined number of unique oligonucleotides based on the evaluation
CC of the parameter. Oligonucleotides in the subset are identified that are
CC clustered along a region of the nucleotide sequence that is hybridisable
CC to the target nucleotide sequence. This is useful for evaluating
CC oligonucleotide probe sequences. The present sequence is an
CC oligonucleotide described in the exemplification of the invention.
XX Sequence 17 BP; 0 A; 2 C; 6 G; 9 T; 0 other;
XX Query Match 1.1%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 TGCTGCTTTGGG 146
 Db ||||| ||||| |||||
 4 TGCTGCTTTGGG 17

RESULT 1628
 ABK00420/c
 ID ABK00420 standard; RNA; 17 BP.
 XX
 AC ABK00420;
 XX
 DT 12-MAR-2002 (first entry)
 DE Human NOGO Hammerhead Ribozyme #420.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 PR 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 PS Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 72; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN
 CC motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinczyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell

CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is a hammerhead ribozyme of the invention.

SQ Sequence 17 BP; 4 A; 4 C; 4 G; 5 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 793 AACTGCAGGACTGA 806

Db ||||| ||||| |||||

17 AACTGCAGGACTGA 4

RESULT 1629

ABK02482

ID ABK02482 standard; RNA; 17 BP.

XX
 AC ABK02482;

DT 12-MAR-2002 (first entry)

XX
 DE Human NOGO Amberzyme #154.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX
 PN WO200159103-A2.

XX
 PD 16-AUG-2001.

XX
 PF 09-FEB-2001; 2001WO-US04273.

XX
 PR 11-FEB-2000; 2000US-181797P.

XX
 PR 28-FEB-2000; 2000US-185516P.

XX
 PR 06-MAR-2000; 2000US-187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, McSwiggen J, Chowrira BM;

XX

DR WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 134; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NAGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inzyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) pr an amberyne (cleaving RNA with an NGN triplet), a zinyne
 CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targetting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NAGO-targetting
 CC nucleic acid is used to cleave RNA of the NAGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NAGO activity of the cell and
 CC treat a patient having a condition associated with the level of NAGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NAGO-targetting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NAGO expression. The
 CC present sequence is an amberyne molecule of the invention.

XX
 SQ Sequence 17 BP; 5 A; 1 C; 8 G; 3 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 78.8%; Pred. No. 1.1e+03;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1008 GAGATGGGGAAGTG 1021
 |||||:|||||:
 Db 3 GAGUAGGGAAGUG 16

RESULT 1630
 ABV85120/c
 ID ABV85120 standard; DNA; 17 BP.
 XX
 AC ABV85120;
 XX
 DT 11-DEC-2002 (first entry)
 XX
 DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:113.
 XX
 KW Human; UDP-GalNAC:polypeptide N-acetylgalactosaminyltransferase 10;
 KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy;
 KW scanning; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN EF1243660-A2.
 XX
 PD 25-SEP-2002.

XX
 PF 25-JAN-2002; 2002EP-0001161.
 XX
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 30-AUG-2001; 2001US-315984P.
 XX
 PA (AEOM-) AEOMICA INC.

XX Zhang J, Gu Y, Nguyen C;

PI WPI; 2002-724954/79.

DR Nucleic acid encoding human UDP-GalNAC:polypeptide
 XX
 PT N-acetylgalactosaminyltransferase 10 protein is useful to diagnose,
 PT prevent and treat disorders associated with reduced or over expression
 PT of the encoded protein -
 XX

PS Example 2; SEQ ID 113; 59pp; English.

XX The present invention describes an isolated nucleic acid (I) encoding a
 CC human UDP-GalNAC:polypeptide N-acetylgalactosaminyltransferase 10
 CC (pp-GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
 CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
 CC present invention can be used in therapy, particularly to prevent or
 CC treat a disorder associated with decreased expression or activity of
 CC pp-GaNTase. The sequences given in ABV85011 to ABV8669 and ABP3502 to
 CC ABP3504 are given in the exemplification of the present invention.
 CC N.B. The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office.

XX Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 AGCCAGCTACCGCG 25

Db 17 AGCCGGCTACCGCG 4

RESULT 1631
 ABV85121/c
 ID ABV85121 standard; DNA; 17 BP.
 XX
 AC ABV85121;
 XX

DT 11-DEC-2002 (first entry)

XX Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:114.

XX Human; UDP-GalNAC:polypeptide N-acetylgalactosaminyltransferase 10;
 KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy;
 KW scanning; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN EF1243660-A2.
 XX
 PD 25-SEP-2002.

XX 25-JAN-2002; 2002EP-0001161.

PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 30-AUG-2001; 2001US-315984P.
 XX
 PA (ABOM-) AEOMICA INC.
 XX

Zhang J, Gu Y, Nguyen C;

WPI; 2002-724954/79.

PT Nucleic acid encoding human UDP-GalNAc:polypeptide

PT N-acetylgalactosaminyltransferase 10 protein is useful to diagnose,
 PT prevent and treat disorders associated with reduced or over expression
 PT of the encoded protein -

XX Example 2; SEQ ID 114; 59pp; English.

CC The present invention describes an isolated nucleic acid (I) encoding a
 CC human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10
 CC (pp-GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
 CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
 CC present invention can be used in therapy, particularly to prevent or
 CC treat a disorder associated with decreased expression or activity of
 CC pp-GaNTase. The sequences given in ABV85011 to ABV86689 and ABP3502 to
 CC ABP3504 are given in the exemplification of the present invention.
 CC N.B. The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office.

SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 ACCGAGCTACCGCG 25

Db 16 AGCGCGCTACCGCG 3

RESULT 1632

ID ABV85122/c

ABV85122 standard; DNA; 17 BP.

XX AC

XX ABV85122;

XX 11-DEC-2002 (first entry)

XX DT

XX DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:115.

XX KW Human; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10;

XX KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy;

XX KW scanning; ss.

XX XX Homo sapiens.

OS Synthetic.

XX PN EP1243660-A2.

XX PD 25-SEP-2002.

XX XX 25-JAN-2002; 2002EP-0001161.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 30-AUG-2001; 2001US-315984P.
 XX
 PA (ABOM-) AEOMICA INC.
 XX

Zhang J, Gu Y, Nguyen C;

WPI; 2002-724954/79.

PT Nucleic acid encoding human UDP-GalNAc:polypeptide

PT N-acetylgalactosaminyltransferase 10 protein is useful to diagnose,
 PT prevent and treat disorders associated with reduced or over expression
 PT of the encoded protein -

XX Example 2; SEQ ID 115; 59pp; English.

CC The present invention describes an isolated nucleic acid (I) encoding a
 CC human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10
 CC (pp-GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
 CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
 CC present invention can be used in therapy, particularly to prevent or
 CC treat a disorder associated with decreased expression or activity of
 CC pp-GaNTase. The sequences given in ABV85011 to ABV86689 and ABP3502 to
 CC ABP3504 are given in the exemplification of the present invention.
 CC N.B. The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office.

SQ Sequence 17 BP; 1 A; 6 C; 6 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 AGCGAGCTACCGCG 25

Db 15 AGCGCGCTACCGCG 2

RESULT 1633

ABV85123/c

ID ABV85123 standard; DNA; 17 BP.

XX AC

XX ABV85123;

XX 11-DEC-2002 (first entry)

XX DT

XX DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:116.

XX KW Human; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10;

XX KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy;

XX KW scanning; ss.

XX XX Homo sapiens.

OS Synthetic.

XX PN EP1243660-A2.

XX PD 25-SEP-2002.

XX XX 25-JAN-2002; 2002EP-0001161.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US00659.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 30-AUG-2001; 2001US-315984P.
 XX (ABOM-) ABOMICA INC.
 XX Zhang J, Gu Y, Nguyen C;
 XX WPI; 2002-724954/79.
 XX Nucleic acid encoding human UDP-GalNAc:polypeptide
 PT N-acetylgalactosaminyltransferase 10 protein is useful to diagnose,
 PT prevent and treat disorders associated with reduced or over expression
 PT of the encoded protein -
 XX Example 2; SEQ ID 116; 59pp; English.
 XX The present invention describes an isolated nucleic acid (I) encoding a
 CC human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10
 CC (pp-GANTase 10, EC 2.4.1.41) protein. Human pp-GANTase 10 is located to
 CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
 CC present invention can be used in therapy, particularly to prevent or
 CC treat a disorder associated with decreased expression or activity of
 CC pp-GANTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
 CC ABP53504 are given in the exemplification of the present invention.
 CC N.B. The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office.
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 7 G; 3 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 AGCCAGCTACCGCG 25
 Db 14 AGCCGGTACCGCG 1
 RESULT 1634
 ABQ99687/c
 ID ABQ99687 standard; DNA; 17 BP.
 XX AC ABQ99687;
 XX 08-NOV-2002 (first entry)
 DT
 DE Murine Ikbkap exon 27 acceptor site.
 XX
 KW Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.
 XX
 OS Mus sp.
 XX
 PN WO200259381-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 07-JAN-2002; 2002WO-US000473.
 XX
 PR 06-JAN-2001; 2001US-260080P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Slangenaupt S, Gusella JF;
 XX WPI; 2002-674806/72.
 XX
 XX New IKBKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes

PT or prenatal diagnosis -
 XX Disclosure; Fig 11; 109pp; English.
 XX
 CC The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
 CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
 CC are associated with FD. The mutation associated with the major haplotype
 CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
 CC patients, although they continue to express varying levels of wild-type
 CC message in a tissue-specific manner. The mutation associated with the
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
 CC This bp mutation causes an arginine to proline missense mutation (R696P)
 CC in the IKBKAP protein, which is predicted to disrupt a potential
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
 CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
 CC gene maps to chromosome 9q31. A mouse model of FD was created in an
 CC example from the invention. Expression of murine Ikbkap was examined
 CC using both mouse embryo and adult mouse multiple tissue Northern blots.
 CC The blots were probed with a 1045bp PCR fragment that contains exons 2
 CC through 11, which was generated using PCR primers ABQ80563-ABQ80564.
 CC ABQ99662-ABQ99733 are the murine Ikbkap exon and intron boundaries.
 XX
 SQ Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAAAAAATAAAAAA 1095
 Db 14 TGAATAAATAAAAAA 1
 RESULT 1635
 ABK55724
 ID ABK55724 standard; RNA; 17 BP.
 XX AC ABK55724;
 XX 02-JUL-2002 (first entry)
 DT
 DE Human CLCA1 gene enzymatic nucleic acid #95.
 XX
 KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX
 OS Homo sapiens.
 XX
 PN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US24970.
 XX
 PR 09-AUG-2000; 2000US-224383P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTAX USA LLC.
 PA (THOM/) THOMPSON J.
 XX
 PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX WPI; 2002-217145/27.
 DR
 XX

PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -

XX Claim 4; Page 54; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.

SQ Sequence 17 BP; 5 A; 5 C; 2 G; 5 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 660 CTCATGCGAGTCAA 673

DB 4 CUCAUUCAGCUGAA 17

RESULT 1636

ABK55725
ID ABK55725 standard; RNA; 17 BP.

AC ABK55725;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #96.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.

OS Homo sapiens.

PN WO200211674-A2.

PD 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US24970.

PR 09-AUG-2000; 2000US-224393P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;

DR WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -

XX
PS
XX

Claim 4; Page 54; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.

SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 660 CTCATGCGAGTCAA 673

DB 3 CUCAUUCAGCUGAA 16

RESULT 1637

ABK56266

ID ABK56266 standard; RNA; 17 BP.

AC ABK56266;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #637.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.

OS Homo sapiens.

PN WO200211674-A2.

PD 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US24970.

PR 09-AUG-2000; 2000US-224383P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;

DR WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -
XX Claim 4; Page 65; 152pp; English.

PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 7667; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 768 GAACTGGAGAGAA 781
Db |||||
4 GAGCTGGAGAGAA 17

RESULT 1640
ABN07679
ID ABN07679 standard; DNA; 17 BP.
XX
AC ABN07679;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7671.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN W0200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
XX 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.

PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX (AEOM-) AEOMICA INC.
PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption ionization, comprises human
PT myosin-like protein hGDMPLP-1 -
XX Disclosure; SEQ ID 7671; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMPLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMPLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMPLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 769 AACTGGAGAGAG 782
Db |||||
1 AGCTGGAGAGAG 14

RESULT 1641
ABN07800/c
ID ABN07800 standard; DNA; 17 BP.
XX
AC ABN07800;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7792.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN W0200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.

XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 05-FEB-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX (AEOM-) AEOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX Disclosure; SEQ ID 7792; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 825 GGTGCTGAAGCTGG 838
 Db 17 GCTGCTGAAGCTGG 4
 RESULT 1642
 ABN07801/c
 ID ABN07801 standard; DNA; 17 BP.
 XX AC ABN07801;
 XX AC ABN07801;
 XX 29-MAY-2002 (first entry)
 DT
 XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7793.
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 XX WO20012524-A2.
 PN 06-DEC-2001.
 XX 25-MAY-2001; 2001WO-US16981.
 XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 05-FEB-2001; 2001US-266860P.
 XX (AEOM-) AEOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX Disclosure; SEQ ID 7793; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 other;
 SQ
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 825 GGTGCTGAAGCTGG 838
 Db 17 GCTGCTGAAGCTGG 4
 RESULT 1642
 ABN07801/c
 ID ABN07801 standard; DNA; 17 BP.
 XX AC ABN07801;
 XX AC ABN07801;
 XX 29-MAY-2002 (first entry)
 DT
 XX

QY 825 GGTCGCTGAAGCTGG 838
 DB 16 GCTGCTGAAGCTGG 3

RESULT 1643
 ABN07802/c
 ID ABN07802 standard; DNA; 17 BP.
 XX
 AC ABN07802;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7794.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US16981.
 XX
 XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX
 XX (ABOM-) ABOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX
 PS Disclosure; SEQ ID 7794; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to

CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 825 GGTCGCTGAAGCTGG 838
 DB 15 GCTGCTGAAGCTGG 2

RESULT 1644
 ABN07803/c
 ID ABN07803 standard; DNA; 17 BP.
 XX
 AC ABN07803;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7795.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US16981.
 XX
 XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX
 XX (ABOM-) ABOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX
 PS Disclosure; SEQ ID 7795; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to

CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.

XX SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 825 GGTGCTGAAGCTGG 838

Db 14 GCTGCTGAAGCTGG 1

RESULT 1645

ABN08112/c

ID ABN08111 standard; DNA; 17 BP.

AC ABN08111;

XX 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8103.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US16981.

XX 26-MAY-2000; 2000US-207456P.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

XX 30-JAN-2001; 2001WO-US00661.

XX 30-JAN-2001; 2001WO-US00662.

XX 30-JAN-2001; 2001WO-US00663.

XX 30-JAN-2001; 2001WO-US00664.

XX 30-JAN-2001; 2001WO-US00665.

XX 30-JAN-2001; 2001WO-US00666.

XX 30-JAN-2001; 2001WO-US00667.

XX 30-JAN-2001; 2001WO-US00668.

XX 30-JAN-2001; 2001WO-US00670.

XX 05-FEB-2001; 2001US-266860P.

XX (ABOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

DR WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption ionization, comprises human
PT myosin-like protein hGDMLP-1 -

PS Disclosure; SEQ ID 8103; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.

XX SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 797 GCAGGACTGACTGA 810

Db 17 GCAGGACTGACGGA 4

RESULT 1646

ABN08112/c

ID ABN08112 standard; DNA; 17 BP.

XX AC ABN08112;

XX 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8104.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US16981.

XX 26-MAY-2000; 2000US-207456P.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

XX 30-JAN-2001; 2001WO-US00661.

XX 30-JAN-2001; 2001WO-US00662.

XX 30-JAN-2001; 2001WO-US00663.

PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX Disclosure; SEQ ID 8104; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 other;
 SQ Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 797 GCAGGACTGACTGA 810
 Db |||||||||
 16 GCAGGACTGACGGA 3
 RESULT 1647
 ABN08113/c
 ID ABN08113 standard; DNA; 17 BP.
 XX AC ABN08113;
 XX XX
 DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8105.
 XX XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX OS Homo sapiens.
 XX XX

PN WO200192524-A2.
 XX 06-DEC-2001.
 XX 25-MAY-2001; 2001WO-US16981.
 XX 26-MAY-2000; 2000US-207456P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 PR 30-JAN-2001; 2001WO-US00661.
 PR 30-JAN-2001; 2001WO-US00662.
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.
 PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 05-FEB-2001; 2001US-266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, or as specific biomolecule capture probes for
 PT surface-enhanced laser desorption/ionization, comprises human
 PT myosin-like protein hGDMPLP-1 -
 XX Disclosure; SEQ ID 8105; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of
 CC hGDMPLP-1 can be used in gene therapy and vaccine production. The
 CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterise
 CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification
 CC substrates, to provide initial substrates for the recombinant engineering
 CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and
 CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may
 CC be used as immunogens to raise antibodies that specifically recognise
 CC hGDMPLP-1 proteins, as standards in assays used to determine the
 CC concentration and/or amount specifically of hGDMPLP proteins, as specific
 CC biomolecule capture probes for surface-enhanced laser desorption
 CC ionisation, as therapeutic supplement in patients having specific
 CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement
 CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for
 CC diagnosing a disorder associated with the expression of hGDMPLP-1, in
 CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to
 CC chromosome 22. The present sequence represents an oligomer used in the
 CC screening of the hGDMPLP-1 sequence in the exemplification of the present
 CC invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.
 XX Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 other;
 SQ Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 797 GCAGGACTGACTGA 810
 Db |||||||||
 15 GCAGGACTGACGGA 2
 RESULT 1648
 ABN08114/c
 ID ABN08114 standard; DNA; 17 BP.

XX AC AEN08114;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8106.
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.
XX PA (ABOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPT; 2002-179446/23.
XX DR New polypeptide, for raising antibodies that recognize hGDMLP-1
XX PT proteins, or as specific biomolecule capture probes for
XX PT surface-enhanced laser desorption/ionization, comprises human
XX PT myosin-like protein hGDMLP-1 -
XX PS Disclosure; SEQ ID 8106; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
XX CC hGDMLP-1 can be used in gene therapy and vaccine production. The
XX CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
XX CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
XX CC substrates, to provide initial substrates for the recombinant engineering
XX CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
XX CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
XX CC be used as immunogens to raise antibodies that specifically recognise
XX CC hGDMLP-1 proteins, as standards in assays used to determine the
XX CC concentration and/or amount specifically of hGDMLP proteins, as specific
XX CC biomolecule capture probes for surface-enhanced laser desorption
XX CC ionisation, as therapeutic supplement in patients having specific
XX CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
XX CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
XX CC diagnosing a disorder associated with the expression of hGDMLP-1, in
XX CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
XX CC chromosome 22. The present sequence represents an oligomer used in the
XX CC screening of the hGDMLP-1 sequence in the exemplification of the present
XX CC invention.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence.
XX SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 797 GCAGGACTGACTGA 810
DB 14 GCAGGACTGACGGA 1
RESULT 1649
ABN08393/c
ID AEN08393 standard; DNA; 17 BP.
XX AC AEN08393;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8385.
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US16981.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR 30-JAN-2001; 2001WO-US00661.
XX PR 30-JAN-2001; 2001WO-US00662.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 30-JAN-2001; 2001WO-US00664.
XX PR 30-JAN-2001; 2001WO-US00665.
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 30-JAN-2001; 2001WO-US00667.
XX PR 30-JAN-2001; 2001WO-US00668.
XX PR 30-JAN-2001; 2001WO-US00669.
XX PR 30-JAN-2001; 2001WO-US00670.
XX PR 05-FEB-2001; 2001US-266860P.
XX PA (ABOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPT; 2002-179446/23.
XX DR New polypeptide, for raising antibodies that recognize hGDMLP-1
XX PT proteins, or as specific biomolecule capture probes for
XX PT surface-enhanced laser desorption/ionization, comprises human
XX PT myosin-like protein hGDMLP-1 -
XX PS Disclosure; SEQ ID 8385; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
XX CC hGDMLP-1 can be used in gene therapy and vaccine production. The
XX CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
XX CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
XX CC substrates, to provide initial substrates for the recombinant engineering
XX CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
XX CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
XX CC be used as immunogens to raise antibodies that specifically recognise
XX CC hGDMLP-1 proteins, as standards in assays used to determine the
XX CC concentration and/or amount specifically of hGDMLP proteins, as specific
XX CC biomolecule capture probes for surface-enhanced laser desorption

ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence.

Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 CACCTGCTCCAGC 414
||| |||||
Db 15 CACTCTGCTCCAGC 2

RESULT 1650
ABN08394/c
ID ABN08394 standard; DNA; 17 BP.
XX AC ABN08394;
XX AC ABN08394;
DT 29-MAY-2002 (first entry)
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8386.
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; Gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS Homo sapiens.
PN WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US16981.
XX 26-MAY-2000; 2000US-207456P.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX 30-JAN-2001; 2001WO-US00661.
XX 30-JAN-2001; 2001WO-US00662.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00666.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 05-FEB-2001; 2001US-266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
XX Disclosure; SEQ ID 8386; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 5 A; 2 C; 8 G; 2 T; 0 other;
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 CACCTGCTCCAGC 414
||| |||||
Db 14 CACTCTGCTCCAGC 1

RESULT 1651
ABN08659/c
ID ABN08659 standard; DNA; 17 BP.
XX AC ABN08659;
XX AC ABN08659;
DT 29-MAY-2002 (first entry)
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8651.
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; Gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS Homo sapiens.
PN WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US16981.
XX 26-MAY-2000; 2000US-207456P.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX 30-JAN-2001; 2001WO-US00661.
XX 30-JAN-2001; 2001WO-US00662.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00666.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 05-FEB-2001; 2001US-266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption/ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
XX Disclosure; SEQ ID 8386; 214pp; English.

XX PA (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX XX WPI; 2002-179446/23.

XX DR

XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1

XX PT proteins, or as specific biomolecule capture probes for

XX PT surface-enhanced laser desorption/ionization, comprises human

XX PT myosin-like protein hGDMPLP-1 -

XX PS Disclosure; SEQ ID 8651; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of

XX CC hGDMPLP-1 can be used in gene therapy and vaccine production. The

XX CC hGDMPLP-1 nucleic acids can be used as probes to detect, characterize

XX CC and quantify hGDMPLP-1 nucleic acids in samples, as amplification

XX CC substrates, to provide initial substrates for the recombinant engineering

XX CC of hGDMPLP-1 protein variants having desired phenotypic improvements, and

XX CC for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may

XX CC be used as immunogens to raise antibodies that specifically recognise

XX CC hGDMPLP-1 proteins, as standards in assays used to determine the

XX CC concentration and/or amount specifically of hGDMPLP proteins, as specific

XX CC biomolecule capture probes for surface-enhanced laser desorption

XX CC ionisation, as therapeutic supplement in patients having specific

XX CC deficiency in hGDMPLP-1 production, and in vaccines or for replacement

XX CC therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for

XX CC diagnosing a disorder associated with the expression of hGDMPLP-1, in

XX CC particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to

XX CC chromosome 22. The present sequence represents an oligomer used in the

XX CC screening of the hGDMPLP-1 sequence in the exemplification of the present

XX CC invention.

XX CC N.B. The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequence.

XX SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 TCCTCCAGGTCGAC 46

Db 17 TCCTCCAGGTCGAC 4

RESULT 1652

ABA93692/c

XX ID ABA93692 standard; DNA; 17 BP.

XX AC ABA93692;

XX XX

XX DT 29-APR-2002 (first entry)

XX DE GAPDH cDNA PCR primer #1.

XX XX

XX KW Neomycin resistance; viral vector; plasmid; pSub201; CMV promoter;

XX KW reversed terminal repetitive sequence; polyclonal site; pRC/CMV;

XX KW cytomegalovirus promoter; GAPDH; PCR primer; ss.

XX XX

XX OS Homo sapiens.

XX XX CN1322840-A.

XX XX

XX PD 21-NOV-2001.

XX XX

XX PF 20-JUN-2001; 2001CN-0118841.

XX XX

XX PR 20-JUN-2001; 2001CN-0118841.

XX XX

PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.

XX XX

XX PI Zhu L, Shi G, Liu Y;

XX XX

XX DR WPI; 2002-148632/20.

XX XX

XX PT Glandular associated viral vector for mediating gene transfer,

XX PT comprises a reversed terminal repetitive sequence of plasmid pSub201 -

XX XX

XX PS Example 3; Page 16; 29pp; Chinese.

XX CC The present invention describes a viral vector as a 7146 base pair

XX CC plasmid including a reversed terminal repetitive sequence of plasmid

XX CC pSub201 and a CMV promoter, polyclonal site and neomycin resistance gene

XX CC of plasmid pRC/CMV. A gene transferred by the vector of the present

XX CC invention may be expressed stably in a host cell for a long period.

XX CC The present sequence represents a PCR primer for GAPDH, which is used in

XX CC an example from the present invention.

XX SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1.1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 211 CCCAGCCCTCTCCA 224

Db 17 CCCAGCCCTCTCCA 4

RESULT 1653

ABK17554

XX ID ABK17554 standard; RNA; 17 BP.

XX AC ABK17554;

XX XX

XX DT 09-APR-2002 (first entry)

XX XX

XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 201.

XX XX

XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

XX KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

XX KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

XX KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

XX KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

XX KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;

XX KW Sturge-Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

XX KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;

XX KW amberzyme.

XX XX

XX OS Homo sapiens.

XX XX

XX PN WO200188124-A2.

XX XX

XX PD 22-NOV-2001.

XX XX

XX PF 16-MAY-2001; 2001WO-US15866.

XX XX

XX PD 16-MAY-2000; 2000US-0572021.

XX XX

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAXO) GLAXO GROUP LTD.

XX XX

XX PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;

XX XX

XX DR WPI; 2002-082995/11.

XX XX

XX PT Novel polynucleotide which down regulates expression of Rts-related

XX PT gene, useful for treating cancer, diabetic retinopathy, macular

XX PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber

XX PT syndrome -

XX PS Claim 4; Page 62; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 2 G; 5 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 445 AGCCAGATGCTTC 458
 ||||| :|||:|
 Db 3 AGCCAUAUGCCUUC 16
 RESULT 1654
 ABK17718/c
 ID ABK17718 standard; RNA; 17 BP.
 XX
 AC ABK17718;
 XX
 XX 09-APR-2002 (first entry)
 XX
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 365.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
 XX
 XX Homo sapiens.
 XX
 XX WO200189124-A2.
 XX
 XX 22-NOV-2001.
 PD
 XX 16-MAY-2001; 2001WO-US15866.
 XX
 XX 16-MAY-2000; 2000US-0572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;

DR WPI; 2002-082995/11.
 XX
 PT Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX
 XX Claim 4; Page 65; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention.
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 882 GAGGTCCTGCATGT 895
 ||||| |||||
 Db 17 GAGTCTCTGAATGT 4
 RESULT 1655
 ABK17723/c
 ID ABK17723 standard; RNA; 17 BP.
 XX
 AC ABK17723;
 XX
 XX 09-APR-2002 (first entry)
 XX
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 370.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
 XX
 XX Homo sapiens.
 XX
 XX WO200189124-A2.
 XX
 XX 22-NOV-2001.
 PD
 XX 16-MAY-2001; 2001WO-US15866.

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XX PR 16-MAY-2000; 2000US-0572021.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
XX DR WPI; 2002-082995/11.
XX PT Novel polynucleotide which down regulates expression of Ets-related
XX PT gene, useful for treating cancer, diabetic retinopathy, macular
XX PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
XX PT syndrome
XX PS Claim 4; Page 65; 149pp; English.
XX CC The invention relates to a nucleic acid molecule (I) which down regulates
XX CC expression of an Ets-related gene (ERG). (I) is useful for treating
XX CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
XX CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
XX CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
XX CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
XX CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
XX CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
XX CC treating a patient having a condition associated with the level of ERG
XX CC by contacting cells of the patient with (I) under conditions suitable for
XX CC the treatment. The method comprises the use of one or more therapies
XX CC under conditions suitable for the treatment. Leukaemia or tumour
XX CC angiogenesis is treated by administering (I) to the patient in
XX CC conjunction with one or more of other therapies such as radiation or
XX CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
XX CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
XX CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
XX CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
XX CC diseases related to the expression of ERG, and as diagnostic tool to
XX CC examine genetic drift and mutations within diseased cells or to detect
XX CC the presence of ERG RNA in a cell. (I) is useful for specifically
XX CC targeting genes that share homology with ERG gene or ERG fusion genes.
XX CC ABK17354-ABK22719 represent nucleic acids, including antisense and
XX CC enzymatic nucleic acid molecules which regulate expression of ERG, and
XX CC related PCR primers of the invention.
XX SQ Sequence 17 BP; 0 A; 4 C; 6 G; 7 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 843 AGAACACAGCCCC 856
Db 15 AGAACAAAGCCCC 2

RESULT 1656
ABK17724/c
ID ABK17724 standard; RNA; 17 BP.
XX AC ABK17724;
XX DT 09-APR-2002 (first entry)
XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 371.
XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
XX KW ophthalmological; antiarthritic; aniposiotic; virucide; osteopathic;
XX KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
XX KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
XX KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
XX KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
XX KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
XX KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
XX KW anberzyme.

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XX OS Homo sapiens.
XX PN WO200188124-A2.
XX PD 22-NOV-2001.
XX PF 16-MAY-2001; 2001WO-US15866.
XX PR 16-MAY-2000; 2000US-0572021.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
XX DR WPI; 2002-082995/11.
XX PT Novel polynucleotide which down regulates expression of Ets-related
XX PT gene, useful for treating cancer, diabetic retinopathy, macular
XX PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
XX PT syndrome
XX PS Claim 4; Page 65; 149pp; English.
XX CC The invention relates to a nucleic acid molecule (I) which down regulates
XX CC expression of an Ets-related gene (ERG). (I) is useful for treating
XX CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
XX CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
XX CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
XX CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
XX CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
XX CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
XX CC treating a patient having a condition associated with the level of ERG
XX CC by contacting cells of the patient with (I) under conditions suitable for
XX CC the treatment. The method comprises the use of one or more therapies
XX CC under conditions suitable for the treatment. Leukaemia or tumour
XX CC angiogenesis is treated by administering (I) to the patient in
XX CC conjunction with one or more of other therapies such as radiation or
XX CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
XX CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
XX CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
XX CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
XX CC diseases related to the expression of ERG, and as diagnostic tool to
XX CC examine genetic drift and mutations within diseased cells or to detect
XX CC the presence of ERG RNA in a cell. (I) is useful for specifically
XX CC targeting genes that share homology with ERG gene or ERG fusion genes.
XX CC ABK17354-ABK22719 represent nucleic acids, including antisense and
XX CC enzymatic nucleic acid molecules which regulate expression of ERG, and
XX CC related PCR primers of the invention.
XX SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 843 AGAACACAGCCCC 856
Db 14 AGAACAAAGCCCC 1

RESULT 1657
ABK18431/c
ID ABK18431 standard; RNA; 17 BP.
XX AC ABK18431;
XX DT 09-APR-2002 (first entry)
XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 1078.
XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

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QV 445 AGCCAGATGCTTC 458
 ||||| :|||:|:|
 Db 1 AGCCAAUGCCUUC 14

RESULT 1659
 ABK19084/c
 ID ABK19084 standard; RNA; 17 BP.
 XX
 AC ABK19084;
 XX
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human ERG DNazyme target sequence Seq ID No 1731.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200188124-A2.
 XX
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US15866.
 XX
 XX
 PR 16-MAY-2000; 2000US-0572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX
 PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 XX
 DR WPI; 2002-082995/11.
 XX
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX
 PS Claim 4; Page 108; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC by contacting cells of the patient having a condition associated with the level of ERG,
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention.
 XX
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 U; 0 other;
 Query Match 1.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QV 881 TGAGGTCTTCATG 894
 ||||| :|||:|:|
 Db 14 TGAGGTCTTCATG 1

RESULT 1660
 ABK19427
 ID ABK19427 standard; RNA; 17 BP.
 XX
 AC ABK19427;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human ERG DNazyme target sequence Seq ID No 2074.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200188124-A2.
 XX
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US15866.
 XX
 XX
 PR 16-MAY-2000; 2000US-0572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX
 PI Jarvis T, Von Carlowitz I, McSwiggen JA, McLaughlin F, Randi AM;
 XX
 DR WPI; 2002-082995/11.
 XX
 XX Novel polynucleotide which down regulates expression of Ets-related
 PT gene, useful for treating cancer, diabetic retinopathy, macular
 PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
 PT syndrome -
 XX
 PS Claim 4; Page 128; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC by contacting cells of the patient having a condition associated with the level of ERG,
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg²⁺. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. AK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention.

Sequence 17 BP; 7 A; 0 C; 8 G; 2 U; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1007 GGAGATGGGAAGT 1020
||||| |||||
Db 1 GGAGAGGGGAGU 14

RESULT 1661
ABK26199
ID ABK26199 standard; DNA; 17 BP.
XX
AC ABK26199;
XX
DT 09-APR-2002 (first entry)
XX
DE Increased starch production genome altering oligonucleotide #51.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Cicer arietinum.
OS Synthetic.
XX
XX WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
XX 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
XX (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production
XX
XX Claim 7; Page 137; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with

CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.

Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1067 GAGTAAAGCAACT 1080
||||| |||||
Db 3 GAGTAAAGGAACT 16

RESULT 1662
ABK26200/c
ID ABK26200 standard; DNA; 17 BP.
XX
AC ABK26200;
XX
DT 09-APR-2002 (first entry)
XX
DE Increased starch production genome altering oligonucleotide #52.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Cicer arietinum.
OS Synthetic.
XX
XX WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
XX 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
XX (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX

PT New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production

XX Claim 7; Page 137; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.

XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1067 GAGGTAAAGCAACT 1080
DB 15 GAGGTAAAGCAACT 2
|||||

RESULT 1663
ABT34415
ID ABT34415 standard; DNA; 17 BP.

XX ABT34415;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 52.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB04208.

XX 17-SEP-2001; 2001FR-0011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases

PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells
XX Disclosure; Page 40; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 8 A; 2 C; 4 G; 2 T; 1 other;

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.1e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 110 GGTCAAGAAAGGGGAA 125
DB 1 GATCAAGAAACTGGAW 16
|||||

RESULT 1664
ABT35404/c
ID ABT35404 standard; DNA; 17 BP.

XX ABT35404;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 1041.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB04208.

XX 17-SEP-2001; 2001FR-0011978.

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XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

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PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells